



# ***STIC Search Report***

## ***Biotech-Chem Library***

**STIC Database Tracking Number: 131140**

**TO: James Schultz**  
**Location: REM/2D18/2C18**  
**Art Unit: 1635**  
**Monday, August 30, 2004**

**Case Serial Number: 09/925139**

**From: David Schreiber**  
**Location: Biotech-Chem Library**  
**Remsen E01A61**  
**Phone: 272-2526**

**david.schreiber@uspto.gov**

### **Search Notes**





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 09:17:56 ; Search time 1 Seconds  
(without alignments)  
3.307 Million cell updates/sec

Title: US-09-925-139-3

Perfect score: 139

Sequence: 1 ggatggggctgttagcagaa.....ctatcctaagggccactgg 139

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 0.5

Searched: 718 seqs, 11895 residues

Total number of hits satisfying chosen parameters: 1436

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 739 summaries

Database : rge3.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	15.1	21	1	B2102270
C 2	17.2	12.4	22	1	ACCESSTION: E25734
C 3	16.8	12.1	21	1	ACCESSTION: BD101979
C 4	16.8	12.1	21	1	ACCESSTION: BD101979
C 5	16.4	11.8	20	1	ACCESSTION: BD131270
C 6	16.2	11.7	22	1	ACCESSTION: AR381288
C 7	15.2	10.9	20	1	ACCESSTION: AR129513
C 8	15.2	10.9	20	1	ACCESSTION: AX323427
C 9	14.4	10.4	20	1	ACCESSTION: AR142933
C 10	14.4	10.4	20	1	ACCESSTION: AX293741
C 11	14.4	10.4	20	1	ACCESSTION: AX488425
C 12	14.2	10.2	20	1	ACCESSTION: BD171443
C 13	14.2	10.2	20	1	ACCESSTION: AR011791
C 14	14.2	10.2	20	1	ACCESSTION: AR025499
C 15	14.2	10.2	20	1	ACCESSTION: E08471
C 16	14.2	10.2	20	1	ACCESSTION: E26707
C 17	14.2	10.2	20	1	ACCESSTION: AR211960
C 18	14.2	10.2	20	1	ACCESSTION: AR281496
C 19	14.2	10.2	20	1	ACCESSTION: BD185884
C 20	14	10.1	20	1	ACCESSTION: AX777492
C 21	13.8	9.9	18	1	ACCESSTION: A06347
C 22	13.8	9.9	20	1	ACCESSTION: BD074024
C 23	13.8	9.9	20	1	ACCESSTION: AR241103
C 24	13.8	9.9	20	1	ACCESSTION: AR281777
C 25	13.8	9.9	20	1	ACCESSTION: AX250715
C 26	13.8	9.9	20	1	ACCESSTION: AX253315
C 27	13.8	9.9	20	1	ACCESSTION: AX283518
C 28	13.8	9.9	20	1	ACCESSTION: BD006136
C 29	13.6	9.8	20	1	ACCESSTION: BD179019
C 30	13.6	9.8	20	1	ACCESSTION: A98445
C 31	13.6	9.8	20	1	ACCESSTION: AR050289
C 32	13.6	9.8	20	1	ACCESSTION: AR100579
C 33	13.6	9.8	20	1	ACCESSTION: AR100585
C 34	13.6	9.8	20	1	ACCESSTION: AR158965
C 35	13.6	9.8	20	1	ACCESSTION: AR158965
C 36	13.6	9.8	20	1	ACCESSTION: AR158965
C 37	13.6	9.8	20	1	ACCESSTION: AR158965
C 38	13.6	9.8	20	1	ACCESSTION: AR158965
C 39	13.6	9.8	20	1	ACCESSTION: AR158965
C 40	13.6	9.8	20	1	ACCESSTION: AR158965
C 41	13.6	9.8	20	1	ACCESSTION: AR158965
C 42	13.6	9.8	20	1	ACCESSTION: AR158965
C 43	13.4	9.6	18	1	ACCESSTION: AX352825
C 44	13.4	9.6	18	1	ACCESSTION: AX362670
C 45	13.4	9.6	18	1	ACCESSTION: AB069639
C 46	13.4	9.6	19	1	ACCESSTION: AX129291
C 47	13.4	9.6	19	1	ACCESSTION: BD088226
C 48	13.4	9.6	19	1	ACCESSTION: BD088234
C 49	13.4	9.6	19	1	ACCESSTION: AB069135
C 50	13.4	9.6	19	1	ACCESSTION: AB069137
C 51	13.4	9.6	20	1	ACCESSTION: AR163797
C 52	13.4	9.6	20	1	ACCESSTION: AR233647
C 53	13.2	9.5	18	1	ACCESSTION: A63088
C 54	13.2	9.5	18	1	ACCESSTION: AR018185
C 55	13.2	9.5	18	1	ACCESSTION: AR106914
C 56	13.2	9.5	18	1	ACCESSTION: AR173918
C 57	13.2	9.5	18	1	ACCESSTION: AR268665
C 58	13.2	9.5	18	1	ACCESSTION: BD089837
C 59	13.2	9.5	18	1	ACCESSTION: AB068204
C 60	13.2	9.5	19	1	ACCESSTION: AR011803
C 61	13.2	9.5	19	1	ACCESSTION: AR361501
C 62	13.2	9.5	20	1	ACCESSTION: A70767
C 63	13.2	9.5	20	1	ACCESSTION: A79251
C 64	13.2	9.5	20	1	ACCESSTION: AR163916
C 65	13.2	9.5	20	1	ACCESSTION: E08376
C 66	13.2	9.5	20	1	ACCESSTION: AR220154
C 67	13.2	9.5	20	1	ACCESSTION: AR315612
C 68	13.2	9.5	20	1	ACCESSTION: AX180379
C 69	13.2	9.5	20	1	ACCESSTION: AX268920
C 70	13.2	9.5	20	1	ACCESSTION: AX287952
C 71	13.2	9.5	20	1	ACCESSTION: BD003481
C 72	13.2	9.5	20	1	ACCESSTION: BD011678
C 73	13.2	9.5	20	1	ACCESSTION: BD011679
C 74	13.2	9.5	20	1	ACCESSTION: BD011680
C 75	12.8	9.2	16	1	ACCESSTION: AX710950
C 76	12.8	9.2	16	1	ACCESSTION: BD001091
C 77	12.8	9.2	16	1	ACCESSTION: BD001520
C 78	12.8	9.2	17	1	ACCESSTION: AR011799
C 79	12.8	9.2	17	1	ACCESSTION: AR192421
C 80	12.8	9.2	17	1	ACCESSTION: AR326290
C 81	12.8	9.2	17	1	ACCESSTION: AX421994
C 82	12.8	9.2	17	1	ACCESSTION: AX422971
C 83	12.8	9.2	17	1	ACCESSTION: AX673768
C 84	12.8	9.2	17	1	ACCESSTION: AX724290
C 85	12.8	9.2	17	1	ACCESSTION: AX753715
C 86	12.8	9.2	17	1	ACCESSTION: AX753716
C 87	12.8	9.2	17	1	ACCESSTION: AX805118
C 88	12.8	9.2	17	1	ACCESSTION: BD104946
C 89	12.8	9.2	18	1	ACCESSTION: AR011802
C 90	12.8	9.2	18	1	ACCESSTION: AR051200
C 91	12.8	9.2	18	1	ACCESSTION: AR106948
C 92	12.8	9.2	18	1	ACCESSTION: AR106981
C 93	12.8	9.2	19	1	ACCESSTION: AX129110
C 94	12.8	9.2	19	1	ACCESSTION: L77467
C 95	12.6	9.1	19	1	ACCESSTION: AR053162
C 96	12.6	9.1	19	1	ACCESSTION: E08539
C 97	12.6	9.1	19	1	ACCESSTION: E11147
C 98	12.6	9.1	19	1	ACCESSTION: AR296543
C 99	12.6	9.1	19	1	ACCESSTION: AX130657
C 100	12.6	9.1	19	1	ACCESSTION: AX131856
C 101	12.4	8.9	15	1	ACCESSTION: A28990
C 102	12.4	8.9	15	1	ACCESSTION: AR030911
C 103	12.4	8.9	15	1	ACCESSTION: I28303
C 104	12.4	8.9	16	1	ACCESSTION: AR127505
C 105	12.4	8.9	16	1	ACCESSTION: I50742
C 106	12.4	8.9	16	1	ACCESSTION: AR328506

ACCESSTION: E26692  
ACCESSTION: I31522  
ACCESSTION: AR298667  
ACCESSTION: AR316120  
ACCESSTION: AR316177  
ACCESSTION: AR370267  
ACCESSTION: AX115823  
ACCESSTION: BD144090  
ACCESSTION: AX723714  
ACCESSTION: AX352825  
ACCESSTION: AX362670  
ACCESSTION: AB069639  
ACCESSTION: AX129291  
ACCESSTION: BD088226  
ACCESSTION: BD088234  
ACCESSTION: AB069135  
ACCESSTION: AB069137  
ACCESSTION: AR163797  
ACCESSTION: AR233647  
ACCESSTION: A63088  
ACCESSTION: AR018185  
ACCESSTION: AR106914  
ACCESSTION: AR173918  
ACCESSTION: AR268665  
ACCESSTION: BD089837  
ACCESSTION: AB068204  
ACCESSTION: AR011803  
ACCESSTION: AR361501  
ACCESSTION: A70767  
ACCESSTION: A79251  
ACCESSTION: AR163916  
ACCESSTION: E08376  
ACCESSTION: AR220154  
ACCESSTION: AR315612  
ACCESSTION: AX180379  
ACCESSTION: AX268920  
ACCESSTION: AX287952  
ACCESSTION: BD003481  
ACCESSTION: BD011678  
ACCESSTION: BD011679  
ACCESSTION: BD011680  
ACCESSTION: AX710950  
ACCESSTION: BD001091  
ACCESSTION: BD001520  
ACCESSTION: AR011799  
ACCESSTION: AR192421  
ACCESSTION: AR326290  
ACCESSTION: AX421994  
ACCESSTION: AX422971  
ACCESSTION: AX673768  
ACCESSTION: AX724290  
ACCESSTION: AX753715  
ACCESSTION: AX753716  
ACCESSTION: AX805118  
ACCESSTION: BD104946  
ACCESSTION: AR011802  
ACCESSTION: AR051200  
ACCESSTION: AR106948  
ACCESSTION: AR106981  
ACCESSTION: AX129110  
ACCESSTION: L77467  
ACCESSTION: AR053162  
ACCESSTION: E08539  
ACCESSTION: E11147  
ACCESSTION: AR296543  
ACCESSTION: AX130657  
ACCESSTION: AX131856  
ACCESSTION: A28990  
ACCESSTION: AR030911  
ACCESSTION: I28303  
ACCESSTION: AR127505  
ACCESSTION: I50742  
ACCESSTION: AR328506

107	12.4	8.9	16	1	AX039862	ACCESSION:AX039862	180	12	8.6	17	1	AX723858	ACCESSION:AX723858
C 108	12.4	8.9	16	1	AX135793	ACCESSION:AX135793	181	12	8.6	18	1	AR169593	ACCESSION:AR169593
C 109	12.4	8.9	17	1	BD255127	ACCESSION:BD255127	C 182	12	8.6	18	1	BD235157	ACCESSION:BD235157
C 110	12.4	8.9	17	1	BD255128	ACCESSION:BD255128	C 183	12	8.6	18	1	BD235175	ACCESSION:BD235175
C 111	12.4	8.9	17	1	AR327591	ACCESSION:AR327591	C 184	12	8.6	18	1	BD235176	ACCESSION:BD235176
C 112	12.4	8.9	17	1	AX266079	ACCESSION:AX266079	C 185	12	8.6	18	1	E33346	ACCESSION:E33346
C 113	12.4	8.9	17	1	AX266080	ACCESSION:AX266080	186	12	8.6	18	1	AX599639	ACCESSION:AX599639
C 114	12.4	8.9	17	1	AX727607	ACCESSION:AX727607	187	11.8	8.5	15	1	A64217	ACCESSION:A64217
C 115	12.4	8.9	17	1	AX753717	ACCESSION:AX753717	C 188	11.8	8.5	15	1	AR011805	ACCESSION:AR011805
C 116	12.4	8.9	17	1	AX753718	ACCESSION:AX753718	C 189	11.8	8.5	15	1	AR102516	ACCESSION:AR102516
C 117	12.4	8.9	17	1	AX757161	ACCESSION:AX757161	C 190	11.8	8.5	15	1	I27821	ACCESSION:I27821
C 118	12.4	8.9	18	1	AR018181	ACCESSION:AR018181	C 191	11.8	8.5	15	1	I36660	ACCESSION:I36660
C 119	12.4	8.9	18	1	AR018183	ACCESSION:AR018183	C 192	11.8	8.5	15	1	I83457	ACCESSION:I83457
C 120	12.4	8.9	18	1	AR018184	ACCESSION:AR018184	C 193	11.8	8.5	15	1	I83461	ACCESSION:I83461
C 121	12.4	8.9	18	1	AR187552	ACCESSION:AR187552	C 194	11.8	8.5	15	1	AR213614	ACCESSION:AR213614
C 122	12.4	8.9	18	1	AR299488	ACCESSION:AR299488	C 195	11.8	8.5	15	1	AR262819	ACCESSION:AR262819
C 123	12.4	8.9	18	1	AR324066	ACCESSION:AR324066	C 196	11.8	8.5	15	1	BD057672	ACCESSION:BD057672
C 124	12.4	8.9	18	1	AR362645	ACCESSION:AR362645	C 197	11.8	8.5	15	1	BD081502	ACCESSION:BD081502
C 125	12.4	8.9	18	1	AR365708	ACCESSION:AR365708	C 198	11.8	8.5	15	1	BD090530	ACCESSION:BD090530
C 126	12.4	8.9	18	1	AX786023	ACCESSION:AX786023	C 199	11.8	8.5	15	1	BD090534	ACCESSION:BD090534
C 127	12.4	8.9	18	1	BD206162	ACCESSION:BD206162	C 200	11.8	8.5	16	1	AR011801	ACCESSION:AR011801
C 128	12.4	8.9	19	1	AR074596	ACCESSION:AR074596	C 201	11.8	8.5	16	1	BD233058	ACCESSION:BD233058
C 129	12.4	8.9	19	1	AR083935	ACCESSION:AR083935	C 202	11.8	8.5	16	1	ACCESSION:AX007612	ACCESSION:AX007612
C 130	12.4	8.9	19	1	I23815	ACCESSION:I23815	C 203	11.8	8.5	16	1	BD234600	ACCESSION:BD234600
C 131	12.4	8.9	19	1	I29969	ACCESSION:I29969	C 204	11.8	8.5	17	1	BD254104	ACCESSION:BD254104
C 132	12.4	8.9	19	1	AR299173	ACCESSION:AR299173	C 205	11.8	8.5	17	1	AR186388	ACCESSION:AR186388
C 133	12.4	8.9	19	1	AX033909	ACCESSION:AX033909	C 206	11.8	8.5	17	1	AR186389	ACCESSION:AR186389
C 134	12.2	8.8	17	1	AR046916	ACCESSION:AR046916	C 207	11.8	8.5	17	1	AR230196	ACCESSION:AR230196
C 135	12.2	8.8	17	1	BD254187	ACCESSION:BD254187	C 208	11.8	8.5	17	1	AR286032	ACCESSION:AR286032
C 136	12.2	8.8	17	1	I53968	ACCESSION:I53968	C 209	11.8	8.5	17	1	AR286132	ACCESSION:AR286132
C 137	12.2	8.8	17	1	AR365741	ACCESSION:AR365741	C 210	11.8	8.5	17	1	AR286133	ACCESSION:AR286133
C 138	12.2	8.8	17	1	AX215134	ACCESSION:AX215134	C 211	11.8	8.5	17	1	AR286141	ACCESSION:AR286141
C 139	12.2	8.8	17	1	AX499445	ACCESSION:AX499445	C 212	11.8	8.5	17	1	AR286177	ACCESSION:AR286177
C 140	12.2	8.8	17	1	AX532097	ACCESSION:AX532097	C 213	11.8	8.5	17	1	AR323019	ACCESSION:AR323019
C 141	12.2	8.8	17	1	AX532099	ACCESSION:AX532099	C 214	11.8	8.5	17	1	AR323020	ACCESSION:AR323020
C 142	12.2	8.8	17	1	AX532103	ACCESSION:AX532103	C 215	11.8	8.5	17	1	AR398022	ACCESSION:AR398022
C 143	12.2	8.8	17	1	AX532253	ACCESSION:AX532253	C 216	11.8	8.5	17	1	AR398122	ACCESSION:AR398122
C 144	12.2	8.8	17	1	AX532254	ACCESSION:AX532254	C 217	11.8	8.5	17	1	AR398123	ACCESSION:AR398123
C 145	12.2	8.8	17	1	AX687667	ACCESSION:AX687667	C 218	11.8	8.5	17	1	AR398131	ACCESSION:AR398131
C 146	12.2	8.8	17	1	AX687850	ACCESSION:AX687850	C 219	11.8	8.5	17	1	AR398167	ACCESSION:AR398167
C 147	12.2	8.8	17	1	AX726673	ACCESSION:AX726673	C 220	11.8	8.5	17	1	AR401998	ACCESSION:AR401998
C 148	12.2	8.8	17	1	AX728392	ACCESSION:AX728392	C 221	11.8	8.5	17	1	AX039622	ACCESSION:AX039622
C 149	12.2	8.8	17	1	AX734168	ACCESSION:AX734168	C 222	11.8	8.5	17	1	AX039652	ACCESSION:AX039652
C 150	12.2	8.8	17	1	AX762563	ACCESSION:AX762563	C 223	11.8	8.5	17	1	AX263012	ACCESSION:AX263012
C 151	12.2	8.8	18	1	AR106981	ACCESSION:AR106981	C 224	11.8	8.5	17	1	AX263013	ACCESSION:AX263013
C 152	12.2	8.8	18	1	A56874	ACCESSION:A56874	C 225	11.8	8.5	17	1	AX263016	ACCESSION:AX263016
C 153	12.2	8.8	18	1	A56885	ACCESSION:A56885	C 226	11.8	8.5	17	1	AX263017	ACCESSION:AX263017
C 154	12.2	8.8	18	1	AR092022	ACCESSION:AR092022	C 227	11.8	8.5	17	1	AX266567	ACCESSION:AX266567
C 155	12.2	8.8	18	1	AR112157	ACCESSION:AR112157	C 228	11.8	8.5	17	1	AX266568	ACCESSION:AX266568
C 156	12.2	8.8	18	1	AR118335	ACCESSION:AR118335	C 229	11.8	8.5	17	1	AX422716	ACCESSION:AX422716
C 157	12.2	8.8	18	1	AR118346	ACCESSION:AR118346	C 230	11.8	8.5	17	1	AX498904	ACCESSION:AX498904
C 158	12.2	8.8	18	1	AR137364	ACCESSION:AR137364	C 231	11.8	8.5	17	1	AX498905	ACCESSION:AX498905
C 159	12.2	8.8	18	1	AR149199	ACCESSION:AR149199	C 232	11.8	8.5	17	1	AX498906	ACCESSION:AX498906
C 160	12.2	8.8	18	1	AR160845	ACCESSION:AR160845	C 233	11.8	8.5	17	1	AX499446	ACCESSION:AX499446
C 161	12.2	8.8	18	1	BD231347	ACCESSION:BD231347	C 234	11.8	8.5	17	1	AX499447	ACCESSION:AX499447
C 162	12.2	8.8	18	1	E10022	ACCESSION:E10022	C 235	11.8	8.5	17	1	AX532098	ACCESSION:AX532098
C 163	12.2	8.8	18	1	I14568	ACCESSION:I14568	C 236	11.8	8.5	17	1	AX532251	ACCESSION:AX532251
C 164	12.2	8.8	18	1	I88615	ACCESSION:I88615	C 237	11.8	8.5	17	1	AX532252	ACCESSION:AX532252
C 165	12.2	8.8	18	1	AR350406	ACCESSION:AR350406	C 238	11.8	8.5	17	1	AX672921	ACCESSION:AX672921
C 166	12.2	8.8	18	1	AR409159	ACCESSION:AR409159	C 239	11.8	8.5	17	1	AX687558	ACCESSION:AX687558
C 167	12.2	8.8	18	1	AR037486	ACCESSION:AR037486	C 240	11.8	8.5	17	1	AX687559	ACCESSION:AX687559
C 168	12.2	8.8	18	1	AX244626	ACCESSION:AX244626	C 241	11.8	8.5	17	1	AX687560	ACCESSION:AX687560
C 169	12.2	8.8	18	1	AX795173	ACCESSION:AX795173	C 242	11.8	8.5	17	1	AX687848	ACCESSION:AX687848
C 170	12.2	8.8	18	1	BD075238	ACCESSION:BD075238	C 243	11.8	8.5	17	1	AX687849	ACCESSION:AX687849
C 171	12.2	8.8	21	1	BD102270	ACCESSION:BD102270	C 244	11.8	8.5	17	1	AX723249	ACCESSION:AX723249
C 172	12	8.6	16	1	BD264860	ACCESSION:BD264860	C 245	11.8	8.5	17	1	AX723448	ACCESSION:AX723448
C 173	12	8.6	17	1	BD254997	ACCESSION:BD254997	C 246	11.8	8.5	17	1	AX725456	ACCESSION:AX725456
C 174	12	8.6	17	1	AX531436	ACCESSION:AX531436	C 247	11.8	8.5	17	1	AX727005	ACCESSION:AX727005
C 175	12	8.6	17	1	AX531437	ACCESSION:AX531437	C 248	11.8	8.5	17	1	AX730367	ACCESSION:AX730367
C 176	12	8.6	17	1	AX531438	ACCESSION:AX531438	C 249	11.8	8.5	17	1	AX732114	ACCESSION:AX732114
C 177	12	8.6	17	1	AX531439	ACCESSION:AX531439	C 250	11.8	8.5	17	1	AX734174	ACCESSION:AX734174
C 178	12	8.6	17	1	AX531440	ACCESSION:AX531440	C 251	11.8	8.5	17	1	AX734182	ACCESSION:AX734182
C 179	12	8.6	17	1	AX531441	ACCESSION:AX531441	C 252	11.8	8.5	17	1	AX736515	ACCESSION:AX736515

[illegible]

C 399	11.2	8.1	17	1	E07498	ACCESSION: E07498	472	11.2	8.1	17	1	AX532451	ACCESSION: AX532451
C 400	11.2	8.1	17	1	E24413	ACCESSION: E24413	473	11.2	8.1	17	1	AX532452	ACCESSION: AX532452
C 401	11.2	8.1	17	1	E27450	ACCESSION: E27450	474	11.2	8.1	17	1	AX532453	ACCESSION: AX532453
C 402	11.2	8.1	17	1	E39008	ACCESSION: E39008	475	11.2	8.1	17	1	AX578661	ACCESSION: AX578661
C 403	11.2	8.1	17	1	E64351	ACCESSION: E64351	476	11.2	8.1	17	1	AX579336	ACCESSION: AX579336
C 404	11.2	8.1	17	1	E50743	ACCESSION: E50743	477	11.2	8.1	17	1	AX615330	ACCESSION: AX615330
C 405	11.2	8.1	17	1	E53622	ACCESSION: E53622	C 477	11.2	8.1	17	1	AX615331	ACCESSION: AX615331
C 406	11.2	8.1	17	1	AR185989	ACCESSION: AR185989	C 478	11.2	8.1	17	1	AX615842	ACCESSION: AX615842
C 407	11.2	8.1	17	1	AR186749	ACCESSION: AR186749	C 479	11.2	8.1	17	1	AX615843	ACCESSION: AX615843
C 408	11.2	8.1	17	1	AR190210	ACCESSION: AR190210	C 480	11.2	8.1	17	1	AX615844	ACCESSION: AX615844
C 409	11.2	8.1	17	1	AR190567	ACCESSION: AR190567	C 481	11.2	8.1	17	1	AX634562	ACCESSION: AX634562
C 410	11.2	8.1	17	1	AR190568	ACCESSION: AR190568	C 482	11.2	8.1	17	1	AX634795	ACCESSION: AX634795
C 411	11.2	8.1	17	1	AR190586	ACCESSION: AR190586	C 483	11.2	8.1	17	1	AX648876	ACCESSION: AX648876
C 412	11.2	8.1	17	1	AR196222	ACCESSION: AR196222	C 484	11.2	8.1	17	1	AX648877	ACCESSION: AX648877
C 413	11.2	8.1	17	1	AR208224	ACCESSION: AR208224	C 485	11.2	8.1	17	1	AX649489	ACCESSION: AX649489
C 414	11.2	8.1	17	1	AR262374	ACCESSION: AR262374	C 486	11.2	8.1	17	1	AX649490	ACCESSION: AX649490
C 415	11.2	8.1	17	1	AR286208	ACCESSION: AR286208	C 487	11.2	8.1	17	1	AX671672	ACCESSION: AX671672
C 416	11.2	8.1	17	1	AR326208	ACCESSION: AR326208	C 488	11.2	8.1	17	1	AX671735	ACCESSION: AX671735
C 417	11.2	8.1	17	1	AR326220	ACCESSION: AR326220	C 489	11.2	8.1	17	1	AX672964	ACCESSION: AX672964
C 418	11.2	8.1	17	1	AR323380	ACCESSION: AR323380	C 490	11.2	8.1	17	1	AX672965	ACCESSION: AX672965
C 419	11.2	8.1	17	1	AR325180	ACCESSION: AR325180	C 491	11.2	8.1	17	1	AX672967	ACCESSION: AX672967
C 420	11.2	8.1	17	1	AR325490	ACCESSION: AR325490	C 492	11.2	8.1	17	1	AX684195	ACCESSION: AX684195
C 421	11.2	8.1	17	1	AR325491	ACCESSION: AR325491	C 493	11.2	8.1	17	1	AX687045	ACCESSION: AX687045
C 422	11.2	8.1	17	1	AR325509	ACCESSION: AR325509	C 494	11.2	8.1	17	1	AX687046	ACCESSION: AX687046
C 423	11.2	8.1	17	1	AR326802	ACCESSION: AR326802	C 495	11.2	8.1	17	1	AX687666	ACCESSION: AX687666
C 424	11.2	8.1	17	1	AR326803	ACCESSION: AR326803	C 496	11.2	8.1	17	1	AX687742	ACCESSION: AX687742
C 425	11.2	8.1	17	1	AR327651	ACCESSION: AR327651	C 497	11.2	8.1	17	1	AX687743	ACCESSION: AX687743
C 426	11.2	8.1	17	1	AR327765	ACCESSION: AR327765	C 498	11.2	8.1	17	1	AX687812	ACCESSION: AX687812
C 427	11.2	8.1	17	1	AR398198	ACCESSION: AR398198	C 499	11.2	8.1	17	1	AX687813	ACCESSION: AX687813
C 428	11.2	8.1	17	1	AR401960	ACCESSION: AR401960	C 500	11.2	8.1	17	1	AX687851	ACCESSION: AX687851
C 429	11.2	8.1	17	1	AR402031	ACCESSION: AR402031	C 501	11.2	8.1	17	1	AX691734	ACCESSION: AX691734
C 430	11.2	8.1	17	1	AR429221	ACCESSION: AR429221	C 502	11.2	8.1	17	1	AX691735	ACCESSION: AX691735
C 431	11.2	8.1	17	1	AR432062	ACCESSION: AR432062	C 503	11.2	8.1	17	1	AX692741	ACCESSION: AX692741
C 432	11.2	8.1	17	1	AR432063	ACCESSION: AR432063	C 504	11.2	8.1	17	1	AX692742	ACCESSION: AX692742
C 433	11.2	8.1	17	1	AX002552	ACCESSION: AX002552	C 505	11.2	8.1	17	1	AX723798	ACCESSION: AX723798
C 434	11.2	8.1	17	1	AX002607	ACCESSION: AX002607	C 506	11.2	8.1	17	1	AX724082	ACCESSION: AX724082
C 435	11.2	8.1	17	1	AX006344	ACCESSION: AX006344	C 507	11.2	8.1	17	1	AX724176	ACCESSION: AX724176
C 436	11.2	8.1	17	1	AX015204	ACCESSION: AX015204	C 508	11.2	8.1	17	1	AX725274	ACCESSION: AX725274
C 437	11.2	8.1	17	1	AX022637	ACCESSION: AX022637	C 509	11.2	8.1	17	1	AX725621	ACCESSION: AX725621
C 438	11.2	8.1	17	1	AX215133	ACCESSION: AX215133	C 510	11.2	8.1	17	1	AX726666	ACCESSION: AX726666
C 439	11.2	8.1	17	1	AX216004	ACCESSION: AX216004	C 511	11.2	8.1	17	1	AX727148	ACCESSION: AX727148
C 440	11.2	8.1	17	1	AX217394	ACCESSION: AX217394	C 512	11.2	8.1	17	1	AX727322	ACCESSION: AX727322
C 441	11.2	8.1	17	1	AX217395	ACCESSION: AX217395	C 513	11.2	8.1	17	1	AX728529	ACCESSION: AX728529
C 442	11.2	8.1	17	1	AX217770	ACCESSION: AX217770	C 514	11.2	8.1	17	1	AX731553	ACCESSION: AX731553
C 443	11.2	8.1	17	1	AX217771	ACCESSION: AX217771	C 515	11.2	8.1	17	1	AX731661	ACCESSION: AX731661
C 444	11.2	8.1	17	1	AX264312	ACCESSION: AX264312	C 516	11.2	8.1	17	1	AX731671	ACCESSION: AX731671
C 445	11.2	8.1	17	1	AX264313	ACCESSION: AX264313	C 517	11.2	8.1	17	1	AX732733	ACCESSION: AX732733
C 446	11.2	8.1	17	1	AX272550	ACCESSION: AX272550	C 518	11.2	8.1	17	1	AX732734	ACCESSION: AX732734
C 447	11.2	8.1	17	1	AX272551	ACCESSION: AX272551	C 519	11.2	8.1	17	1	AX734016	ACCESSION: AX734016
C 448	11.2	8.1	17	1	AX272840	ACCESSION: AX272840	C 520	11.2	8.1	17	1	AX734043	ACCESSION: AX734043
C 449	11.2	8.1	17	1	AX273034	ACCESSION: AX273034	C 521	11.2	8.1	17	1	AX736388	ACCESSION: AX736388
C 450	11.2	8.1	17	1	AX326513	ACCESSION: AX326513	C 522	11.2	8.1	17	1	AX738496	ACCESSION: AX738496
C 451	11.2	8.1	17	1	AX33401	ACCESSION: AX33401	C 523	11.2	8.1	17	1	AX756774	ACCESSION: AX756774
C 452	11.2	8.1	17	1	AX423730	ACCESSION: AX423730	C 524	11.2	8.1	17	1	AX757120	ACCESSION: AX757120
C 453	11.2	8.1	17	1	AX423731	ACCESSION: AX423731	C 525	11.2	8.1	17	1	AX757252	ACCESSION: AX757252
C 454	11.2	8.1	17	1	AX475293	ACCESSION: AX475293	C 526	11.2	8.1	17	1	AX757657	ACCESSION: AX757657
C 455	11.2	8.1	17	1	AX475294	ACCESSION: AX475294	C 527	11.2	8.1	17	1	AX761860	ACCESSION: AX761860
C 456	11.2	8.1	17	1	AX498962	ACCESSION: AX498962	C 528	11.2	8.1	17	1	AX762374	ACCESSION: AX762374
C 457	11.2	8.1	17	1	AX498963	ACCESSION: AX498963	C 529	11.2	8.1	17	1	AX762744	ACCESSION: AX762744
C 458	11.2	8.1	17	1	AX498964	ACCESSION: AX498964	C 530	11.2	8.1	17	1	BD067531	ACCESSION: BD067531
C 459	11.2	8.1	17	1	AX499444	ACCESSION: AX499444	C 531	11.2	8.1	17	1	BD091426	ACCESSION: BD091426
C 460	11.2	8.1	17	1	AX531276	ACCESSION: AX531276	C 532	11.2	8.1	17	1	BD104174	ACCESSION: BD104174
C 461	11.2	8.1	17	1	AX531277	ACCESSION: AX531277	C 533	11.2	8.1	17	1	BD105057	ACCESSION: BD105057
C 462	11.2	8.1	17	1	AX532096	ACCESSION: AX532096	C 534	11.2	8.1	17	1	BD137018	ACCESSION: BD137018
C 463	11.2	8.1	17	1	AX532100	ACCESSION: AX532100	C 535	11.2	8.1	17	1	BD198908	ACCESSION: BD198908
C 464	11.2	8.1	17	1	AX532102	ACCESSION: AX532102	C 536	11.2	8.1	17	1	BD199121	ACCESSION: BD199121
C 465	11.2	8.1	17	1	AX532104	ACCESSION: AX532104	C 537	11.2	8.1	17	1	BD200826	ACCESSION: BD200826
C 466	11.2	8.1	17	1	AX532255	ACCESSION: AX532255	C 538	11.2	8.1	17	1	BD223385	ACCESSION: BD223385
C 467	11.2	8.1	17	1	AX532275	ACCESSION: AX532275	C 539	11.2	8.1	18	1	AR106914	ACCESSION: AR106914
C 468	11.2	8.1	17	1	AX532276	ACCESSION: AX532276	C 540	11.2	8.1	20	1	AR381288	ACCESSION: AR381288
C 469	11.2	8.1	17	1	AX532448	ACCESSION: AX532448	C 541	11.2	8.1	20	1	AX623106	ACCESSION: AX623106
C 470	11.2	8.1	17	1	AX532449	ACCESSION: AX532449	C 542	11.2	8.1	11	1	AX630527	ACCESSION: AX630527
C 471	11.2	8.1	17	1	AX532450	ACCESSION: AX532450	C 543	11.2	8.1	15	1	AX15061	ACCESSION: AX15061
							C 544	11.2	8.1	15	1	BD251646	ACCESSION: BD251646

545	11	7.9	15	1	AR180150	ACCESSION:AR180150	618	10.4	7.5	14	1	BD197859	ACCESSION:BD197859
546	11	7.9	15	1	AR180787	ACCESSION:AR180787	c 619	10.4	7.5	15	1	A07567	ACCESSION:A07567
c 547	11	7.9	15	1	AX028347	ACCESSION:AX028347	620	10.4	7.5	15	1	A07569	ACCESSION:A07569
548	11	7.9	16	1	AR008042	ACCESSION:AR008042	c 621	10.4	7.5	15	1	AR033573	ACCESSION:AR033573
549	11	7.9	16	1	AR029494	ACCESSION:AR029494	c 622	10.4	7.5	15	1	AR113395	ACCESSION:AR113395
550	11	7.9	16	1	AR110507	ACCESSION:AR110507	623	10.4	7.5	15	1	AR132845	ACCESSION:AR132845
551	11	7.9	16	1	AR137060	ACCESSION:AR137060	c 624	10.4	7.5	15	1	AR143397	ACCESSION:AR143397
c 552	11	7.9	16	1	I26587	ACCESSION:I26587	625	10.4	7.5	15	1	E05479	ACCESSION:E05479
c 553	11	7.9	16	1	AX349231	ACCESSION:AX349231	c 626	10.4	7.5	15	1	I15197	ACCESSION:I15197
c 554	10.8	7.8	14	1	A64216	ACCESSION:A64216	c 627	10.4	7.5	15	1	I57802	ACCESSION:I57802
c 555	10.8	7.8	14	1	A98858	ACCESSION:A98858	c 628	10.4	7.5	15	1	I61657	ACCESSION:I61657
c 556	10.8	7.8	14	1	AR029990	ACCESSION:AR029990	629	10.4	7.5	15	1	AR180368	ACCESSION:AR180368
557	10.8	7.8	14	1	AR102515	ACCESSION:AR102515	c 630	10.4	7.5	15	1	AR040907	ACCESSION:AR040907
558	10.8	7.8	14	1	AR262818	ACCESSION:AR262818	c 631	10.4	7.5	15	1	AX166714	ACCESSION:AX166714
559	10.8	7.8	14	1	AX467088	ACCESSION:AX467088	c 632	10.4	7.5	15	1	AX586996	ACCESSION:AX586996
c 560	10.8	7.8	14	1	BD066371	ACCESSION:BD066371	c 633	10.4	7.5	15	1	AX636078	ACCESSION:AX636078
561	10.8	7.8	15	1	A42347	ACCESSION:A42347	c 634	10.4	7.5	15	1	BD207306	ACCESSION:BD207306
562	10.8	7.8	15	1	A44378	ACCESSION:A44378	c 635	10.4	7.5	15	1	BD208694	ACCESSION:BD208694
563	10.8	7.8	15	1	A47165	ACCESSION:A47165	c 636	10.4	7.5	15	1	S45933	ACCESSION:S45933
564	10.8	7.8	15	1	A56641	ACCESSION:A56641	c 637	10.4	7.5	15	1	I28863	ACCESSION:I28863
565	10.8	7.8	15	1	A80362	ACCESSION:A80362	638	10.4	7.5	16	1	AR328508	ACCESSION:AR328508
c 566	10.8	7.8	15	1	A88333	ACCESSION:A88333	c 639	10.4	7.5	16	1	AR329723	ACCESSION:AR329723
c 567	10.8	7.8	15	1	A89423	ACCESSION:A89423	640	10.4	7.5	16	1	AX349227	ACCESSION:AX349227
c 568	10.8	7.8	15	1	A90300	ACCESSION:A90300	c 641	10.4	7.5	18	1	AX103735	ACCESSION:AX103735
c 569	10.8	7.8	15	1	AR041808	ACCESSION:AR041808	642	10.4	7.5	20	1	A70767	ACCESSION:A70767
c 570	10.8	7.8	15	1	AR041809	ACCESSION:AR041809	643	10.4	7.5	20	1	A79251	ACCESSION:A79251
571	10.8	7.8	15	1	AR073553	ACCESSION:AR073553	644	10.2	7.3	20	1	BD003481	ACCESSION:BD003481
572	10.8	7.8	15	1	AR111765	ACCESSION:AR111765	c 645	10.2	7.3	15	1	A20991	ACCESSION:A20991
573	10.8	7.8	15	1	AR133622	ACCESSION:AR133622	c 646	10.2	7.3	15	1	A64273	ACCESSION:A64273
574	10.8	7.8	15	1	I20495	ACCESSION:I20495	c 647	10.2	7.3	15	1	A78578	ACCESSION:A78578
c 575	10.8	7.8	15	1	I33987	ACCESSION:I33987	c 648	10.2	7.3	15	1	AR026479	ACCESSION:AR026479
576	10.8	7.8	15	1	I33988	ACCESSION:I33988	c 649	10.2	7.3	15	1	AR041292	ACCESSION:AR041292
577	10.8	7.8	15	1	I84720	ACCESSION:I84720	650	10.2	7.3	15	1	AR041361	ACCESSION:AR041361
578	10.8	7.8	15	1	AR179805	ACCESSION:AR179805	651	10.2	7.3	15	1	AR041957	ACCESSION:AR041957
579	10.8	7.8	15	1	AR193504	ACCESSION:AR193504	652	10.2	7.3	15	1	AR056148	ACCESSION:AR056148
580	10.8	7.8	15	1	AR254155	ACCESSION:AR254155	c 653	10.2	7.3	15	1	AR056220	ACCESSION:AR056220
581	10.8	7.8	15	1	AX081337	ACCESSION:AX081337	c 654	10.2	7.3	15	1	AR056325	ACCESSION:AR056325
582	10.8	7.8	15	1	AX283167	ACCESSION:AX283167	c 655	10.2	7.3	15	1	AR102572	ACCESSION:AR102572
c 583	10.8	7.8	15	1	AX283281	ACCESSION:AX283281	656	10.2	7.3	15	1	AR113906	ACCESSION:AR113906
c 584	10.8	7.8	15	1	AX637264	ACCESSION:AX637264	c 657	10.2	7.3	15	1	AR113978	ACCESSION:AR113978
c 585	10.8	7.8	15	1	AX637266	ACCESSION:AX637266	c 658	10.2	7.3	15	1	AR114083	ACCESSION:AR114083
c 586	10.8	7.8	15	1	AX742553	ACCESSION:AX742553	c 659	10.2	7.3	15	1	AR131838	ACCESSION:AR131838
c 587	10.8	7.8	15	1	BD065846	ACCESSION:BD065846	c 660	10.2	7.3	15	1	AR132776	ACCESSION:AR132776
c 588	10.8	7.8	15	1	BD066936	ACCESSION:BD066936	c 661	10.2	7.3	15	1	BD233013	ACCESSION:BD233013
c 589	10.8	7.8	15	1	BD184406	ACCESSION:BD184406	662	10.2	7.3	15	1	BD233078	ACCESSION:BD233078
590	10.8	7.8	16	1	AR057424	ACCESSION:AR057424	663	10.2	7.3	15	1	BD233297	ACCESSION:BD233297
591	10.8	7.8	16	1	AR15182	ACCESSION:AR15182	664	10.2	7.3	15	1	BD233300	ACCESSION:BD233300
592	10.8	7.8	16	1	BD233053	ACCESSION:BD233053	c 665	10.2	7.3	15	1	BD233341	ACCESSION:BD233341
593	10.8	7.8	16	1	E39140	ACCESSION:E39140	c 666	10.2	7.3	15	1	I05468	ACCESSION:I05468
c 594	10.8	7.8	16	1	I50741	ACCESSION:I50741	c 667	10.2	7.3	15	1	I30549	ACCESSION:I30549
595	10.8	7.8	16	1	AR203385	ACCESSION:AR203385	c 668	10.2	7.3	15	1	I39340	ACCESSION:I39340
596	10.8	7.8	16	1	AR328401	ACCESSION:AR328401	669	10.2	7.3	15	1	I61786	ACCESSION:I61786
597	10.8	7.8	16	1	AR328478	ACCESSION:AR328478	c 670	10.2	7.3	15	1	AR180274	ACCESSION:AR180274
c 598	10.8	7.8	16	1	AR328510	ACCESSION:AR328510	c 671	10.2	7.3	15	1	AR180399	ACCESSION:AR180399
599	10.8	7.8	16	1	AX007607	ACCESSION:AX007607	672	10.2	7.3	15	1	AR242642	ACCESSION:AR242642
600	10.8	7.8	16	1	AX011283	ACCESSION:AX011283	c 673	10.2	7.3	15	1	AR262875	ACCESSION:AR262875
601	10.8	7.8	16	1	AX384636	ACCESSION:AX384636	c 674	10.2	7.3	15	1	AR279380	ACCESSION:AR279380
c 602	10.8	7.8	16	1	AX419931	ACCESSION:AX419931	c 675	10.2	7.3	15	1	AX007567	ACCESSION:AX007567
c 603	10.8	7.8	16	1	AX521635	ACCESSION:AX521635	676	10.2	7.3	15	1	AX007632	ACCESSION:AX007632
604	10.8	7.8	16	1	AX634479	ACCESSION:AX634479	677	10.2	7.3	15	1	AX007851	ACCESSION:AX007851
c 605	10.8	7.8	18	1	AR106948	ACCESSION:AR106948	678	10.2	7.3	15	1	AX007854	ACCESSION:AX007854
c 606	10.6	7.6	17	1	AX532451	ACCESSION:AX532451	c 679	10.2	7.3	15	1	AX007973	ACCESSION:AX007973
c 607	10.6	7.6	17	1	AX532452	ACCESSION:AX532452	680	10.2	7.3	15	1	AX456739	ACCESSION:AX456739
c 608	10.4	7.5	13	1	AR382702	ACCESSION:AR382702	c 681	10.2	7.3	15	1	AX572218	ACCESSION:AX572218
c 609	10.4	7.5	14	1	A09968	ACCESSION:A09968	c 682	10.2	7.3	15	1	AX572222	ACCESSION:AX572222
c 610	10.4	7.5	14	1	A40553	ACCESSION:A40553	c 683	10.2	7.3	15	1	AX587077	ACCESSION:AX587077
c 611	10.4	7.5	14	1	A89078	ACCESSION:A89078	684	10.2	7.3	15	1	AX633179	ACCESSION:AX633179
c 612	10.4	7.5	14	1	AR328833	ACCESSION:AR328833	c 685	10.2	7.3	15	1	AX633279	ACCESSION:AX633279
c 613	10.4	7.5	14	1	AR403509	ACCESSION:AR403509	c 686	10.2	7.3	15	1	AX633526	ACCESSION:AX633526
c 614	10.4	7.5	14	1	AX030128	ACCESSION:AX030128	c 687	10.2	7.3	15	1	AX635641	ACCESSION:AX635641
c 615	10.4	7.5	14	1	AX316449	ACCESSION:AX316449	688	10.2	7.3	15	1	AX636135	ACCESSION:AX636135
c 616	10.4	7.5	14	1	BD066591	ACCESSION:BD066591	c 689	10.2	7.3	15	1	AX636741	ACCESSION:AX636741
c 617	10.4	7.5	14	1	BD069009	ACCESSION:BD069009	690	10.2	7.3	15	1	AX636781	ACCESSION:AX636781

```
691 10.2 7.3 15 1 AX637368
c 692 10.2 7.3 15 1 BD007196
693 10.2 7.3 17 1 AX687848
c 694 10.2 7.3 17 1 AX532453
695 10.2 7.3 17 1 AX687851
c 696 10.2 7.3 17 1 AX757657
c 697 10 7.2 10 1 AR098907
c 698 10 7.2 10 1 I79747
c 699 10 7.2 10 1 AX301720
c 700 10 7.2 10 1 BD161179
c 701 10 7.2 10 1 BD161279
c 702 10 7.2 11 1 AX471317
c 703 10 7.2 11 1 AX471659
c 704 10 7.2 11 1 AX471723
c 705 10 7.2 11 1 AX622975
c 706 10 7.2 11 1 AX624360
c 707 10 7.2 11 1 AX625117
c 708 10 7.2 11 1 AX625409
c 709 10 7.2 11 1 AX625899
c 710 10 7.2 11 1 AX626201
c 711 10 7.2 11 1 AX626758
c 712 10 7.2 11 1 AX627300
c 713 10 7.2 11 1 AX627599
c 714 10 7.2 11 1 AX628274
c 715 10 7.2 11 1 AX629280
c 716 10 7.2 11 1 AX630396
c 717 10 7.2 11 1 AX631781
c 718 10 7.2 11 1 AX632538
c 719 10 7.2 11 1 BD187463
c 720 10 7.2 11 1 BD189593
c 721 10 7.2 11 1 BD190136
c 722 10 7.2 12 1 AR030066
c 723 10 7.2 12 1 AR303946
c 724 10 7.2 14 1 A08720
c 725 10 7.2 14 1 A08721
c 726 10 7.2 14 1 E03997
c 727 10 7.2 14 1 E04001
c 728 10 7.2 14 1 I39737
c 729 10 7.2 15 1 AR055901
c 730 10 7.2 15 1 AR055902
c 731 10 7.2 15 1 AR113659
c 732 10 7.2 15 1 AR113660
c 733 10 7.2 15 1 AR116338
c 734 10 7.2 15 1 AX084987
c 735 10 7.2 15 1 AX374605
c 736 10 7.2 15 1 AX632978
c 737 10 7.2 15 1 AX632980
c 738 10 7.2 15 1 AX763334
c 739 10 7.2 15 1 AX763665

ALIGNMENTS
BD102270/c 21 bp DNA linear PAT 27-AUG-2002
LOCUS Method of detecting risk factor for onset of arteriosclerosis.
DEFINITION BD102270
VERSION BD102270.1 GI:22647844
KEYWORDS WO 0171032-A/33.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 21)
Yamashita, S. and Matsuzawa, Y.
Nagano, M., Ito, M., Sageshashi, Y., Hattori, H., Egashira, T.,
Method of detecting risk factor for onset of arteriosclerosis
Patent: WO 0171032-A 33 27-SEP-2001;
BML INC, MAKOTO NAGANO, MAYUMI ITO, YUKIKO SAGESHASHI, HIROAKI HATTORI,
TORU EGASHIRA, SHIZUYA YAMASHITA, YUJI MATSUZAWA
OS Homo sapiens (human)

RESULT 1
BD102270/c
LOCUS Method of detecting risk factor for onset of arteriosclerosis.
DEFINITION BD102270
VERSION BD102270.1 GI:22647844
KEYWORDS WO 0171032-A/33.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 21)
Yamashita, S. and Matsuzawa, Y.
Nagano, M., Ito, M., Sageshashi, Y., Hattori, H., Egashira, T.,
Method of detecting risk factor for onset of arteriosclerosis
Patent: WO 0171032-A 33 27-SEP-2001;
BML INC, MAKOTO NAGANO, MAYUMI ITO, YUKIKO SAGESHASHI, HIROAKI HATTORI,
TORU EGASHIRA, SHIZUYA YAMASHITA, YUJI MATSUZAWA
OS Homo sapiens (human)

ACCESSION:AX637368
ACCESSION:BD007196
ACCESSION:AX687848
ACCESSION:AX532453
ACCESSION:AX687851
ACCESSION:AX757657
ACCESSION:AR098907
ACCESSION:I79747
ACCESSION:AX301720
ACCESSION:BD161179
ACCESSION:BD161279
ACCESSION:AX471317
ACCESSION:AX471659
ACCESSION:AX471723
ACCESSION:AX622975
ACCESSION:AX624360
ACCESSION:AX625117
ACCESSION:AX625409
ACCESSION:AX625899
ACCESSION:AX626201
ACCESSION:AX626758
ACCESSION:AX627300
ACCESSION:AX627599
ACCESSION:AX628274
ACCESSION:AX629280
ACCESSION:AX630396
ACCESSION:AX631781
ACCESSION:AX632538
ACCESSION:BD187463
ACCESSION:BD189593
ACCESSION:BD190136
ACCESSION:AR030066
ACCESSION:AR303946
ACCESSION:A08720
ACCESSION:A08721
ACCESSION:E03997
ACCESSION:E04001
ACCESSION:I39737
ACCESSION:AR055901
ACCESSION:AR055902
ACCESSION:AR113659
ACCESSION:AR113660
ACCESSION:AR116338
ACCESSION:AX084987
ACCESSION:AX374605
ACCESSION:AX632978
ACCESSION:AX632980
ACCESSION:AX763334
ACCESSION:AX763665

PN WO 0171032-A/33
PD 27-SEP-2001
PF 23-MAR-2001 WO 2001JP002327
PI 24-MAR-2000 JP 00P 084264
PI MAKOTO NAGANO, MAYUMI ITO, YUKIKO SAGESHASHI, HIROAKI HATTORI, TORU EGASHIRA, SHIZUYA YAMASHITA, YUJI MATSUZAWA
PI C1201/68, C12N15/12
PC Method of detecting risk factor for onset of arteriosclerosis
FH Key Location/Qualifiers
FT source 1..21
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..21
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 15.1%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1665 TCACAGCTGGACCCCTGGTGT 1685
Db 21 TCACAGCTGGACCCCTGGTGT 1
RESULT 2
E25734 22 bp DNA linear PAT 18-JUN-2001
LOCUS Method for assaying HBV gene by real time detection PCR method and
DEFINITION primer and probe to be used therein.
E25734
VERSION E25734.1 GI:13024922
KEYWORDS JP 1999103897-A/8.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 22)
AUTHORS Aki, A., Naotake, K., Kazuo, T. and Ryuji, K.
TITLE Method for assaying HBV gene by real time detection PCR method and
JOURNAL primer and probe to be used therein
Patent: JP 1999103897-A 8 20-APR-1999;
COMMENT SRL INC
OS Unidentified
PN JP 1999103897-A/8
PD 20-APR-1999
PF 30-SEP-1997 JP 1997282612
PI AKI ABE, NAO TAKE KAJIYAMA, KAZUO TAKEMURA, RYUJI KAWAGUCHI PC
C1201/70, C12N15/09, G01N21/78, G01N33/566, G01N33/576, G01N33/58, PC
C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..22
FT /organism='Unidentified'.
FEATURES
source
1..22
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 12.4%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1738 CCCAACTCTCCCTATCCTAAA 1759
Db 1 CCCAACTCTCCAGTCTTAA 22
RESULT 3
```

BD101979  
LOCUS Novel G protein coupled receptor and its DNA. 21 bp DNA linear PAT 27-AUG-2002  
DEFINITION  
ACCESSION BD101979  
VERSION BD101979.1 GI:22647553  
KEYWORDS WO 0177325-A/4.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Miwa,M., Matsui,H. and Shintani,Y.  
TITLE Novel G protein coupled receptor and its DNA  
JOURNAL Patent: WO 0177325-A 4 18-OCT-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD, MASANORI MIWA, HIDEKI MATSUI, YASUSHI SHINTANI  
COMMENT  
OS Artificial Sequence  
PN WO 0177325-A/4  
PD 18-OCT-2001  
PF 12-APR-2001 WO 2001JP003143  
PI MASANORI MIWA, HIDEKI MATSUI, YASUSHI SHINTANI  
PC C12N15/12, C07K14/705, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC  
C12N5/10,  
PC C12Q1/68, A61K45/00, A61P25/00, A61P29/00, A61P35/00, A61P11/06, PC  
A61P9/00,  
PC G01N33/53, G01N33/566, G01N33/15, G01N33/50//C12P21/02 CC  
Primer  
FH Key Location/Qualifiers  
FT source 1..21 /organism='Artificial Sequence'.  
FEATURES  
source 1..21 Location/Qualifiers  
/mol\_type='synthetic construct'  
/db\_xref='taxon:32630'  
Query Match 12.1%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1732 TTGGCTCCCAACTCTCCCT 1751  
|||||  
DB 1 TTGGCTCCCAACTCTCCCT 20  
RESULT 4  
BD131270  
LOCUS Novel G protein-coupled receptor protein and its DNA. 21 bp DNA linear PAT 18-SEP-2002  
DEFINITION  
ACCESSION BD131270  
VERSION BD131270.1 GI:23226215  
KEYWORDS JP 2002000281-A/4.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Miwa,M., Matsui,H. and Shintani,Y.  
TITLE Novel G protein-coupled receptor protein and its DNA  
JOURNAL Patent: JP 2002000281-A 4 08-JAN-2002;  
TAKEDA CHEMICAL INDUSTRIES LTD  
COMMENT  
OS Artificial Sequence  
PN JP 2002000281-A/4  
PD 08-JAN-2002  
PF 12-APR-2001 JP 2001114136  
PI MASANORI MIWA, HIDEKI MATSUI, YASUSHI SHINTANI  
PC C12N15/09, A61K45/00, A61P3/10, A61P9/00, A61P25/00, A61P29/00, PC  
A61P35/00,  
PC C07K14/705, C07K16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/10, PC  
C12P21/02,  
PC C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/566//  
PC C12P21/08,  
PC C12N15/00, C12N5/00  
CC Primer

PH Key Location/Qualifiers  
FT source 1..21 /organism='Artificial Sequence'.  
FEATURES  
source 1..21 Location/Qualifiers  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
Query Match 12.1%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1732 TTGGCTCCCAACTCTCCCT 1751  
|||||  
DB 1 TTGGCTCCCAACTCTCCCT 20  
RESULT 5  
AR381288  
LOCUS Sequence 19 from patent US 6607915. 20 bp DNA linear PAT 18-DEC-2003  
DEFINITION  
ACCESSION AR381288  
VERSION AR381288.1 GI:40089107  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Wanciewicz,E.  
TITLE Antisense inhibition of E2A-Pbx1 expression  
JOURNAL Patent: US 6607915-A 19 13-AUG-2003;  
FEATURES  
source 1..20 Location/Qualifiers  
/organism='unknown'  
/mol\_type='genomic DNA'  
Query Match 11.8%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 30;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1658 ACCAGGCTCACAGCTGGA 1675  
|||||  
DB 1 ACCAGGCTGACAGCTGGA 18  
RESULT 6  
AR129513  
LOCUS Sequence 102 from patent US 6187533. 22 bp DNA linear PAT 16-MAY-2001  
DEFINITION  
ACCESSION AR129513  
VERSION AR129513.1 GI:14117410  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Bell,G.I., Yamagata,K., Oda,N., Kaisaki,P.J., Furuta,H.,  
Horikawa,Y. and Menzel,S.  
TITLE Mutations in the diabetes susceptibility genes hepatocyte nuclear  
factor (HNF) 1 alpha (alpha.), HNF1.beta. and HNF4.alpha  
JOURNAL Patent: US 6187533-A 102 13-FEB-2001;  
FEATURES  
source 1..22 Location/Qualifiers  
/organism='unknown'  
/mol\_type='unassigned DNA'  
Query Match 11.7%; Score 16.2; DB 1; Length 22;  
Best Local Similarity 85.7%; Pred. No. 40;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1658 ACCAGGCTCACAGCTGGAACC 1678  
|||||

```

Db          2 ACCAGACTCAGCGCTGAACC 22

RESULT 7
AX323427
LOCUS      20 bp      DNA      linear      PAT 07-JAN-2002
DEFINITION Sequence 19 from Patent WO0192578.
ACCESSION  AX323427
VERSION     AX323427.1 GI:18094190
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Roninson, I.B., Dokmanovic, M. and Chang, B.D.
TITLE       Reagents and methods for identifying and modulating expression of
            genes regulated by retinoids
JOURNAL     Patent: WO 0192578-A 19 06-DEC-2001;
            Board of Trustees of the University of Illinois (US)
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="Antisense primer for beta IG-H3"

Query Match      10.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 55;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1653 CAAGCACCAGGCTCACAGCT 1672
      |||||
      1 CATGCACAAGGCTCACATCT 20

RESULT 8
ARI142933
LOCUS      23 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 19 from patent US 6204025.
ACCESSION  ARI142933
VERSION     ARI142933.1 GI:15104219
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 23)
AUTHORS     Liu, Q.
TITLE       Efficient linking of nucleic acid segments
JOURNAL     Patent: US 6204025-A 19 20-MAR-2001;
            Location/Qualifiers
FEATURES    Location/Qualifiers
            source
            1..23
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      10.9%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1713 AGGAGTACGGAGATGGAGAT 1732
      |||||
      4 AGGAGGAGGGAGATGGACAT 23

RESULT 9
AX293741/c
LOCUS      20 bp      DNA      linear      PAT 21-NOV-2001
DEFINITION Sequence 5503 from Patent WO0179548.
ACCESSION  AX293741
VERSION     AX293741.1 GI:17055424
SOURCE      synthetic construct
ORGANISM    synthetic construct

artificial sequences.
1
REFERENCE   1
AUTHORS     Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE       Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
JOURNAL     Patent: WO 0179548-A 5503 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Hypothetical Probe Sequence"

Query Match      10.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1728 GAGATTGGCTCCGCAAC 1743
      |||||
      18 GAGATTGGCTCGCAAC 3

RESULT 10
AX488425
LOCUS      20 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION Sequence 5725 from Patent WO02053728.
ACCESSION  AX488425
VERSION     AX488425.1 GI:22322505
SOURCE      Candida albicans
ORGANISM    Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
AUTHORS     Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L.
TITLE       Gene disruption methodologies for drug target discovery
JOURNAL     Patent: WO 02053728-A 5725 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="Candida albicans"
            /mol_type="unassigned DNA"
            /db_xref="taxon:5476"

Query Match      10.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1737 TCCCAACTCTCCCTA 1752
      |||||
      1 TCCCAACTCTCCCAA 16

RESULT 11
BD171443/c
LOCUS      20 bp      DNA      linear      PAT 18-FEB-2003
DEFINITION Nucleic acid molecule derived from actinomycetes plasmid.
ACCESSION  BD171443
VERSION     BD171443.1 GI:28412733
KEYWORDS    JP 2002233380-A/2.
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
            1 (bases 1 to 23)
REFERENCE   1
AUTHORS     Kawai, T., Onji, Y., Hiraki, J., Inoue, S., Takagi, H. and Nakamori, S.
TITLE       Nucleic acid molecule derived from actinomycetes plasmid
JOURNAL     Patent: JP 2002233380-A 2 20-AUG-2002;
            CHISSO CORP
COMMENT     OS Artificial Sequence
            PN JP 2002233330-A/2
            PD 20-AUG-2002
            PF 08-FEB-2001 JP 2001031958

```



PI TAKAHIRO KAWAI,YUICHI ONJI,JUN HIRAKI,SATOSHI INOUE,HIROSHI  
PI TAKAGI,  
PI SHIGERU NAKAMORI  
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10/(C12N15/09,PC  
C12R1.465),  
PC (C12N1/21,C12R1.19),C12N15/00,C12N5/00,(C12N15/00,C12R1.465)  
CC Nucleic acid molecule derived from actinomycetes plasmid FH  
Key Location/Qualifiers  
FT source 1..20  
FT /organism='Artificial Sequence'.  
FEATURES  
source  
Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
Query Match 10.4%; Score 14.4; DB 1; Length 20;  
Best Local Similarity 93.8%; Pred. No. 82;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1636 GGGCTTGTAGCAGAAG 1651  
Db 17 GGGCTTGTAGCAGATG 2  
RESULT 12  
AR011791/c  
LOCUS  
DEFINITION Sequence 4 from patent US 5763172.  
ACCESSION AR011791  
VERSION AR011791.1 GI:3969781  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Magda,D., Sessler,J.L., Wright,M., Miller,R.A. and Dow,W.C.  
TITLE Method of phosphate ester hydrolysis  
JOURNAL Patent: US 5763172-A 4 09-JUN-1998;  
FEATURES  
source  
Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 10.2%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1655 AGCACCGGCTCACAGCTG 1673  
Db 19 AACACCGGCTCACAGATG 1  
RESULT 13  
AR025499/c  
LOCUS  
DEFINITION Sequence 1 from patent US 5798491.  
ACCESSION AR025499  
VERSION AR025499.1 GI:3978127  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Magda,D. and Sessler,J.L.  
TITLE Multi-mechanistic chemical cleavage using certain metal complexes  
JOURNAL Patent: US 5798491-A 1 25-AUG-1998;  
FEATURES  
source  
Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 10.2%; Score 14.2; DB 1; Length 20;  
QY 1655 AGCACCGGCTCACAGCTG 1673  
Db 19 AACACCGGCTCACAGATG 1  
RESULT 15  
AR025499/c  
LOCUS  
DEFINITION Sequence 1 from patent US 5798491.  
ACCESSION AR025499  
VERSION AR025499.1 GI:3978127  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Magda,D. and Sessler,J.L.  
TITLE Multi-mechanistic chemical cleavage using certain metal complexes  
JOURNAL Patent: US 5798491-A 1 25-AUG-1998;  
FEATURES  
source  
Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 10.2%; Score 14.2; DB 1; Length 20;  
QY 1655 AGCACCGGCTCACAGCTG 1673  
Db 19 AACACCGGCTCACAGATG 1  
RESULT 15  
AR025499/c  
LOCUS  
DEFINITION Sequence 1 from patent US 5798491.  
ACCESSION AR025499  
VERSION AR025499.1 GI:3978127  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Magda,D. and Sessler,J.L.  
TITLE Multi-mechanistic chemical cleavage using certain metal complexes  
JOURNAL Patent: US 5798491-A 1 25-AUG-1998;  
FEATURES  
source  
Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Best Local Similarity 84.2%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1655 AGCACCGGCTCACAGCTG 1673  
Db 19 AACACCGGCTCACAGATG 1  
RESULT 14  
E08471/c  
LOCUS  
DEFINITION  
ACCESSION E08471  
VERSION E08471.1 GI:2176587  
KEYWORDS JP 1994321991-A/7.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Uchida,T. and Shikata,T.  
TITLE POLYPEPTIDE DERIVED FROM HEPATITIS B VIRUS AND GENE CODING THE SAME  
JOURNAL Patent: JP 1994321991-A 7 22-NOV-1994;  
COMMENT MITSUBISHI KASEI CORP  
OC None  
CC Artificial sequences.  
PN JP 1994321991-A/7  
PD 22-NOV-1994  
PF 14-MAY-1993 JP 1993113136  
PI UCHIDA TOSHIKAZU, SHIKATA TOSHIO  
PC C07K13/00,C12N15/51,C12P21/02,C12Q1/68,G01N33/53,PC  
G01N33/576//A61K37/02,  
PC A61K39/29;  
CC strandedness: Single;  
CC topology: Linear;  
CC hypothetical: No;  
FH Key Location/Qualifiers  
FT source 1..20  
FT /organism='Artificial sequences'.  
FEATURES  
source  
Location/Qualifiers  
1..20  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
Query Match 10.2%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1736 CTCGCCAACTCCTCCCTATC 1754  
Db 19 CCCCAACTCCTCCAGTC 1  
RESULT 15  
I26707/c  
LOCUS  
DEFINITION Sequence 2 from patent US 5559207.  
ACCESSION I26707  
VERSION I26707.1 GI:1606577  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Sessler,J.L., Smith,D.A., Miller,R.A., Ross,K.L., Wright,M.,  
Dow,W.C., Kr al V.A., Iverson,B. and Magda,D.  
TITLE Tetaphyrin metal complex mediated ester hydrolysis  
JOURNAL Patent: US 5559207-A 2 24-SEP-1996;  
FEATURES  
source  
Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

```
Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTACAGCTG 1673
Db 19 AACACCCGGCTCAGATG 1

RESULT 16
LOCUS AR211960/c
DEFINITION Sequence 16 from patent US 6399378.
ACCESSION AR211960
VERSION AR211960.1 GI:21515420
KEYWORDS
SOURCE
ORGANISM Unknown.
UNCLASIFIED.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ward,D.T. and Watt,A.T.
TITLE Antisense modulation of RECOL2 expression
JOURNAL Patent: US 6399378-A 16 04-JUN-2002;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCAGACCTGGAACCTT 1680
Db 20 GGCTCAGACCTGTAATCT 2

RESULT 17
LOCUS AR281496
DEFINITION Sequence 109 from patent US 6518411.
ACCESSION AR281496
VERSION AR281496.1 GI:29717183
KEYWORDS
SOURCE
ORGANISM Unknown.
UNCLASIFIED.
REFERENCE 1 (bases 1 to 20)
AUTHORS Murray,J.C. and Semina,E.
TITLE RGS compositions and therapeutic and diagnostic uses therefor
JOURNAL Patent: US 6518411-A 109 11-FEB-2003;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
                /mol_type="mrna"

Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1733 TGGCTCCCACTCTCCCT 1751
Db 2 TGTCTCCCAATTCCTCACT 20

RESULT 18
LOCUS BD185884/c
DEFINITION A stabilization method and a preservation method for a reagent for
ACCESSION BD185884
VERSION BD185884.1 GI:31878084

Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTACAGCTG 1673
Db 19 AACACCCGGCTCAGATG 1

RESULT 16
LOCUS AR211960/c
DEFINITION Sequence 16 from patent US 6399378.
ACCESSION AR211960
VERSION AR211960.1 GI:21515420
KEYWORDS
SOURCE
ORGANISM Unknown.
UNCLASIFIED.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ward,D.T. and Watt,A.T.
TITLE Antisense modulation of RECOL2 expression
JOURNAL Patent: US 6399378-A 16 04-JUN-2002;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCAGACCTGGAACCTT 1680
Db 20 GGCTCAGACCTGTAATCT 2

RESULT 17
LOCUS AR281496
DEFINITION Sequence 109 from patent US 6518411.
ACCESSION AR281496
VERSION AR281496.1 GI:29717183
KEYWORDS
SOURCE
ORGANISM Unknown.
UNCLASIFIED.
REFERENCE 1 (bases 1 to 20)
AUTHORS Murray,J.C. and Semina,E.
TITLE RGS compositions and therapeutic and diagnostic uses therefor
JOURNAL Patent: US 6518411-A 109 11-FEB-2003;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
                /mol_type="mrna"

Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1733 TGGCTCCCACTCTCCCT 1751
Db 2 TGTCTCCCAATTCCTCACT 20

RESULT 18
LOCUS BD185884/c
DEFINITION A stabilization method and a preservation method for a reagent for
ACCESSION BD185884
VERSION BD185884.1 GI:31878084

Query Match      10.2%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 99;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1679 CTGGTGTCTCTCTCCAGCGT 1697
```

```
KEYWORDS
SOURCE WO 02101042-A/80.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Sagawa,H., Uemori,T., Mukai,H., Yamamoto,J., Tomono,J., Kobayashi,E., Eroki,T., Asada,K. and Kato,I.
TITLE A stabilization method and a preservation method for a reagent for
JOURNAL nucleic acid amplification or detection reaction
COMMENT TAKARA BIO INC, FIIROAKI SAGAWA, TAKASHI UEMORI, HIROYUKI MUKAI, JUNKO YAMAMOTO, JUN TOMONO, EIJI KOBAYASHI, TATSUJI ENOKI, KIYOZO ASADA, IKUNOSHIN KATO
OS Artificial Sequence
PN WO 02101042-A/80
PD 19-DEC-2002
PF 12-JUN-2002 WO 2002JP005832
PR 12-JUN-2001 JP 01P 177737.20-AUG-2001 JP 01P 249689 PI
HIROAKI SAGAWA, TAKASHI UEMORI, HIROYUKI MUKAI, JUNKO YAMAMOTO, PI
JUN TOMONO,
PI EIJI KOBAYASHI, TATSUJI ENOKI, KIYOZO ASADA, IKUNOSHIN KATO
PC
C12N15/09,C12Q1/68
CC Designed oligonucleotide probe as HBV-probe2 to detect a DNA
CC fragment
CC amplifying a portion of X-protein-encoding sequence from CC
Hepatitis B virus.
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.

FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 CTCCCAACTCTCTCCCTATC 1754
Db 19 CCCCCAACTCTCTCCCTAGTC 1

RESULT 19
LOCUS AX777492
DEFINITION Sequence 40 from Patent WO03029458.
ACCESSION AX777492
VERSION AX777492.1 GI:32694510
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Breitling,F., Moldenhauer,G., Poustka,A. and Kuehlwein,T.
TITLE Method for producing protein libraries and for selecting proteins
JOURNAL from said libraries
PATENT: WO 03029458-A 40 10-APR-2003;
DEUTSCHES Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
(DE)

FEATURES
    source
        Location/Qualifiers
            1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Primer vH3-11"

Query Match      10.2%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 99;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1679 CTGGTGTCTCTCTCCAGCGT 1697
```

```

Db      1  CTGCCCTCTCCTCCAGCGT 19
      |||  |||||  |||||  |||||
      |||  |||||  |||||  |||||
      |||  |||||  |||||  |||||

RESULT 20
A06347/c
LOCUS      20 bp      RNA      linear      PAT 22-JUL-1993
DEFINITION      oligonucleotide d.
ACCESSION      A06347
VERSION      A06347.1  GI:412830
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
              artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Hilder, V.A., Gatehouse, A.M.R., Gatehouse, J.A. and Boulter, D.
TITLE      DNA molecules useful in plant protection
JOURNAL      Patent: EP 0272144-A 7 22-JUN-1988;
              AGRICULTURAL GENETICS COMPANY LIMITED
FEATURES
  source      Location/Qualifiers
              1..20
                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"

Query Match      10.1%; Score 14; DB 1; Length 20;
Best Local Similarity      61.1%; Pred. No. 1e+02;
Matches      11; Conservative      6; Mismatches      1; Indels      0; Gaps      0;

QY      1637  GGCTTGATGAGGAGGCA 1654
      |||  |||||  |||||  |||||
      |||  |||||  |||||  |||||
      |||  |||||  |||||  |||||

Db      20  GGYTTTATCAAAATCT 3

RESULT 21
BD074024
LOCUS      18 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION      Human glial cell-line derived neurotrophic factor promoter, vector
              containing the promoter, and method for screening a compound by the
              promoter.
ACCESSION      BD074024
VERSION      BD074024.1  GI:22619627
KEYWORDS      JP 2001512679-A/6.
SOURCE      unidentified
ORGANISM      unidentified
              unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS      Albert, B.P., Mels, J.R., Lee, W.O. and Nei, B.A.
TITLE      Human glial cell-line derived neurotrophic factor promoter, vector
              containing the promoter, and method for screening a compound by the
              promoter
JOURNAL      Patent: JP 2001512679-A 6 28-AUG-2001;
              F. HOFFMANN LA ROCHE AG
COMMENT      OS      Unidentified
              PN      JP 2001512679-A/6
              PD      28-AUG-2001
              PF      23-JUL-1998  JP 2000506328
              PR      05-AUG-1997  US  60/054812.14-APR-1998  US  60/081751  PI
              BECKER PRESTON ALBERT, JOHNSON RADOLF MELS, WALTER OM LEE, BERITY
              PI      ADRIAN NEIL
              PC      C12N15/09, A61K45/00, A61P25/28, C12N5/10, C12Q1/68, G01N33/15, PC
              G01N33/50,
              PC      C12N15/00, C12N5/00
              CC      Strandedness: Single;
              CC      Topology: Linear;
              CC      Human glial cell-line derived neurotrophic factor promoter,
              CC      vector
              CC      containing the promoter, and method for screening a compound
              CC      by the
              CC      promoter
              CC      key
              FH      key
              FT      source
              /organism='Unidentified'.

RESULT 22
AR241103/c
LOCUS      20 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION      Sequence 74 from patent US 6468796.
ACCESSION      AR241103
VERSION      AR241103.1  GI:27286320
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
              unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Watt, A.T.
TITLE      Antisense modulation of bifunctional apoptosis regulator expression
JOURNAL      Patent: US 6468796-A 74 22-OCT-2002;
              Location/Qualifiers
FEATURES
  source      Location/Qualifiers
              1..20
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match      9.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity      88.2%; Pred. No. 92;
Matches      15; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      1655  AGCACCAGGCTCAGC 1671
      |||||  |||||  |||||
      |||||  |||||  |||||
      |||||  |||||  |||||

Db      2  AGCACCAGGAGACAGC 18

RESULT 23
AR281777
LOCUS      20 bp      DNA      linear      PAT 10-APR-2003
DEFINITION      Sequence 4 from patent US 6521225.
ACCESSION      AR281777
VERSION      AR281777.1  GI:29717571
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
              unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Srivastava, A., Ponnazhagan, S., Chloemer, R.H., Wang, X.-S.,
              Yoder, M.C., Zhou, S.-Z., Escobedo, J. and Dwarki, V.
TITLE      AAV vectors
JOURNAL      Patent: US 6521225-A 4 18-FEB-2003;
              Location/Qualifiers
FEATURES
  source      Location/Qualifiers
              1..20
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match      9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity      88.2%; Pred. No. 1.1e+02;
Matches      15; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      1681  GGTGTCTCTCTCCAGCGT 1697
      |||  |||||  |||||
      |||  |||||  |||||
      |||  |||||  |||||

Db      2  GGTTCCTCTCTCCAGCAT 18

RESULT 24

```

```

AX250715
LOCUS AX250715 20 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 7 from Patent WO0168670.
ACCESSION AX250715
VERSION AX250715.1 GI:15984453
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lazdunski,M., Lesage,F. and Maingret,F.
TITLE Novel family of mechanically sensitive human potassium channels
activated by polyunsaturated fatty acids and use thereof
JOURNAL Patent: WO 0168670-A 7 20-SEP-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
Source 1..20
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 1..20
/note="Oligonucleotide utilise pour l'analyse des biots,
marque au P32"

Query Match 9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1659 CCAGGCTCACAGTGGGA 1675
Db 1 CCAGGCTCCAGCTGGA 17

RESULT 25
AX253315/c
LOCUS AX253315 20 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 21 from Patent WO0170993.
ACCESSION AX253315
VERSION AX253315.1 GI:16073855
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Winther,M.D., Smith,H.L., Allen,S.J., Ponton,A. and de Antueno R.J.
TITLE Polynucleotides that control delta-6-desaturase genes and methods
for identifying compounds for modulating delta-6-desaturase
JOURNAL Patent: WO 0170993-A 21 27-SEP-2001;
Scotia Holdings plc (GB)
FEATURES
Source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match 9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1685 TCTCTCCAGCGTGGTG 1701
Db 19 TCTTCTCCAGCGTAGTG 3

RESULT 26
AX283518/c
LOCUS AX283518 20 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 1 from Patent WO0178754.
ACCESSION AX283518
VERSION AX283518.1 GI:17044265
KEYWORDS

AX250715
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Chancellor,M.B., Huard,J., Capelli,C.C. and Qu,Z.
TITLE Soft tissue and bone augmentation and bulking utilizing
muscle-derived progenitor cells, compositions and treatments
thereof
JOURNAL Patent: WO 0178754-A 1 25-OCT-2001;
University of Pittsburgh (US)
FEATURES
Source 1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="CD34 UP OLIGONUCLEOTIDE SEQUENCE"

Query Match 5.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1640 TTGTAGCAGAGGCAAG 1656
Db 20 TGGTAGCAGAGTCAAG 4

RESULT 27
BD006136
LOCUS BD006136 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Methods and compositions for liver specific delivery of therapeutic
molecules using recombinant AAV vectors.
ACCESSION BD006136
VERSION BD006136.1 GI:18634507
KEYWORDS JP 2001500376-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Srivastava,A., Ponnazhagan,S., Chloemer,R.H., Wang,X.S.,
Yoder,M.C., Zhou,S.Z., Escobedo,J. and Dwariki,V.
TITLE Methods and compositions for liver specific delivery of therapeutic
molecules using recombinant AAV vectors
JOURNAL Patent: JP 2001500376-A 4 16-JAN-2001;
CHIRON CORP, INDIANA UNIVERSITY
COMMENT OS Homo sapiens (human)
PN JP 2001500376-A/4
PD 16-JAN-2001
PF 02-SEP-1997 JP 1998512823
PR 06-SEP-1996 US 60/025616 11-SEP-1996 US 60/025649 PI XU
ARON SRIVASTAVA,SELVARANGAN PONNAZHAGAN,ROBERT H CHLOEMER,PI SHAN WANG,
PI MERVIN C YODER,SHANG ZEHU,ZHOU,JAIME ESCOBEDO,VARAVANI DWARKI
PC A01N43/04,A51K31/70,C12N15/63
CC
FH Key Location/Qualifiers
FT source 1..20
/organism="Homo sapiens (human)"
FEATURES
Source Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1681 GGTCTCTCTCCAGCGT 1697
Db 2 GGTCTCTCTCCAGCAT 18

```

```
RESULT 28
BD179019/c
LOCUS          BD179019          20 bp    DNA        linear    PAT 16-APR-2003
DEFINITION    A method of secreting and producing proteins.
ACCESSION     BD179019
VERSION       BD179019.1 GI:30016287
KEYWORDS      WO 02081694-A/45.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 20)
AUTHORS      Kikuchi.Y., Date,M., Umezawa.Y., Yokoyama.K., Heima,H. and
              Matsui,H.
TITLE         A method of secreting and producing proteins
JOURNAL       Patent: WO 02081694-A 45 17-OCT-2002;
              AJINOMOTO CO INC, YOSHIMI KIKUCHI, MASAYO DATE, YUKIKO UMEZAWA,
              KEIICHI YOKOYAMA, HARUO HEIMA, HIROSHI MATSUI
COMMENT       OS Artificial Sequence
              PN WO 02081694-A/45
              PD 17-OCT-2002
              PF 27-MAR-2002 WO 2002JP002978
              PR 30-MAR-2001 JP 01P 098808
              PI YOSHIMI KIKUCHI, MASAYO DATE, YUKIKO UMEZAWA, KEIICHI YOKOYAMA,
              PI HARUO HEIMA,
              PI HIROSHI MATSUI
              PC .C12N15/09,C12N1/21,C12P21/02,C07K19/00,C07K7/06,C07K7/08 CC
              Description of Artificial Sequence:PCR primer FH Key
              Location/Qualifiers
              FT source 1..20
              /organism='Artificial Sequence'.
FEATURES      source
              Location/Qualifiers
              1..20
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
Query Match 9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1725 ATGGAGATTGGCTCCCA 1741
|||||
Db 19 ATGGAGATAGCTCCCA 3

RESULT 29
A98445/c
LOCUS          A98445          20 bp    DNA        linear    PAT 07-SEP-2000
DEFINITION    Sequence 29 from Patent WO9912948.
ACCESSION     A98445
VERSION       A98445.1 GI:6781546
KEYWORDS      unidentified
SOURCE        unclassified.
ORGANISM      unclassified.
REFERENCE     1
AUTHORS      Landt,O.
TITLE         Protein-coated polynucleic acids, method for the production
              thereof, and use of the same
JOURNAL       Patent: WO 9912948-A 29 18-MAR-1999;
              LANDT OLFERT (DE)
FEATURES      Location/Qualifiers
              source 1..20
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1631 CGATGGGCTTGTACAGAA 1650
|||||

RESULT 30
AR050289
LOCUS          AR050289          20 bp    DNA        linear    PAT 29-SEP-1999
DEFINITION    Sequence 2 from patent US 5827661.
ACCESSION     AR050289
VERSION       AR050289.1 GI:5973014
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unknown.
REFERENCE     1 (bases 1 to 20)
AUTHORS      Blais,B.W.
TITLE         Enhancing detection polymerase chain reaction assays by RNA
              transcription and immunodetection of RNA:DNA hybrids
              Patent: US 5827661-A 2 27-OCT-1998;
              Location/Qualifiers
              FEATURES      source 1..20
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1684 GTCTCTCCAGCGGTGGGA 1703
|||||
Db 1 GTATCTCCAGATGATCGA 20

RESULT 31
AR100579
LOCUS          AR100579          20 bp    DNA        linear    PAT 14-FEB-2001
DEFINITION    Sequence 95 from patent US 6080588.
ACCESSION     AR100579
VERSION       AR100579.1 GI:12811027
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unknown.
REFERENCE     1 (bases 1 to 20)
AUTHORS      Glick,G.D.
TITLE         Therapeutic methods for benzodiazepine derivatives
              Patent: US 6080588-A 95 27-JUN-2000;
              Location/Qualifiers
              FEATURES      source 1..20
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1692 CAGCGTGTGCACTGGGT 1711
|||||
Db 1 CACTGTGTGACGTTCGGT 20

RESULT 32
AR100585
LOCUS          AR100585          20 bp    DNA        linear    PAT 14-FEB-2001
DEFINITION    Sequence 103 from patent US 6080588.
ACCESSION     AR100585
VERSION       AR100585.1 GI:12811033
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unknown.
REFERENCE     1 (bases 1 to 20)
AUTHORS      Glick,G.D.
TITLE         Therapeutic methods for benzodiazepine derivatives
```

```

JOURNAL Patent: US 6080588-A 103 27-JUN-2000;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1692 CAGCGTGGTGAAGTTGGGT 1711
  |||||
  1 CACTGTGGTGAAGTTGGGT 20

Db

RESULT 33
LOCUS AR158965 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 587 from patent US 6251588.
ACCESSION AR158965
VERSION AR158965.1 GI:16221399
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and Kincaid,R.H.
TITLE Method for evaluating oligonucleotide probe sequences
JOURNAL Patent: US 6251588-A 587 26-JUN-2001;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1701 GGAAGTTGGTTAGGAGTAC 1720
  |||||
  20 GGAAGTTCAATTAGGAATAC 1

Db

RESULT 34
LOCUS E26692 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Improved method for measuring cytokine gene expression.
ACCESSION E26692
VERSION E26692.1 GI:13026279
KEYWORDS JP 1999155600-A/42.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Michio,S., Takeshi,H., Masato,H. and Hideyuki,I.
TITLE Improved method for measuring cytokine gene expression
JOURNAL Patent: JP 1999155600-A 42 15-JUN-1999;
SHISEIDO CO LTD
COMMENT OS Unidentified
PN JP 1999155600-A/42
PD 15-JUN-1999
PF
PR 28-NOV-1997 JP 1997328171
PI
PR MICHIO SHIBATA,TAKESHI HARIYA,MASATO HATAO,HIDEYUKI ICHIKAWA
PC C12Q1/68,C07K14/52,C07K14/54,C07K14/55,C07K14/56,C07K14/57, PC
PC C12N15/09,
CC G01N33/50//C12Q1/68,C12R1:91
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.

JOURNAL Patent: US 6080588-A 103 27-JUN-2000;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

Query Match
  5.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGCTCCC 1740
  |||||
  1 GAAGATGGTATGGGCTTCC 20

Db

RESULT 35
LOCUS I31522 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 434 from patent US 5582979.
ACCESSION I31522
VERSION I31522.1 GI:1822313
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 434 10-DEC-1996;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1713 AGGAGTAGGAGATGGAGAT 1732
  |||||
  1 AGGAGTTAGGAGCTGGAGT 20

Db

RESULT 36
LOCUS AR298667/c 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 10402 from patent US 6537751.
ACCESSION AR298667
VERSION AR298667.1 GI:31685951
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 10402 25-MAR-2003;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match
  9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1746 CTCCTATCTCTAAAGCCCCA 1765
  |||||
  20 CTCCTATCTCTCTCTCCCA 1

Db

```

```
RESULT 37
AR316120/c
LOCUS AR316120 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6657 from patent US 6559294.
ACCESSION AR316120
VERSION AR316120.1 GI:31709546
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,I.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6657 06-MAY-2003;
FEATURES
    source
        1..20
        /organism="unknown"
        /mol_type="genomic DNA"
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1633 ATGGGGCTTGTAGCAGAGG 1652
|||||
Db 20 ATGGTGTAGTATCAGCAGG 1

RESULT 38
AR316177/c
LOCUS AR316177 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6714 from patent US 6559294.
ACCESSION AR316177
VERSION AR316177.1 GI:31709603
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,I.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6714 06-MAY-2003;
FEATURES
    source
        1..20
        /organism="unknown"
        /mol_type="genomic DNA"
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1633 ATGGGGCTTGTAGCAGAGG 1652
|||||
Db 20 ATGGTGTAGTATCAGCAGG 1

RESULT 39
AR370267
LOCUS AR370267 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 88 from patent US 6300132.
ACCESSION AR370267
VERSION AR370267.1 GI:34606773
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Cowsett,L.M.
TITLE Antisense inhibition of telomeric repeat binding factor 2
JOURNAL Patent: US 6300132-A 88 09-OCT-2001;

FEATURES
    source
        1..20
        /organism="unknown"
        /mol_type="genomic DNA"
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1720 CGGAGATGGAGATGGCTCC 1739
|||||
Db 20 CGGATAGGGAGACTGGCTGC 1

RESULT 40
AR315823/c
LOCUS AX115823 20 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 946 from Patent WO0129262.
ACCESSION AX115823
VERSION AX115823.1 GI:14032765
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 946 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
    source
        1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer"
Query Match 9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1737 TCCCAACTCTCCCTATCCT 1756
|||||
Db 20 TCCCAACTCTCCCTATCCT 1

RESULT 41
BD144090
LOCUS BD144090 20 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid of uncoupling protein-1, -2 or -3
and reagent therefor, and method for screening diet drug.
ACCESSION BD144090
VERSION BD144090.1 GI:27849848
KEYWORDS JP 2002125680-A/14.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Horiya,T., Shibata,M., Soma,T. and Ichikawa,H.
TITLE Method for assaying nucleic acid of uncoupling protein-1, -2 or -3
and reagent therefor, and method for screening diet drug
JOURNAL Patent: JP 2002125680-A 14 08-MAY-2002;
SHISEIDO CO LTD
COMMENT OS Artificial Sequence
PN JP 2002125680-A/14
PD 08-MAY-2002
PF 24-OCT-2000 JP 2000324581
PI TAKESHI HARIYA, MICHIO SHIBATA, TSUTOMU SOMA, HIDEYUKI ICHIKAWA
PC C12N15/09, A61K45/00, A61P3/04, C12Q1/68, G01N33/53, G01N33/566//
PC C12N9/02,
PC C12N15/00
CC Reverse primer for amplification of gene for glyceroldehyde-3-
phosphate
CC dehydrogenase
CC CC
```

```

FH Key      Location/Qualifiers
FT source   1..20
FT          /organism='Artificial Sequence'.

FEATURES             source
    source       1..20
                Location/Qualifiers
                1..20
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match      9.6%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGGCTCC 1740
Db 1 GAAGATGGTGGTGGCTCC 20

RESULT 42
AX723714
LOCUS AX723714 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1401 from Patent WO03025176.
ACCESSION AX723714
VERSION AX723714.1 GI:30503057
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 1401 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES             source
    source       1..17
                Location/Qualifiers
                1..17
                /organism="Mus musculus"
                /mol_type="unassigned DNA"
                /db_xref="taxon:10090"

Query Match      9.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 GCTCCCAACTCTCTCC 1749
Db 1 GATCCCAACTCTCTCC 15

RESULT 43
AX352825
LOCUS AX352825 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 31 from Patent EP1174518.
ACCESSION AX352825
VERSION AX352825.1 GI:18617907
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Loukachov,V.V., van Gemen,B. and Goudsmit,J.
TITLE Collection of binding molecules
JOURNAL Patent: EP 1174518-A 31 23-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES             source
    source       1..18
                Location/Qualifiers
                1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="position 41"

Query Match      9.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1717 GTACGAGATGGAGA 1731
Db 1 GTACAGAGATGGAGA 15

RESULT 44
AX362670
LOCUS AX362670 18 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 31 from Patent WO0208463.
ACCESSION AX362670
VERSION AX362670.1 GI:18694810
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Loukachov,V.V., Goudsmit,J. and van Gemen,B.
TITLE Collection of binding molecules
JOURNAL Patent: WO 0208463-A 31 31-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES             source
    source       1..18
                Location/Qualifiers
                1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="position 41"

Query Match      9.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1717 GTACGAGATGGAGA 1731
Db 1 GTACAGAGATGGAGA 15

RESULT 45
AB069639/c
LOCUS AB069639/c 18 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-A007F44
at 1p36
ACCESSION AB069639
VERSION AB069639.1 GI:15130443
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
and Soeda,E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human
chromosome 1p35-36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE 2 (bases 1 to 13)
AUTHORS Horii,A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             source
    source       1..18
                Location/Qualifiers
                1..18
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

```



```
misc_feature 1. .19
/note="reverse primer for human STS sts-A007F44 at 1p36
sts-A007F44 obtained from clones B22K3, B24C10, B30U5,
B358124, B242E21, Human BAC library RPCI-11"

Query Match 9.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1654 AAGCACCAGGCTCAC 1668
|||||
Db 17 AAGCACCAGGCTCTC 3

RESULT 46
AX129291/c AX129291 19 bp DNA linear PAT 15-MAY-2001
LOCUS
DEFINITION Sequence 509 from Patent WO0130362.
ACCESSION AX129291
VERSION AX129291.1 GI:14135596
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 509 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source 1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cdk4 ribozyme binding site"

Query Match 9.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 GCTCCCACTCCTCC 1749
|||||
Db 16 GCTCCCACTCCTCC 2

RESULT 47
BD088226/c BD088226 19 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION A method of arraying genome clone.
ACCESSION BD088226
VERSION BD088226.1 GI:22633836
KEYWORDS JP 2001321190-A/470.
SOURCE Synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 470 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECs
OS Artificial Sequence
PN JP 2001321190-A/470
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
FT source 1. .19
/organism="Artificial Sequence".
FEATURES
source 1. .19
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 9.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAGGCGAAGCA 1658
|||||
Db 18 AGCAGAGGCGATGCA 4

RESULT 48
BD088234/c BD088234 19 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION A method of arraying genome clone.
ACCESSION BD088234
VERSION BD088234.1 GI:22633844
KEYWORDS JP 2001321190-A/478.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 478 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECs
OS Artificial Sequence
PN JP 2001321190-A/478
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
FT source 1. .19
/organism="Artificial Sequence".
FEATURES
source 1. .19
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 9.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAGGCGAAGCA 1658
|||||
Db 18 AGCAGAGGCGATGCA 4

RESULT 49
AB069135/c AB069135 19 bp DNA linear SYN 21-MAY-2003
LOCUS
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-stSG8994
at 1p36.
ACCESSION AB069135
VERSION AB069135.1 GI:15129939
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
```

Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,  
Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.  
and Soeda,E.

A BAC-based STS-content map spanning a 35-Mb region of human

chromosome 1p35-p36  
Genomics 74 (1), 55-70 (2001)

Medline  
21269192

REFERENCE  
2 (bases 1 to 19)

AUTHORS  
Horii,A.

TITLE  
Direct Submission

Submitted (04-AUG-2001) Akira Horii, Tohoku University School of  
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,  
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,  
Tel:81-22-717-8042, Fax:81-22-717-8047)

FEATURES  
Location/Qualifiers

source  
1..19

/organism="synthetic construct"

/mol\_type="genomic DNA"

/db\_xref="taxon:32630"

misc\_feature

1..19

/note="reverse primer for human STS sts-stSG994 at 1p36  
sts-stSG994 obtained from clones B369B23, B18717,  
B305A18, B372M12, B225E8, B45E6, B258116, B194113, Human  
BAC library RFCl-11"

Query Match 9.6%; Score 13.4; DB 1; Length 19;

Best Local Similarity 93.3%; Pred. No. 1.2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAAGCGAAGCA 1658

Db 18 AGCAGAAGCGATGCA 4  
|||||

RESULT 50

AB069137/c

LOCUS

AB069137 Synthetic construct DNA, reverse primer for human STS sts-stSG9952  
at 1p36.

DEFINITION

19 bp DNA linear SYN 21-MAY-2003

ACCESSION

AB069137

VERSION

AB069137.1 GI:15129941

KEYWORDS

synthetic construct

synthetic construct

artificial sequences.

SOURCE

ORGANISM

REFERENCE

AUTHORS

Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,  
Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,  
Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.  
and Soeda,E.

A BAC-based STS-content map spanning a 35-Mb region of human

chromosome 1p35-p36

Genomics 74 (1), 55-70 (2001)

Medline

21269192

REFERENCE

2 (bases 1 to 19)

AUTHORS

Horii,A.

TITLE

Direct Submission

Submitted (04-AUG-2001) Akira Horii, Tohoku University School of  
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,  
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,  
Tel:81-22-717-8042, Fax:81-22-717-8047)

FEATURES  
Location/Qualifiers

source  
1..19

/organism="synthetic construct"

/mol\_type="genomic DNA"

/db\_xref="taxon:32630"

Query Match 9.6%; Score 13.4; DB 1; Length 19;

Best Local Similarity 93.3%; Pred. No. 1.2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAAGCGAAGCA 1658

Db 18 AGCAGAAGCGATGCA 4  
|||||

RESULT 51

AR163797

LOCUS

AR163797

DEFINITION

Sequence 84 from patent US 6271029.

ACCESSION

AR163797

VERSION

AR163797.1 GI:16234547

KEYWORDS

Unknown.

SOURCE

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 20)

AUTHORS

Bennett,C.Frank. and Cowsert,L.M.

TITLE

Antisense inhibition of cytohesin-2 expression

JOURNAL

Patent: US 6271029-A 84 07-AUG-2001;

FEATURES

Location/Qualifiers

source  
1..20

/organism="unknown"

/mol\_type="unassigned DNA"

Query Match 9.6%; Score 13.4; DB 1; Length 20;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1685 TCTCTCCAGGTG 1699

Db 5 TCTCTCTCCGTG 19  
|||||

RESULT 52

AR233647/c

LOCUS

AR233647

DEFINITION

Sequence 9 from patent US 6458536.

ACCESSION

AR233647

VERSION

AR233647.1 GI:27276271

KEYWORDS

Unknown.

SOURCE

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 20)

AUTHORS

Gatti,R.A.

TITLE

Modified SSCP method using sequential electrophoresis of multiple

nucleic acid segments

JOURNAL

Patent: US 6458536-A 9 01-OCT-2002;

FEATURES

Location/Qualifiers

source  
1..20

/organism="unknown"

/mol\_type="genomic DNA"

Query Match 9.6%; Score 13.4; DB 1; Length 20;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1742 ACTCTCCCTATCCT 1756

Db 15 ACTCTCCCTCTCCT 1  
|||||

RESULT 53

AG3088/c

LOCUS

AG3088

DEFINITION

Sequence 15 from Patent WO9720197.

ACCESSION

AG3088

VERSION

AG3088.1 GI:3716952

18 bp DNA linear PAT 12-MAR-1998

```
KEYWORDS
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE 1
AUTHORS     Arguello,R., Avakian,H. and Madrigal,A.
TITLE       METHOD FOR IDENTIFYING AN UNKNOWN ALLELE
JOURNAL     Patent: WO 9720197-A 15 05-JUN-1997;
COMMENT     ANTHONY NOLAN BONE MARROW TRUS (GB)
FEATURES    Other publication AU 7703796 19970619.
            Location/Qualifiers
            source
              1. .18
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"
            Query Match      9.5%; Score 13.2; DB 1; Length 18;
            Best Local Similarity 83.3%; Pred. No. 1.2e+02;
            Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1732 TTGGCTCCCACTCTCTCC 1749
Db 18 TAGGCTCTCAACTGCTCC 1

RESULT 54
AR018185/c
LOCUS      AR018185
DEFINITION Sequence 12 from patent US 5780611.
ACCESSION AR018185
VERSION   AR018185.1 GI:3973788
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unassigned.
REFERENCE 1 (bases 1 to 18)
AUTHORS     Guntaka,R.V., Weber,K.Theodore., Kovacs,A. and Kandala,J.
TITLE       Oligomers which inhibit expression of collagen genes
JOURNAL     Patent: US 5780611-A 12 14-JUL-1998;
FEATURES    Location/Qualifiers
            source
              1. .18
                /organism="unknown"
                /mol_type="unassigned DNA"
            Query Match      9.5%; Score 13.2; DB 1; Length 18;
            Best Local Similarity 83.3%; Pred. No. 1.2e+02;
            Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1736 CTCCCACTCTCTCTAT 1753
Db 18 CTCCCCCTCTCTCTTT 1

RESULT 55
AR106914
LOCUS      AR106914
DEFINITION Sequence 75 from patent US 6107092.
ACCESSION AR106914
VERSION   AR106914.1 GI:12821444
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unassigned.
REFERENCE 1 (bases 1 to 18)
AUTHORS     Cowser,L.M., Bennett,C.Frank. and O'Malley,B.W.
TITLE       Antisense modulation of SRA expression
JOURNAL     Patent: US 6107092-A 75 22-AUG-2000;
FEATURES    Location/Qualifiers
            source
              1. .18
                /organism="unknown"
                /mol_type="unassigned DNA"
            Query Match      9.5%; Score 13.2; DB 1; Length 18;

Qy 1732 TTGGCTCCCACTCTCTCC 1749
Db 18 TAGGCTCTCAACTGCTCC 1

RESULT 56
AR173918/c
LOCUS      AR173918
DEFINITION Sequence 116 from patent US 6306606.
ACCESSION AR173918
VERSION   AR173918.1 GI:17914238
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unassigned.
REFERENCE 1 (bases 1 to 18)
AUTHORS     Weber,M.J., Wyatt,J. and Cowser,L.M.
TITLE       Antisense modulation of MP-1 expression
JOURNAL     Patent: US 6306606-A 116 23-OCT-2001;
FEATURES    Location/Qualifiers
            source
              1. .18
                /organism="unknown"
                /mol_type="unassigned DNA"
            Query Match      9.5%; Score 13.2; DB 1; Length 18;
            Best Local Similarity 83.3%; Pred. No. 1.2e+02;
            Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1664 CTCACAGCTGGACCCCTG 1681
Db 18 CTCAGTCGAGCAACCCCTG 1

RESULT 57
AR268665/c
LOCUS      AR268665
DEFINITION Sequence 15 from patent US 650614.
ACCESSION AR268665
VERSION   AR268665.1 GI:29699280
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unassigned.
REFERENCE 1 (bases 1 to 18)
AUTHORS     Arguello,R., Avakian,H. and Madrigal,A.
TITLE       Method for identifying an unknown allele
JOURNAL     Patent: US 650614-A 15 31-DEC-2002;
FEATURES    Location/Qualifiers
            source
              1. .18
                /organism="unknown"
                /mol_type="genomic DNA"
            Query Match      9.5%; Score 13.2; DB 1; Length 18;
            Best Local Similarity 83.3%; Pred. No. 1.2e+02;
            Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1732 TTGGCTCCCACTCTCTCC 1749
Db 18 TAGGCTCTCAACTGCTCC 1

RESULT 58
BD089837/c
LOCUS      BD089837
DEFINITION A method of arraying genome clone.
ACCESSION BD089837
VERSION   BD089837.1 GI:22635447
KEYWORDS   JP 2001321190-A/2081.
SOURCE      synthetic construct
ORGANISM    synthetic construct
```

```

artificial sequences.
1 (bases 1 to 18)
A method of arraying genome clone
Soeda,E.
TITLE
JOURNAL
COMMENT
OS Artificial Sequence
PN JP 2001321190-A/2081
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
CC Description of Artificial Sequence:Synthetic DNA FH Key
FT source
FT 1. .18
/organism='Artificial Sequence'.
FEATURES
source
1. .18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match
Best Local Similarity 9.5%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1720 CGGAGATGGAGTTGGCT 1737
Db 18 CTGAGATGGAGTTGGCT 1
RESULT 59
AB068204/c
LOCUS
DEFINITION
Synthetic construct DNA, forward primer for human STS sts-DIS2666
at lp36.
ACCESSION
AB068204
VERSION
AB068204.1 GI:15129008
KEYWORDS
synthetic construct
synthetic construct
artificial sequences.
ORGANISM
Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
and Soeda,E.
TITLE
A BAC-based STS-content map spanning a 35-Mb region of human
chromosome 1p35-p36
JOURNAL
Genomics 74 (1), 55-70 (2001)
MEDLINE
21269192
PUBMED
11374902
REFERENCE
2 (bases 1 to 18)
AUTHORS
Horii,A.
TITLE
Direct Submission
JOURNAL
Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-Ku, Sendai,
Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
misc_feature
1. .18
/note="forward primer for human STS sts-DIS2666 at lp36
sts-DIS2666 obtained from clones B279H/6, B332E8,
B156C13, B370L6, B310A20, B359J17, B45N15, B63P6, Human
BAC library RPCI-11"
artificial sequences.
9.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1720 CGGAGATGGAGTTGGCT 1737
Db 18 CTGAGATGGAGTTGGCT 1
RESULT 60
AR011803/c
LOCUS
DEFINITION
Sequence 16 from patent US 5763172.
ACCESSION
AR011803
VERSION
AR011803.1 GI:3969793
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Magda,D., Sessler,J.L., Wright,M., Miller,R.A. and Dow,W.C.
TITLE
Method of phosphate ester hydrolysis
JOURNAL
Patent: US 5763172-A 16 09-JUN-1998;
FEATURES
Location/Qualifiers
1. .19
source
/organism="unknown"
/mol_type="unassigned DNA"
Query Match
Best Local Similarity 9.5%; Score 13.2; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1655 AGCACCGAGCTCACAGCT 1672
Db 18 AACACCGGCTCACAGAT 1
RESULT 61
AR361501
LOCUS
DEFINITION
Sequence 27 from patent US 6599728.
ACCESSION
AR361501
VERSION
AR361501.1 GI:33769349
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Morin,G.B., Funk,W.D. and Piatyszek,M.A.
TITLE
Second mammalian tankyrase
JOURNAL
Patent: US 6599728-A 27 29-JUL-2003;
FEATURES
Location/Qualifiers
1. .19
source
/organism="unknown"
/mol_type="genomic DNA"
Query Match
Best Local Similarity 9.5%; Score 13.2; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1715 GAGTACGAGATGGAGAT 1732
Db 1 GAGCACAGAGATGGAGGT 18
RESULT 62
A70767/c
LOCUS
DEFINITION
Sequence 88 from Patent WO9813490.
ACCESSION
A70767
VERSION
A70767.1 GI:4774770
KEYWORDS
unidentified
SOURCE

```

```
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS Ophoff,R.A., Terwindt,G.M., Ferrari,M.D. and Frants,R.R.
TITLE A gene related to migraine in man
JOURNAL Patent: WO 9813490-A 88 02-APR-1998;
OPHOFF ROEL ANDRE (NL)
FEATURES
source
location/Qualifiers
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1689 CTCGAGCGTGGTGAAGT 1706
Db 20 CACCAGGGTGGCGGAAGT 3

RESULT 63
A79251/c
LOCUS A79251 20 bp DNA linear PAT 20-OCT-1999
DEFINITION Sequence 88 from Patent EP0834561.
ACCESSION A79251
VERSION A79251.1 GI:6092296
KEYWORDS
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS
TITLE A GENE RELATED TO MIGRAINE IN MAN
JOURNAL Patent: EP 0834561-A 88 08-APR-1998;
UNIV LEIDEN (NL)
FEATURES
source
location/Qualifiers
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1689 CTCGAGCGTGGTGAAGT 1706
Db 20 CACCAGGGTGGCGGAAGT 3

RESULT 64
AR163916
LOCUS AR163916 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 114 from patent US 6271030.
ACCESSION AR163916
VERSION AR163916.1 GI:16234741
KEYWORDS
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP beta expression
JOURNAL Patent: US 6271030-A 114 07-AUG-2001;
FEATURES
source
location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;

ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS Ophoff,R.A., Terwindt,G.M., Ferrari,M.D. and Frants,R.R.
TITLE A gene related to migraine in man
JOURNAL Patent: WO 9813490-A 88 02-APR-1998;
OPHOFF ROEL ANDRE (NL)
FEATURES
source
location/Qualifiers
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1689 CTCGAGCGTGGTGAAGT 1706
Db 20 CACCAGGGTGGCGGAAGT 3

RESULT 65
E08376
LOCUS E08376 20 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer for enterovirus complementary to the downstream gene coding
partially Vp4 and Vp2 proteins.
ACCESSION E08376
VERSION E08376.1 GI:2176493
KEYWORDS JP 1994311900-A/2.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS Marisawa,T., Ishiko,H., Sakae,K., Ishihara,Y., Takeda,N.,
Miyamura,K. and Inoue,S.
TITLE DETECTION OF ENTEROVIRUS AND DISCRIMINATION OF THE SAME
JOURNAL Patent: JP 1994311900-A 2 08-NOV-1994;
MITSUBISHI YUKA B C L.KK, INOUE SAKAE
COMMENT OS None
OC Artificial sequences.
PN JP 1994311900-A/2
PD 08-NOV-1994
PF 28-APR-1993 JP 1993102254
PI NARISAWA TADASHI, ISHIKO HIROAKI, SAKAE KENJI, PI ISHIHARA
YUICHI,
PI TAKEDA NAOKAZU, MIYAMURA KIKUKO, INOUE SAKAE
PC C12Q1/70//C12N15/41;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FH
FT
FT source 1..20
/organism='Artificial sequences'.
FEATURES
source
location/Qualifiers
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1696 GTGGTGAAGTTGGTTA 1713
Db 3 GTGGTGAAGTTGCCTGA 20

RESULT 66
AR220154/c
LOCUS AR220154 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 19 from patent US 6423543.
ACCESSION AR220154
VERSION AR220154.1 GI:23324597
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Marcotte,P.A. and Cowseert,L.M.
TITLE Antisense modulation of hepsin expression
JOURNAL Patent: US 6423543-A 19 23-JUL-2002;
FEATURES
source
location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"
```

```

Query Match          9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGAACCTG 1681
    ||||| ||||| |||||
Db 19 CTCAC TGGGGGACCTG 2

RESULT 67
AR315612
LOCUS AR315612
DEFINITION Sequence 6149 from patent US 6559294.
ACCESSION AR315612
VERSION AR315612
KEYWORDS AR315612.1 GI:31709038
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
TITLE Sankaran,B. and Fletcher,L.D.
JOURNAL Chlamydia pneumoniae polynucleotides and uses thereof
FEATURES Patent: US 6559294-A 6149 06-MAY-2003;
Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match          9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1744 TCCTCCTATCTCTAAGG 1761
    ||||| ||||| |||||
Db 3 TCCTCTCTACCTAAAGG 20

RESULT 68
AX180379
LOCUS AX180379
DEFINITION Sequence 16 from Patent WO0146260.
ACCESSION AX180379
VERSION AX180379.1 GI:15132316
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Starling,G.C. and Finger,J.
TITLE Novel immunoglobulin superfamily members apex-1, apex-2 and apex-3
JOURNAL and uses thereof
FEATURES Patent: WO 0146260-A 16 28-JUN-2001;
Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="JNF14 PRIMER"

Query Match          9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCACAGCTGAACCC 1679
    ||||| ||||| |||||
Db 2 GGCTCACAGCTGAATCC 19

RESULT 69
AX268920/c
LOCUS AX268920
DEFINITION Sequence 1 from Patent WO0175165.
ACCESSION AX268920
VERSION AX268920.1 GI:16541939
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Mcconlogue,L.C., Games,K.D., Yednock,T.A., Hua,T., Messersmith,E.
and Bard,F.
TITLE Screening markers and methods for neurodegenerative disorders
JOURNAL Patent: WO 0175165-A 1 11-OCT-2001;
FEATURES Elan Pharmaceuticals, Inc. (US)
Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="forward primer MoGapdh251P"

Query Match          9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1723 AGATGGAGATTGGCTCCC 1740
    ||||| ||||| |||||
Db 19 AGATGGTGTGGCTTCC 2

RESULT 70
AX287952
LOCUS AX287952
DEFINITION Sequence 338 from Patent WO0179481.
ACCESSION AX287952
VERSION AX287952.1 GI:17049698
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Ladner,R.C., Cohen,E.H., Nastri,H.G., Rookey,K.L. and Hoet,R.
TITLE Novel methods of constructing libraries of genetic packages that
collectively display the members of a diverse family of peptides,
polypeptides or proteins
JOURNAL Patent: WO 0179481-A 338 25-OCT-2001;
Dyax Corp. (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

Query Match          9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGGCTC 1738
    ||||| ||||| |||||
Db 3 GAAGATGGAGACTGGGTC 20

RESULT 71
BD003481/c
LOCUS BD003481
DEFINITION A gene related to migraine in man.
ACCESSION BD003481
VERSION BD003481.1 GI:18631442
KEYWORDS JP 2001500743-A/50.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE 1 (bases 1 to 20)  
AUTHORS Prantz,R.R.I.E., Ferrari,M.D., Teruvinto,H.M. and Opuhofu,R.A.  
TITLE A gene related to migraine in man  
JOURNAL Patent: JP 2001500743-A 50 23-JAN-2001;  
RYUKUS UNIVERSITYTAT TO RAIDEN  
COMMENT OS Homo sapiens (human)  
PN JP 2001500743-A/50  
PD 23-JAN-2001  
PF 26-SEP-1997 JP 1998515527  
PI RENE ROBERT ISAAC ERIK PRANTZ, MICHEL DOMINIQUE FERRARI, PI  
HISERA MARRY TERUVINTO, RURU ANDRE OPUHOFU  
PC C12N15/09,A01K67/027,C07K14/435,C07K16/18,C12N1/15,C12N1/19,  
C12N1/21,  
PC C12N5/10,C12Q1/02,C12Q1/68,C12N15/00,C12N5/00 CC  
FH Key Location/Qualifiers  
FT primer bind (1)..(20).  
  
FEATURES  
source  
1..20  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
  
Query Match 9.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1689 CTCACGGCTGCTGGAAGT 1706  
||||| ||||| |||||  
Db 20 CACCAGGTTGCGGGAAGT 3  
  
RESULT 72  
BD011678  
LOCUS 20 bp DNA linear PAT 02-AUG-2002  
DEFINITION Method for detecting Pseudomonas bacteria.  
ACCESSION BD011678  
VERSION BD011678.1 GI:22091867  
KEYWORDS JP 2001190279-A/4.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Sawai,H. and Nakamura,T.  
TITLE Method for detecting Pseudomonas bacteria  
JOURNAL Patent: JP 2001190279-A 4 17-JUL-2001;  
MITSUBISHI HEAVY IND LTD  
COMMENT OS Artificial sequence  
PN JP 2001190279-A/4  
PD 17-JUL-2001  
PF 13-JAN-2000 JP 2000004160  
PI HIDEKI SAWAI,TSUYOSHI NAKAMURA  
PC C12N15/09,C12Q1/04,C12Q1/68//((C12N15/09,C12R1:40),(C12Q1/04,  
C12R1:40),  
PC C12N15/00,(C12N15/00,C12R1:40)  
CC primer  
FH Key Location/Qualifiers  
source  
1..20  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
  
Query Match 9.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1657 CACCAGGCTACAGCTGG 1674  
||||| ||||| |||||  
Db 2 CACCAGTTTCACTGCTGG 19  
  
RESULT 73  
BD011678  
LOCUS 20 bp DNA linear PAT 02-AUG-2002  
DEFINITION Method for detecting Pseudomonas bacteria.  
ACCESSION BD011678  
VERSION BD011678.1 GI:22091867  
KEYWORDS JP 2001190279-A/6.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Sawai,H. and Nakamura,T.  
TITLE Method for detecting Pseudomonas bacteria  
JOURNAL Patent: JP 2001190279-A 6 17-JUL-2001;  
MITSUBISHI HEAVY IND LTD  
COMMENT OS Artificial sequence  
PN JP 2001190279-A/6  
PD 17-JUL-2001  
PF 13-JAN-2000 JP 2000004160  
PI HIDEKI SAWAI,TSUYOSHI NAKAMURA  
PC C12N15/09,C12Q1/04,C12Q1/68//((C12N15/09,C12R1:40),(C12Q1/04,  
C12R1:40),  
PC C12N15/00,(C12N15/00,C12R1:40)  
CC primer  
FH Key Location/Qualifiers  
source  
1..20  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
  
Query Match 9.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1657 CACCAGGCTACAGCTGG 1674  
||||| ||||| |||||  
Db 2 CACCAGTTTCACTGCTGG 19  
  
RESULT 73

BD011679  
LOCUS 20 bp DNA linear PAT 02-AUG-2002  
DEFINITION Method for detecting Pseudomonas bacteria.  
ACCESSION BD011679  
VERSION BD011679.1 GI:22091868  
KEYWORDS JP 2001190279-A/5.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Sawai,H. and Nakamura,T.  
TITLE Method for detecting Pseudomonas bacteria  
JOURNAL Patent: JP 2001190279-A 5 17-JUL-2001;  
MITSUBISHI HEAVY IND LTD  
COMMENT OS Artificial sequence  
PN JP 2001190279-A/5  
PD 17-JUL-2001  
PF 13-JAN-2000 JP 2000004160  
PI HIDEKI SAWAI,TSUYOSHI NAKAMURA  
PC C12N15/09,C12Q1/04,C12Q1/68//((C12N15/09,C12R1:40),(C12Q1/04,  
C12R1:40),  
PC C12N15/00,(C12N15/00,C12R1:40)  
CC primer  
FH Key Location/Qualifiers  
source  
1..20  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
  
Query Match 9.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1657 CACCAGGCTACAGCTGG 1674  
||||| ||||| |||||  
Db 2 CACCAGTTTCACTGCTGG 19  
  
RESULT 74  
BD011680  
LOCUS 20 bp DNA linear PAT 02-AUG-2002  
DEFINITION Method for detecting Pseudomonas bacteria.  
ACCESSION BD011680  
VERSION BD011680.1 GI:22091869  
KEYWORDS JP 2001190279-A/6.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Sawai,H. and Nakamura,T.  
TITLE Method for detecting Pseudomonas bacteria  
JOURNAL Patent: JP 2001190279-A 6 17-JUL-2001;  
MITSUBISHI HEAVY IND LTD  
COMMENT OS Artificial sequence  
PN JP 2001190279-A/6  
PD 17-JUL-2001  
PF 13-JAN-2000 JP 2000004160  
PI HIDEKI SAWAI,TSUYOSHI NAKAMURA  
PC C12N15/09,C12Q1/04,C12Q1/68//((C12N15/09,C12R1:40),(C12Q1/04,  
C12R1:40),  
PC C12N15/00,(C12N15/00,C12R1:40)  
CC primer  
FH Key Location/Qualifiers  
source  
1..20  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
  
Query Match 9.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1657 CACCAGGCTACAGCTGG 1674  
||||| ||||| |||||  
Db 2 CACCAGTTTCACTGCTGG 19  
  
RESULT 74  
BD011680  
LOCUS 20 bp DNA linear PAT 02-AUG-2002  
DEFINITION Method for detecting Pseudomonas bacteria.  
ACCESSION BD011680  
VERSION BD011680.1 GI:22091869  
KEYWORDS JP 2001190279-A/6.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Sawai,H. and Nakamura,T.  
TITLE Method for detecting Pseudomonas bacteria  
JOURNAL Patent: JP 2001190279-A 6 17-JUL-2001;  
MITSUBISHI HEAVY IND LTD  
COMMENT OS Artificial sequence  
PN JP 2001190279-A/6  
PD 17-JUL-2001  
PF 13-JAN-2000 JP 2000004160  
PI HIDEKI SAWAI,TSUYOSHI NAKAMURA  
PC C12N15/09,C12Q1/04,C12Q1/68//((C12N15/09,C12R1:40),(C12Q1/04,  
C12R1:40),  
PC C12N15/00,(C12N15/00,C12R1:40)  
CC primer  
FH Key Location/Qualifiers  
source  
1..20  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
  
Query Match 9.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1657 CACCAGGCTACAGCTGG 1674  
||||| ||||| |||||  
Db 2 CACCAGTTTCACTGCTGG 19  
  
RESULT 74

```

QY 1657 CACCAAGGCTCACAGCTGG 1674
      ||||| ||||| ||||| |||||
Db 2 CACCAAGTTCAGTCTGG 19

RESULT 75
AX710950
LOCUS AX710950 16 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 250 from Patent EP1288296.
ACCESSION AX710950
VERSION AX710950.1 GI:29787331
KEYWORDS
SOURCE Human herpesvirus 5
ORGANISM Human herpesvirus 5
REFERENCE
AUTHORS Macejak,D.G. and Mamone,J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 250 03-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
Location/Qualifiers
1..16
/organism="Human herpesvirus 5"
/mol_type="unassigned RNA"
/db_xref="taxon:10359"

Query Match 9.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1679 CTGGTGCTCTCCCTCCAG 1694
      ||||| ||||| ||||| |||||
Db 1 CTGGGTGCACCCCCAG 16

RESULT 77
BD001520
LOCUS BD001520 16 bp RNA linear PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001520
VERSION BD001520.1 GI:18626079
KEYWORDS JP 2000342286-A/251.
SOURCE synthetic construct
ORGANISM RIBOZYME PHARMACEUTICALS INC
REFERENCE
AUTHORS Draper,K.G., Mcewigen,J.A., Holecsek,J.J., Dudycz,L.W.,
Holecsek,J.J. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342286-A 251 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Artificial Sequence
PN JP 2000342286-A/251
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132651
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PR
KENNETH G DRAPER,LEC W DADYKIZ,JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK,ANTHONY J MAMONE
PC C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
PC A61K39/135,
PC A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
PC A61P1/16,
PC A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12Q1/68, PC
(C12N15/09,C12N1/93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
C12R1:93)
CC Key Location/Qualifiers
FH source 1..16
FT /organism="Artificial Sequence".
FEATURES
source
Location/Qualifiers
1..16
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match 9.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1679 CTGGTGCTCTCCCTCCAG 1694
      ||||| ||||| ||||| |||||
Db 1 CTGGGTGCACCCCCAG 16

RESULT 77
BD001520
LOCUS BD001520 16 bp RNA linear PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001520
VERSION BD001520.1 GI:18626079
KEYWORDS JP 2000342286-A/251.
SOURCE synthetic construct
ORGANISM RIBOZYME PHARMACEUTICALS INC
REFERENCE
AUTHORS Draper,K.G., Dadykiz,L.W., Macswigen,J.A., Maysejak,D.G.,
Holecsek,J.J. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342286-A 251 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Artificial Sequence
PN JP 2000342286-A/251
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132651
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PR
KENNETH G DRAPER,LEC W DADYKIZ,JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK,ANTHONY J MAMONE
PC C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
PC A61K39/135,
PC A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
PC A61P1/16,
PC A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12Q1/68, PC
(C12N15/09,C12N1/93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
C12R1:93)
CC Key Location/Qualifiers
FH source 1..16
FT /organism="Artificial Sequence".
FEATURES
source
Location/Qualifiers
1..16
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

```



```
source 1. .16
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match 9.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1679 CTGGTGCTCTCCAG 1694
||||| |||||
Db 1 CTGGTGTCACCCCGAG 16

RESULT 78
AR011799/c
LOCUS AR011799 17 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 12 from patent US 5763172.
ACCESSION AR011799
VERSION AR011799.1 GI:3969789
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Magda,D., Sessler,J.L., Wright,M., Miller,R.A. and Dow,W.C.
TITLE Method of phosphate ester hydrolysis
JOURNAL Patent: US 5763172-A 12 09-JUN-1998;
FEATURES
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 AGCACCGGCTCAG 1670
||||| |||||
Db 16 AACACCGGCTCAG 1

RESULT 79
AR192421/c
LOCUS AR192421 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7909 from patent US 6346398.
ACCESSION AR192421
VERSION AR192421.1 GI:20238386
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 7909 12-FEB-2002;
FEATURES
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAGCGCACCA 1661
||||| |||||
Db 17 CAGAAGCCAGCGCCA 2

RESULT 80
AR326290/c
LOCUS AR326290 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1307 from Patent WO0188124.
ACCESSION AR326290
VERSION AR326290.1 GI:21526353
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
Randi,A.M.
```

---

```
LOCUS AR326290 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3692 from patent US 6566127.
ACCESSION AR326290
VERSION AR326290.1 GI:33712098
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3692 20-MAY-2003;
FEATURES
source 1. .17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAAGCGCACCA 1661
||||| |||||
Db 17 CAGAAGCCAGCGCCA 2

RESULT 81
AX421994/c
LOCUS AX421994 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 330 from Patent WO0188124.
ACCESSION AX421994
VERSION AX421994.1 GI:21525376
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 330 22-NOV-2001; GLAXO GROUP LIMITED (GB)
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1674 GAACCCGTGCTCTCC 1689
||||| |||||
Db 17 GAACCCGTGAGTCTCC 2

RESULT 82
AX422971/c
LOCUS AX422971 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1307 from Patent WO0188124.
ACCESSION AX422971
VERSION AX422971.1 GI:21526353
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
Randi,A.M.
```

```

TITLE      Method and reagent for the inhibition of erg
JOURNAL    Patent: WO 0188124-A 1307 22-NOV-2001; GLAXO GROUP LIMITED (GB)
FEATURES
  source
    1..17
      /organism="Homo sapiens"
      /mol_type="unassigned RNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 9.2%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1674 GAACCTCGTGCTCC 1689
Db 16 GAACCTCGAGTCTCC 1

RESULT 83
LOCUS      AX673768 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 2213 from Patent WO03004526.
ACCESSION  AX673768
VERSION     AX673768.1 GI:29332116
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijinder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Molecular Engines Laboratories (FR)
  PATENT    Patent: WO 03004526-A 2213 16-JAN-2003;
            Molecular Engines Laboratories (FR)
  FEATURES
    source
      1..17
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
Best Local Similarity 9.2%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1693 ACCGTGTGGAAGTTG 1708
Db 2 ATCGTGTGGAAGTTG 17

RESULT 84
LOCUS      AX724290/c 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1977 from Patent WO03025176.
ACCESSION  AX724290
VERSION     AX724290.1 GI:30503633
KEYWORDS    Mus musculus (house mouse)
SOURCE      Mus musculus
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijinder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 1977 27-MAR-2003;
            Molecular Engines Laboratories (FR)
  FEATURES
    source
      1..17
        /organism="Mus musculus"
        /mol_type="unassigned DNA"

/db_xref="taxon:10090"

Query Match
Best Local Similarity 9.2%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1717 GTACGGAGATGGAGAT 1732
Db 17 GTAGGGAGGTGGAGAT 2

RESULT 85
LOCUS      AX753715 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 62 from Patent WO03037931.
ACCESSION  AX753715
VERSION     AX753715.1 GI:32166412
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M. and Paan,T.
  TITLE     Human angiotensin-like protein 1
  JOURNAL   Patent: WO 03037331-A 62 08-MAY-2003;
            Amersham Biosciences SV Corp. (US)
  FEATURES
    source
      1..17
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
Best Local Similarity 9.2%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1716 AGTACGGAGATGGAGA 1731
Db 2 AATACGGTGTGGAGA 17

RESULT 86
LOCUS      AX753716 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 63 from Patent WO03037931.
ACCESSION  AX753716
VERSION     AX753716.1 GI:32166413
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M. and Paan,T.
  TITLE     Human angiotensin-like protein 1
  JOURNAL   Patent: WO 03037331-A 63 08-MAY-2003;
            Amersham Biosciences SV Corp. (US)
  FEATURES
    source
      1..17
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
Best Local Similarity 9.2%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1716 AGTACGGAGATGGAGA 1731
Db 1 AATACGGTGTGGAGA 16
```

```

RESULT 87
AX805118
LOCUS          AX805118          17 bp      DNA          linear          PAT 25-NOV-2003
DEFINITION     Sequence 1286 from Patent WO03060160.
ACCESSION      AX805118
VERSION        AX805118.1  GI:38522259
KEYWORDS
SOURCE
ORGANISM       Oreochromis niloticus (Nile tilapia)
               Oreochromis niloticus
               Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
               Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
               Labroidae; Cichlidae; Oreochromis.
REFERENCE      1
AUTHORS        Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,P.
TITLE          Verification of food origin based on nucleic acid pattern
               recognition
JOURNAL        Genomaz ASA (NO)
FEATURES       source
               1. .17
               /organism="Oreochromis niloticus"
               /mol_type="unassigned DNA"
               /db_xref="taxon:8128"

Query Match          9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1677 CCTGGTGTCTCCTCC 1692
||||| ||||| |||||
Db 1 CCTGGTGTCTCCTCC 16

RESULT 88
BD104946/c
LOCUS          BD104946          17 bp      DNA          linear          PAT 27-AUG-2002
DEFINITION     Kit and method for determining HLA type.
ACCESSION      BD104946
VERSION        BD104946.1  GI:22650520
KEYWORDS       WO 0192572-A/1050.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 17)
AUTHORS        Inoko,H.; Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
               Nishida,M.
TITLE          Kit and method for determining HLA type
JOURNAL        Patent: WO 0192572-A 1050 06-DEC-2001;
               NISSHINO INDUSTRIES INC.SYSTEM RESEARCH INC.HIDETOSHI INOKO, TAEKO
               KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
               NISHIDA
COMMENT        OS Artificial Sequence
               PN WO 0192572-A/1050
               PD 06-DEC-2001
               PE 01-JUN-2001 WO 2001JP004662
               PR 01-JUN-2000 JP ODP 164798
               PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
               MATSUMURA,
               PI SHOGO MORIYA,MICHIO NISHIDA
               PC C1201/68,C12M1/00,C12N15/09,G01N33/53
               CC Description of Artificial Sequence:capture
               FH key Location/Qualifiers
               FT source 1. .17
               /organism='Artificial Sequence'.
               /mol_type='genomic DNA'
               /db_xref='taxon:32630'

FEATURES       source
               1. .17
               Location/Qualifiers

Query Match          9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;

RESULT 89
AR011802/c
LOCUS          AR011802          18 bp      DNA          linear          PAT 04-DEC-1998
DEFINITION     Sequence 15 from patent US 5763172.
ACCESSION      AR011802
VERSION        AR011802.1  GI:3969792
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Magda,D., Sessler,J.L., Wright,M., Miller,R.A. and Dow,W.C.
TITLE          Method of phosphate ester hydrolysis
JOURNAL        Patent: US 5763172-A 15 09-JUN-1998;
FEATURES       Location/Qualifiers
               source 1. .18
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match          9.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCAG 1670
||||| ||||| |||||
Db 17 AACACCGGCTCAG 2

RESULT 90
AR051200
LOCUS          AR051200          18 bp      DNA          linear          PAT 29-SEP-1999
DEFINITION     Sequence 7 from patent US 5830656.
ACCESSION      AR051200
VERSION        AR051200.1  GI:5974564
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Milo,G.E. Jr., Casto,B.C., Li,D., Chen,J., Shuler,C.F.,
               Ribovich,M.L., Noyes,I., Sun,X.Li. and Theil,K.S.
TITLE          Detecting the expression of the catrl gene in squamous cell
               carcinoma
JOURNAL        Patent: US 5830656-A 7 03-NOV-1998;
FEATURES       Location/Qualifiers
               source 1. .18
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match          9.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1691 CCAGCGTGGTGAAGT 1706
||||| ||||| |||||
Db 2 CCAGTGTGGTGAAT 17

RESULT 91
AR106948
LOCUS          AR106948          18 bp      DNA          linear          PAT 14-FEB-2001
DEFINITION     Sequence 109 from patent US 6107092.
ACCESSION      AR106948
VERSION        AR106948.1  GI:12821478
KEYWORDS
SOURCE         Unknown.

```

```
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 18)
AUTHORS Cowsett,L.M., Bennett,C.Frank, and O'Malley,B.W.
TITLE Antisense modulation of SRA expression
JOURNAL Patent: US 6107092-A 109 22-AUG-2000;
FEATURES
  Location/Qualifiers
    source
      1..18
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match
  Best Local Similarity 9.2%; Score 12.8; DB 1; Length 18;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1670 GCTGGAACCTGGTGT 1695
Db 2 GCTGGAAGCTGGTAT 17

RESULT 92
LOCUS AX106981 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 142 from patent US 6107092.
ACCESSION AR106981
VERSION AR106981.1 GI:12821511
KEYWORDS
SOURCE
  ORGANISM
    Unknown.
  Unclassified.
REFERENCE
  1 (bases 1 to 18)
AUTHORS Cowsett,L.M., Bennett,C.Frank, and O'Malley,B.W.
TITLE Antisense modulation of SRA expression
JOURNAL Patent: US 6107092-A 142 22-AUG-2000;
FEATURES
  Location/Qualifiers
    source
      1..18
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match
  Best Local Similarity 9.2%; Score 12.8; DB 1; Length 18;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1668 CAGCTGGAACCTGGT 1683
Db 2 CTGCTGGAAGCTGGT 17

RESULT 93
LOCUS AX129110 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 328 from Patent WO0130362.
ACCESSION AX129110
VERSION AX129110.1 GI:14135415
KEYWORDS
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
  diseases
JOURNAL Patent: WO 0130362-A 328 03-MAY-2001;
FEATURES
  IMMUSON, INC. (US)
  Location/Qualifiers
    source
      1..19
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
        /note="cdk3 ribozyme binding site"
Query Match
  Best Local Similarity 9.2%; Score 12.8; DB 1; Length 19;
  Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 18)
AUTHORS Cowsett,L.M., Bennett,C.Frank, and O'Malley,B.W.
TITLE Antisense modulation of SRA expression
JOURNAL Patent: US 6107092-A 109 22-AUG-2000;
FEATURES
  Location/Qualifiers
    source
      1..18
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match
  Best Local Similarity 9.2%; Score 12.8; DB 1; Length 18;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1670 GCTGGAACCTGGTGT 1695
Db 2 GCTGGAAGCTGGTAT 17

RESULT 92
LOCUS AX106981 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 142 from patent US 6107092.
ACCESSION AR106981
VERSION AR106981.1 GI:12821511
KEYWORDS
SOURCE
  ORGANISM
    Unknown.
  Unclassified.
REFERENCE
  1 (bases 1 to 18)
AUTHORS Cowsett,L.M., Bennett,C.Frank, and O'Malley,B.W.
TITLE Antisense modulation of SRA expression
JOURNAL Patent: US 6107092-A 142 22-AUG-2000;
FEATURES
  Location/Qualifiers
    source
      1..18
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match
  Best Local Similarity 9.2%; Score 12.8; DB 1; Length 18;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1668 CAGCTGGAACCTGGT 1683
Db 2 CTGCTGGAAGCTGGT 17

RESULT 93
LOCUS AX129110 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 328 from Patent WO0130362.
ACCESSION AX129110
VERSION AX129110.1 GI:14135415
KEYWORDS
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
  diseases
JOURNAL Patent: WO 0130362-A 328 03-MAY-2001;
FEATURES
  IMMUSON, INC. (US)
  Location/Qualifiers
    source
      1..19
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
        /note="cdk3 ribozyme binding site"
Query Match
  Best Local Similarity 9.2%; Score 12.6; DB 1; Length 19;
  Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1657 CACCAGGCTCAGAGT 1672
Db 1 CCCCAGGCTCAGAGT 16

RESULT 94
LOCUS DOGCTRB 19 bp DNA linear STS 11-APR-1996
DEFINITION Canis familiaris chymotrypsinogen (CTRB) STS DNA, primer, sequence
  tagged site.
ACCESSION L77467
VERSION L77467.1 GI:1261683
KEYWORDS STS; PCR identification; PCR primer; chymotrypsinogen; sequence
  tagged site; universal mammalian STS.
SOURCE
  Canis familiaris (dog)
  ORGANISM
    Canis familiaris
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
  1 (bases 1 to 19)
AUTHORS Venter,P.J., Brouillette,J.A., Yuzbasiyan-Gurkan,V. and Brewer,G.J.
TITLE Gene-specific universal mammalian sequence-tagged sites:
  application to the canine genome
JOURNAL Unpublished (1996)
COMMENT Original source text: Canis familiaris DNA.
  Gene-specific universal mammalian sequence-tagged site for CTRB.
  Primer for the 3' end is in exon 6. Human product is 1000 bp.
  Canine kproduct is 1000 bp. PCR conditions: 1 min, 94 C, 2 min, 57
  C, 5 min, 72 C, 35 cycles (hot start).
FEATURES
  Location/Qualifiers
    source
      1..19
        /organism="Canis familiaris"
        /mol_type="genomic DNA"
        /db_xref="taxon:9615"
    primer_bind
      1..19
        /note="3PCR primer binding site"
        /evidence=experimental
    STS
      1..19
        Query Match
          Best Local Similarity 9.2%; Score 12.8; DB 1; Length 19;
          Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1680 TGGGTCTCTCTCCAC 1695
Db 17 TGGGTCTCTCTCTCTCT 2

RESULT 95
LOCUS AR053162 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 68 from patent US 5834183.
ACCESSION AR053162
VERSION AR053162.1 GI:5378024
KEYWORDS
  Unknown.
  SOURCE
    Unknown.
  ORGANISM
    Unknown.
  Unclassified.
REFERENCE
  1 (bases 1 to 19)
AUTHORS Orr,H.T., Ranum,P.W., Chung,M.-Y. and Zoghbi,H.Y.
TITLE Gene sequence for spinocerebellar ataxia type 1 and method for
  diagnosis
JOURNAL Patent: US 5834133-A 68 10-NOV-1998;
FEATURES
  Location/Qualifiers
    source
      1..19
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match
  Best Local Similarity 9.1%; Score 12.6; DB 1; Length 19;
  Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```

QY 1657 CACCAAGCTCACAGCTGGA 1675
||||| ||||| |||||
1 CACCAAGCTCCTGATGGA 19

RESULT 96
E08539
LOCUS 19 bp DNA linear PAT 29-SEP-1997
DEFINITION PCR primer to detect Aspergillus sp. and Penicillium sp. rDNA.
ACCESSION E08539
VERSION E08539.1 GI:2176654
KEYWORDS JP 1994339400-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Makimura,K., Murayama,S. and Yamaguchi,H.
TITLE PRIMER FOR PATHOGENIC MOULD GENE AMPLIFICATION
JOURNAL Patent: JP 1994339400-A 2 13-DEC-1994;
YAMAGUCHI HIDEYO
COMMENT OS None
OC Artificial sequences.
PN JP 1994339400-A/2
PD 13-DEC-1994
PF 01-JUN-1993 JP 1993130778
PI MAKIMURA KOUICHI, MURAYAMA SOUMEI, YAMAGUCHI HIDEYO PC
C12Q1/68,C12N15/11,(C12Q1/68,C12R1:66),(C12Q1/68,C12R1:80); CC
strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..19
FT /organism='Artificial sequences'.
FEATURES
source 1..19
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 9.1%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1646 CAGAAGCGACGACCCAGGC 1664
||||| ||||| |||||
1 CAGAAGGAAAGTCCAGCC 19

RESULT 98
E08539
LOCUS 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 8278 from patent US 6537751.
ACCESSION AR296543
VERSION AR296543.1 GI:31683827
KEYWORDS Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 8278 25-MAR-2003;
FEATURES
source 1..19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 9.1%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1694 GCGTGTGGAGTGGGTT 1712
||||| ||||| |||||
19 GAGTTGTGGATGTTGGGT 1

RESULT 99
AX130657
LOCUS 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 1875 from Patent WO0130362.
ACCESSION AX130657
VERSION AX130657.1 GI:14136962
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 1875 03-MAY-2001;
IMMUSOL, INC. (US)

QY 1657 CACCAAGCTCACAGCTGGA 1675
||||| ||||| |||||
1 CACCAAGCTCCTGATGGA 19

RESULT 96
E08539
LOCUS 19 bp DNA linear PAT 29-SEP-1997
DEFINITION PCR primer to detect Aspergillus sp. and Penicillium sp. rDNA.
ACCESSION E08539
VERSION E08539.1 GI:2176654
KEYWORDS JP 1994339400-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Makimura,K., Murayama,S. and Yamaguchi,H.
TITLE PRIMER FOR PATHOGENIC MOULD GENE AMPLIFICATION
JOURNAL Patent: JP 1994339400-A 2 13-DEC-1994;
YAMAGUCHI HIDEYO
COMMENT OS None
OC Artificial sequences.
PN JP 1994339400-A/2
PD 13-DEC-1994
PF 01-JUN-1993 JP 1993130778
PI MAKIMURA KOUICHI, MURAYAMA SOUMEI, YAMAGUCHI HIDEYO PC
C12Q1/68,C12N15/11,(C12Q1/68,C12R1:66),(C12Q1/68,C12R1:80); CC
strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..19
FT /organism='Artificial sequences'.
FEATURES
source 1..19
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 9.1%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1646 CAGAAGCGACGACCCAGGC 1664
||||| ||||| |||||
1 CAGAAGGAAAGTCCAGCC 19

RESULT 98
E08539
LOCUS 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 8278 from patent US 6537751.
ACCESSION AR296543
VERSION AR296543.1 GI:31683827
KEYWORDS Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 8278 25-MAR-2003;
FEATURES
source 1..19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 9.1%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1694 GCGTGTGGAGTGGGTT 1712
||||| ||||| |||||
19 GAGTTGTGGATGTTGGGT 1

RESULT 99
AX130657
LOCUS 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 1875 from Patent WO0130362.
ACCESSION AX130657
VERSION AX130657.1 GI:14136962
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 1875 03-MAY-2001;
IMMUSOL, INC. (US)

```

```
FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
        /note="Cyclin D1 ribozyme binding site"

Query Match
  Best Local Similarity 9.1%; Score 12.6; DB 1; Length 19;
  Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1739 CCAACTCTCTCCATCCTA 1757
Db 1 CCAACAACCTCTCTGCTTA 19

RESULT 100
AX131856
LOCUS AX131856 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3074 from Patent WO0130362.
ACCESSION AX131856
VERSION AX131856.1 GI:14138161
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  TITLE Robbins, J.M. and Tritz, R.
  JOURNAL Ribozyme therapy for the treatment of proliferative skin and eye
  diseases
  PATENT: WO 0130362-A 3074 03-MAY-2001;
  IMMUSOL, INC. (US)
FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
        /note="Cyclin A1 ribozyme binding site"

Query Match
  Best Local Similarity 9.1%; Score 12.6; DB 1; Length 19;
  Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1698 GGTGAAGTGGGTTAGGA 1716
Db 1 GGTGAGGTTGGGAGAA 19

RESULT 101
A28990
LOCUS A28990 15 bp DNA linear PAT 30-JUN-1995
DEFINITION Oligo 9 from patent EP0522880.
ACCESSION A28990
VERSION A28990.1 GI:1248843
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
  AUTHORS 1 (bases 1 to 15)
  TITLE artificial sequences.
  JOURNAL Holton, T.A., Cornish, E.C., Kovacic, F., Tanaka, Y. and Lester, D.R.
  TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
  therefor
  PATENT: EP 0522880-A 9 13-JAN-1993;
  INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd
FEATURES
  source
    Location/Qualifiers
      1..15
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"

Query Match
  Best Local Similarity 8.9%; Score 12.4; DB 1; Length 15;

FEATURES
  source
    Location/Qualifiers
      1..15
        /organism="unassigned DNA"

Query Match
  Best Local Similarity 8.9%; Score 12.4; DB 1; Length 15;
  Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1683 TGTCTCTCTCCAGCG 1696
Db 2 TGTCTCTCTCCAGTG 15

RESULT 102
AR030911
LOCUS AR030911 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5861487.
ACCESSION AR030911
VERSION AR030911.1 GI:5344125
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  AUTHORS 1 (bases 1 to 15)
  TITLE Holton, T. Albert., Cornish, E. Cecily., Kovacic, F., Tanaka, Y. and
  Lester, D. Ruth.
  JOURNAL Genetic sequences encoding flavonoid pathway enzymes and uses
  therefor
  PATENT: US 5861437-A 11 19-JAN-1999;
  Location/Qualifiers
    source
      1..15
        /organism="unassigned DNA"

Query Match
  Best Local Similarity 8.9%; Score 12.4; DB 1; Length 15;
  Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1683 TGTCTCTCTCCAGCG 1696
Db 2 TGTCTCTCTCCAGTG 15

RESULT 103
I28303
LOCUS I28303 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 11 from patent US 5569832.
ACCESSION I28303
VERSION I28303.1 GI:1813079
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  AUTHORS 1 (bases 1 to 15)
  TITLE Holton, T.A., Cornish, E.C., Kovacic, F., Tanaka, Y. and Lester, D.R.
  TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
  therefor
  JOURNAL Patent: US 5569832-A 11 29-OCT-1996;
  Location/Qualifiers
    source
      1..15
        /organism="unassigned DNA"

Query Match
  Best Local Similarity 8.9%; Score 12.4; DB 1; Length 15;
  Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1683 TGTCTCTCTCCAGCG 1696
Db 2 TGTCTCTCTCCAGTG 15

RESULT 104
AR127505/c
LOCUS AR127505/c 16 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 20 from patent US 6180766.
ACCESSION AR127505
VERSION AR127505.1 GI:14114100
KEYWORDS
```

```

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Schinazi,R.F., Fulcrand-El Kattan,G. and Lesnikowski,Z.Jan.
TITLE        Nucleosides and oligonucleotides containing boron clusters
JOURNAL      Patent: US 6180766-A 20 30-JAN-2001;
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      8.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1677 CCTCGGTGTCTCCT 1690
Db      16 CCTGGTGCTCAT 3

RESULT 105
LOCUS      I50742              16 bp      DNA              linear      PAT 07-OCT-1997
DEFINITION Sequence 24 from patent US 5643724.
ACCESSION  I50742
VERSION     I50742.1 GI:2472445
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Fildes,N.Jane. and Reynolds,R.Lynne.
TITLE        Methods and reagents for Glycophorin A typing
JOURNAL      Patent: US 5643724-A 24 01-JUL-1997;
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      8.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1698 GGTGGAAGTTGGGT 1711
Db      16 GGTGGAAGCTGGGT 3

RESULT 106
LOCUS      AR328506/c          16 bp      RNA              linear      PAT 17-AUG-2003
DEFINITION Sequence 5908 from patent US 6566127.
ACCESSION  AR328506
VERSION     AR328506.1 GI:33714314
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL      Patent: US 6566127-A 5908 20-MAY-2003;
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="unknown"
                /mol_type="unassigned RNA"

Query Match      8.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Schinazi,R.F., Fulcrand-El Kattan,G. and Lesnikowski,Z.Jan.
TITLE        Nucleosides and oligonucleotides containing boron clusters
JOURNAL      Patent: US 6180766-A 20 30-JAN-2001;
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      8.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1677 CCTCGGTGTCTCCT 1690
Db      16 CCTGGTGCTCAT 3

RESULT 109
LOCUS      BD255127/c          17 bp      DNA              linear      PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION  BD255127
```

---

```

Qy      1663 GCTCACAGCTGGAA 1676
Db      16 GCCCACAGCTGGAA 3

RESULT 107
LOCUS      AX039862              16 bp      DNA              linear      PAT 18-NOV-2000
DEFINITION Sequence 251 from Patent WO0063441.
ACCESSION  AX039862
VERSION     AX039862.1 GI:11229891
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1
AUTHORS      Herrstadt,C. and Davis,R.E.
TITLE        Single nucleotide polymorphisms in mitochondrial genes that segregate with alzheimer's disease
JOURNAL      Patent: WO 0063441-A 251 26-OCT-2000;
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="PCR primer"

Query Match      8.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1709 GGTAGGAGTACGG 1722
Db      3 GGTAGGCGTACGG 16

RESULT 108
LOCUS      AX135793              16 bp      DNA              linear      PAT 29-MAY-2001
DEFINITION Sequence 20 from Patent EP1113020.
ACCESSION  AX135793
VERSION     AX135793.1 GI:14272029
KEYWORDS    Human immunodeficiency virus 1 (HIV-1)
SOURCE      Human immunodeficiency virus 1
ORGANISM     Viruses; Retrovirdae; Retroviridae; Lentivirus; Primate lentivirus group.
REFERENCE    1
AUTHORS      Lesnikowski,Z.J., Kattan,G.F. and Schinazi,R.F.
TITLE        Nucleosides and oligonucleotides containing boron clusters
JOURNAL      Patent: EP 1113020-A 20 04-JUL-2001;
EMORY UNIVERSITY (US)
FEATURES     Location/Qualifiers
              source
                1..16
                /organism="Human immunodeficiency virus 1"
                /mol_type="unassigned DNA"
                /db_xref="taxon:11676"

Query Match      8.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1677 CCTCGGTGTCTCCT 1690
Db      16 CCTGGTGCTCAT 3

RESULT 109
LOCUS      BD255127/c          17 bp      DNA              linear      PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION  BD255127
```

```

VERSION BD255127.1 GI:33064897
KEYWORDS JP 2002541795-A/2920.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt L., Zwick M., Pavco P. and Mcswiggen J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2920 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2920
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source 1..17 Location/Qualifiers
FT source 1..17 /organism='Eukaryote'.
FEATURES
source
Location/Qualifiers
1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1696 GTGGTGAAGTTGG 1709
Db 16 GAGGTGAAGTTGG 3
RESULT 110
BD255128/2
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255128
VERSION BD255128.1 GI:33064898
KEYWORDS JP 2002541795-A/2921.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt L., Zwick M., Pavco P. and Mcswiggen J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2921 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2921
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source 1..17 Location/Qualifiers
FT source 1..17 /organism='Eukaryote'.
FEATURES
source
Location/Qualifiers
1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1696 GTGGTGAAGTTGG 1709
Db 16 GAGGTGAAGTTGG 3
RESULT 110
BD255128/2
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255128
VERSION BD255128.1 GI:33064898
KEYWORDS JP 2002541795-A/2921.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt L., Zwick M., Pavco P. and Mcswiggen J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2921 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2921
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source 1..17 Location/Qualifiers
FT source 1..17 /organism='Eukaryote'.
FEATURES
source
Location/Qualifiers
1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1696 GTGGTGAAGTTGG 1709
Db 16 GAGGTGAAGTTGG 3
RESULT 111
AR327591/1
LOCUS 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4993 from patent US 6566127.
ACCESSION AR327591
VERSION AR327591.1 GI:33711399
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco P., McSwiggen J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4993 20-MAY-2003;
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1663 GCTCACAGCTGAA 1676
Db 15 GCCACAGCTGAA 2
RESULT 112
AX266079/1
LOCUS 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 3470 from Patent WO0173002.
ACCESSION AX266079
VERSION AX266079.1 GI:16514878
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kmiec, E.B., Gamper, H.B. and Rice, M.C.
TITLE Targeted chromosomal genomic alterations with modified single stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 3470 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1663 GCTCACAGCTGAA 1676
Db 15 GCCACAGCTGAA 2
RESULT 112
AX266079/1
LOCUS 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 3470 from Patent WO0173002.
ACCESSION AX266079
VERSION AX266079.1 GI:16514878
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kmiec, E.B., Gamper, H.B. and Rice, M.C.
TITLE Targeted chromosomal genomic alterations with modified single stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 3470 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1663 GCTCACAGCTGAA 1676
Db 15 GCCACAGCTGAA 2

```



[illegible][illegible]

TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines  
JOURNAL Patent: WO 03040369-A 482 15-MAY-2003;  
FEATURES Molecular Engines Laboratories (FR)  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 8.9%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 92.9%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1674 GAACCTGGTGCT 1687  
Db 1 GATCCCTGGTGCT 14

RESULT 118  
AR018181/c  
LOCUS AR018181 18 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 8 from patent US 5780611.  
ACCESSION AR018181  
VERSION AR018181.1 GI:3973784  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Guntaka,R.V., Weber,K.Theodore., Kovacs,A. and Kandala,J.  
TITLE Oligomers which inhibit expression of collagen genes  
JOURNAL Patent: US 5780611-A 8 14-JUL-1998;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 8.9%; Score 12.4; DB 1; Length 18;  
Best Local Similarity 92.9%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756  
Db 17 CTCCTCCCTTTCCT 4

RESULT 119  
AR018183/c  
LOCUS AR018183 18 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 10 from patent US 5780611.  
ACCESSION AR018183  
VERSION AR018183.1 GI:3973786  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Guntaka,R.V., Weber,K.Theodore., Kovacs,A. and Kandala,J.  
TITLE Oligomers which inhibit expression of collagen genes  
JOURNAL Patent: US 5780611-A 10 14-JUL-1998;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 8.9%; Score 12.4; DB 1; Length 18;  
Best Local Similarity 92.9%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756  
Db 17 CTCCTCCCTTTCCT 4

RESULT 120  
AR018184/c  
LOCUS AR018184 18 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 11 from patent US 5780611.  
ACCESSION AR018184  
VERSION AR018184.1 GI:3973787  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Guntaka,R.V., Weber,K.Theodore., Kovacs,A. and Kandala,J.  
TITLE Oligomers which inhibit expression of collagen genes  
JOURNAL Patent: US 5780611-A 11 14-JUL-1998;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 8.9%; Score 12.4; DB 1; Length 18;  
Best Local Similarity 92.9%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756  
Db 17 CTCCTCCCTTTCCT 4

RESULT 121  
AR187552/c  
LOCUS AR187552 18 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 3040 from patent US 6346398.  
ACCESSION AR187552  
VERSION AR187552.1 GI:23233517  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 3040 12-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 8.9%; Score 12.4; DB 1; Length 18;  
Best Local Similarity 92.9%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1663 GCTCACAGCTGAA 1676  
Db 16 GCCCAGCTGAA 3

RESULT 122  
AR299488  
LOCUS AR299488 18 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 11223 from patent US 6537751.  
ACCESSION AR299488  
VERSION AR299488.1 GI:3.686772  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.  
TITLE Biallelic markers for use in constructing a high density

```

disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 11223 25-MAR-2003;
FEATURES Location/Qualifiers
    source
        1..18
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match      8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1722 GAGATGGAGATTGG 1735
Db 5 GAGATGGAGATTGG 18

RESULT 123
AR324066/c
LOCUS AR324066 18 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1468 from patent US 6566127.
ACCESSION AR324066
VERSION AR324066.1 GI:33709874
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1468 20-MAY-2003;
FEATURES Location/Qualifiers
    source
        1..18
        /organism="unknown"
        /mol_type="unassigned RNA"

Query Match      8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1663 GCTCACAGCTGGAA 1676
Db 16 GCCCACAGCTGGAA 3

RESULT 124
AR362645
LOCUS AR362645 18 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 15 from patent US 5179198.
ACCESSION AR362645
VERSION AR362645.1 GI:34422997
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Okada,H., Okada,N., Nagami,Y., Takahashi,K., Takizawa,H. and Kondo,J.
TITLE Glycoprotein and gene coding therefor
JOURNAL Patent: US 5179198-A 15 12-JAN-1993;
FEATURES Location/Qualifiers
    source
        1..18
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match      8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1702 GAAGTTGGTTAGG 1715
Db 5 GCAGTTGGTTAGG 18

RESULT 125
AR365708
LOCUS AR365708 18 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 11 from patent US 5521296.
ACCESSION AR365708
VERSION AR365708.1 GI:34429630
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Okada,H., Okada,N., Nagami,Y., Takahashi,K., Takizawa,H. and Kondo,J.
TITLE Glycoprotein and gene coding therefor
JOURNAL Patent: US 5521296-A 11 28-MAY-1996;
FEATURES Location/Qualifiers
    source
        1..18
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match      8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1702 GAAGTTGGTTAGG 1715
Db 5 GCAGTTGGTTAGG 18

RESULT 126
AX786023/c
LOCUS AX786023 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 19 from Patent WO03050272.
ACCESSION AX786023
VERSION AX786023.1 GI:32953643
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bandelier,M.A., Denys,P., Denormandie,P., Sapena,R., Lepailleur-Enouf,D. and Youssefian,T.
TITLE Bone development model
JOURNAL Patent: WO 03050272-A 19 19-JUN-2003;
FEATURES Location/Qualifiers
    source
        1..18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Amorce PCR sens pour l'amplification specifique du
        gene du collagene de type I alpha 1 (COL1A1)"

Query Match      8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1655 AGCACAGGCTCAC 1668
Db 14 AGCACAGGCTTAC 1

RESULT 127
BD206162
LOCUS BD206162 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Human antithrombin III and method concerning the same.
ACCESSION BD206162
VERSION BD206162.1 GI:33015932
KEYWORDS JP 2002514579-A/16.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18)
AUTHORS Brook,J.David., Housman,D.E., Shaw,D.J., Harley,H.G. and
TITLE Johnson,K.J.
JOURNAL DNA sequence encoding the myotonic dystrophy gene and uses thereof
PATENT: JP 2002514579-A 16 21-MAY-2002;
SUSAN C BOCK,VERONIQUE PICARD,PEDRAM ZENDEHROUH
OS Homo sapiens (human)
PN JP 2002514579-A/16
PD 21-MAY-2002
PF 12-MAY-1999 JP 2000547950
PR 12-MAY-1998 US 60/085197,05-MAY-1999 US 09/305.588 P1
SUSAN C BOCK,VERONIQUE PICARD,PEDRAM ZENDEHROUH PC
AG1K38/00,AG1K38/55,AG1P7/02,AG1P43/00,C07K14/47,C07K14/81, PC
C12N15/09,
PC AG1K37/02,AG1K37/64,C12N15/00
CC Human antithrombin III and method concerning the same. FH
Key Location/Qualifiers
FT source 1..18
/organism="Homo sapiens (human)".
FEATURES
source
1..18
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1640 TTGTAGCAGAGGC 1653
|||||:|||||
Db 3 TTGTTGCAGAGGC 16
RESULT 128
AR074596/c
LOCUS 19 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 13 from patent US 5955265.
ACCESSION AR074596
VERSION AR074596.1 GI:10001349
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Brook,J.David., Housman,D.E., Shaw,D.J., Harley,H.G. and
TITLE Johnson,K.J.
JOURNAL DNA sequence encoding the myotonic dystrophy gene and uses thereof
PATENT: US 5955265-A 13 21-SEP-1999;
FEATURES
source
1..19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 2e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCAGCTGGACCC 1679
|||||:|||||
Db 18 GGCTCAYRCCTGTATCC 1
RESULT 129
AR083935/c
LOCUS 19 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 13 from patent US 5977333.
ACCESSION AR083935
VERSION AR083935.1 GI:10010706
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Brook,J.David., Housman,D.E., Shaw,D.J., Harley,H.G. and
TITLE Johnson,K.J.
JOURNAL DNA sequence encoding the myotonic dystrophy gene and uses thereof
PATENT: US 5977333-A 13 02-NOV-1999;
FEATURES
source
1..19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 2e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCAGCTGGACCC 1679
|||||:|||||
Db 18 GGCTCAYRCCTGTATCC 1
RESULT 130
I23815/c
LOCUS 19 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 1 from patent US 5538869.
ACCESSION I23815
VERSION I23815.1 GI:1603685
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Siciliano,M.J. and Liu,P.
TITLE In-situ hybridization probes for identification and banding of
specific human chromosomes and regions
JOURNAL Patent: US 5538869-A 1 23-JUL-1996;
FEATURES
source
1..19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 2e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCAGCTGGACCC 1679
|||||:|||||
Db 18 GGCTCAYRCCTGTATCC 1
RESULT 131
I29969/c
LOCUS 19 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5578493.
ACCESSION I29969
VERSION I29969.1 GI:1820760
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Gilliam,T.Conrad. and Tanzi,R.E.
TITLE Wilson's disease gene
JOURNAL Patent: US 5578493-A 1 26-NOV-1996;
FEATURES
source
1..19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 2e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCAGCTGGACCC 1679
|||||:|||||

```

```

Db      18  GGCTCAVRCCTGTATCC 1

RESULT 132
LOCUS      AR299173/c
DEFINITION Sequence 10908 from patent US 6537751.
ACCESSION  AR299173
VERSION     AR299173.1  GI:31686457
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
JOURNAL     disequilibrium map of the human genome
JOURNAL     Patent: US 6537751-A 10908 25-MAR-2003;
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1631  GGATGGGCTTGTA 1644
Db      19  GGTTGGGGCTTGTA 6

RESULT 133
LOCUS      AX033909/c
DEFINITION Sequence 1 from Patent WO9851790.
ACCESSION  AX033909
VERSION     AX033909.1  GI:10280477
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1
AUTHORS     Cancilla,M.R., Choo,K.H. and Du,S.D.
TITLE       A novel nucleic acid molecule
JOURNAL     Patent: WO 9851790-A 1 19-NOV-1998;
JOURNAL     CANCELLA MICHAEL ROBERT (AU) ; CHOO KONG HONG ANDY (AU) ; SART
JOURNAL     DESIRBE DU (AU) ; AMRAD OPERATIONS PTY LTD (AU)
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 2e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1662  GGCTCAGCTGGAAACC 1679
Db      18  GGCTCAVRCCTGTATCC 1

RESULT 134
LOCUS      AR046916
DEFINITION Sequence 1709 from patent US 5817796.
ACCESSION  AR046916
VERSION     AR046916.1  GI:5968381
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
JOURNAL     disequilibrium map of the human genome
JOURNAL     Patent: US 6537751-A 10908 25-MAR-2003;
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1638  GCTTGTAGCAGGAGCCA 1654
Db      17  GCTTGTAGTAGAGGCCA 1

RESULT 136
LOCUS      I53968
DEFINITION Sequence 1709 from patent US 5646042.
ACCESSION  I53968
VERSION     I53968.1  GI:2475171
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1
AUTHORS     Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE       C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL     Patent: US 5817796-A 1709 06-OCT-1998;
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1665  TCACAGCTGGAACCCCTG 1681
Db      1  TCTCAGCTCGAACTCTG 17

RESULT 135
LOCUS      BD254187/c
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION  BD254187
VERSION     BD254187.1  GI:33063957
KEYWORDS   JP 2002541795-A/1980.
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 17)
AUTHORS     Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE       Regulation of repressor genes using nucleic acid molecules
JOURNAL     Patent: JP 2002541795-A 1980 10-DEC-2002;
JOURNAL     RIBOZYME PHARMACEUTICALS INC
COMMENT     OS Eukaryote
            PN JP 2002541795-A/1980
            PD 10-DEC-2002
            PF 11-APR-2000 JP 2000611654
            PR 12-APR-1999 US 60/129390
            PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
            C12R1:91),
            PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC A61K37/02,
            PC (C12N5/00,C12R1:91)
            CC Regulation of repressor genes using nucleic acid molecules FH
            Key source
            1..17
            Location/Qualifiers
            FT
            /organism='Eukaryote'.
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1638  GCTTGTAGCAGGAGCCA 1654
Db      17  GCTTGTAGTAGAGGCCA 1

RESULT 136
LOCUS      I53968
DEFINITION Sequence 1709 from patent US 5646042.
ACCESSION  I53968
VERSION     I53968.1  GI:2475171
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1
AUTHORS     Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE       C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL     Patent: US 5817796-A 1709 06-OCT-1998;
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="unassigned DNA"

```

```

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      1 (bases 1 to 17)
TITLE        Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
JOURNAL      C-myb targeted ribozymes
JOURNAL      Patent: US 5646042-A 1709 08-JUL-1997;
FEATURES     Location/Qualifiers
             source
             1..17
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1665 TCACAGCTGGAACCTG 1681
Db      1 TCTCAGCTCGAAGCTG 17

RESULT 137
AX365741
LOCUS      AR365741
DEFINITION Sequence 6 from patent US 6328971.
ACCESSION  AR365741
VERSION     AR365741.1 GI:34597897
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      van der Bruggen,P. and Boon-Palleur,T.
TITLE        MAGE-1 derived nona peptides, and compositions thereof
JOURNAL      Patent: US 6328971-A 6 11-DEC-2001;
FEATURES     Location/Qualifiers
             source
             1..17
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1653 CAAGCACCAGGCTCACA 1669
Db      1 CAAGCGCCAGGCACAGA 17

RESULT 138
AX215134
LOCUS      AX215134
DEFINITION Sequence 576 from Patent WO0159103.
ACCESSION  AX215134
VERSION     AX215134.1 GI:15525177
KEYWORDS    synthetic construct
SOURCE      synthetic construct
             artificial sequences.
ORGANISM     1
REFERENCE    Blatt,L., McSwiggen,J. and Chowrira,B.M.
AUTHORS      Method and reagent for the modulation and diagnosis of cd20 and
TITLE        nogo gene expression
JOURNAL      Patent: WO 0159103-A 576 16-AUG-2001;
JOURNAL      RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
JOURNAL      McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES     Location/Qualifiers
             source
             1..17
             /organism="synthetic construct"
             /mol_type="unassigned RNA"
             /db_xref="taxon:32630"
             /note="Nucleic Acid"

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      1 (bases 1 to 17)
TITLE        Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
JOURNAL      C-myb targeted ribozymes
JOURNAL      Patent: US 5646042-A 1709 08-JUL-1997;
FEATURES     Location/Qualifiers
             source
             1..17
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1665 TCACAGCTGGAACCTG 1681
Db      1 TCTCAGCTCGAAGCTG 17

RESULT 137
AX365741
LOCUS      AR365741
DEFINITION Sequence 6 from patent US 6328971.
ACCESSION  AR365741
VERSION     AR365741.1 GI:34597897
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      van der Bruggen,P. and Boon-Palleur,T.
TITLE        MAGE-1 derived nona peptides, and compositions thereof
JOURNAL      Patent: US 6328971-A 6 11-DEC-2001;
FEATURES     Location/Qualifiers
             source
             1..17
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1653 CAAGCACCAGGCTCACA 1669
Db      1 CAAGCGCCAGGCACAGA 17

RESULT 138
AX215134
LOCUS      AX215134
DEFINITION Sequence 576 from Patent WO0159103.
ACCESSION  AX215134
VERSION     AX215134.1 GI:15525177
KEYWORDS    synthetic construct
SOURCE      synthetic construct
             artificial sequences.
ORGANISM     1
REFERENCE    Blatt,L., McSwiggen,J. and Chowrira,B.M.
AUTHORS      Method and reagent for the modulation and diagnosis of cd20 and
TITLE        nogo gene expression
JOURNAL      Patent: WO 0159103-A 576 16-AUG-2001;
JOURNAL      RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
JOURNAL      McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES     Location/Qualifiers
             source
             1..17
             /organism="synthetic construct"
             /mol_type="unassigned RNA"
             /db_xref="taxon:32630"
             /note="Nucleic Acid"

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      1 (bases 1 to 17)
TITLE        Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
JOURNAL      C-myb targeted ribozymes
JOURNAL      Patent: US 5646042-A 1709 08-JUL-1997;
FEATURES     Location/Qualifiers
             source
             1..17
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1704 AGTTGGTTAGAGTAC 1720
Db      1 AGTTGGTTTCAGAGTAC 17

RESULT 139
AX499445
LOCUS      AX499445
DEFINITION Sequence 752 from Patent EP1229046.
ACCESSION  AX499445
VERSION     AX499445.1 GI:23381738
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Zhan,J.
TITLE        Human testis expressed patched like protein
JOURNAL      Patent: EP 1229046-A 752 07-AUG-2002;
JOURNAL      Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
             source
             1..17
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1662 GGCTCAGCTGGAACC 1678
Db      1 GACTCACTGCTGGACCC 17

RESULT 140
AX532097
LOCUS      AX532097
DEFINITION Sequence 1606 from Patent EP1239051.
ACCESSION  AX532097
VERSION     AX532097.1 GI:25255956
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Shannon,M.
TITLE        Human posh-like protein 1
JOURNAL      Patent: EP 1239051-A 1606 11-SEP-2002;
JOURNAL      Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
             source
             1..17
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      3.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1671 CTGGAACCCGTGTCT 1687
Db      1 CCGGAGCCCTGGTCTCT 17

RESULT 141
AX532099
```

```
LOCUS AX532099 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1608 from Patent EP1239051.
ACCESSION AX532099
VERSION AX532099.1 GI:25255985
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1608 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1673 GGAGCCCTGGTCTCTCC 1689
| | | | | | | | | | | | | | |
Db 1 GGAGCCCTGGTCTCTAC 17

RESULT 142
AX532103
LOCUS AX532103 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1612 from Patent EP1239051.
ACCESSION AX532103
VERSION AX532103.1 GI:25255993
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1612 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1673 GGAGCCCTGGTCTCTCC 1689
| | | | | | | | | | | | | | |
Db 1 GGAGCCCTGGTCTCTAC 17

RESULT 143
AX532253/c
LOCUS AX532253 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1762 from Patent EP1239051.
ACCESSION AX532253
VERSION AX532253.1 GI:25256291
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
```

```
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1762 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1749 CCTATCCTAAAGGCCCA 1765
| | | | | | | | | | | | | | |
Db 17 CTGTGCTTAAGTCCCA 1

RESULT 144
AX532254/c
LOCUS AX532254 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1763 from Patent EP1239051.
ACCESSION AX532254
VERSION AX532254.1 GI:25256293
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1763 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1748 CCCTATCCTAAAGGCC 1764
| | | | | | | | | | | | | | |
Db 17 CCTGTGCTTAAGTCCC 1

RESULT 145
AX687667
LOCUS AX687667 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 399 from Patent EP1281758.
ACCESSION AX687667
VERSION AX687667.1 GI:29410363
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 399 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.8%; Score 12.2; DB 1; Length 17;
```

<p>Best Local Similarity 82.4%; Pred. No. 1.8e+02; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>		<p>AX728392 17 bp DNA linear PAT 08-MAY-2003 Sequence 26 from Patent WO03025175. AX728392 AX728392.1 GI:30507735</p>	
QY	1740 CAACCTCCCTCCCTATCCT 1756		
Db	1 CAGTTCCTCACTATCCT 17		
<p>RESULT 146 AX687850/c LOCUS DEFINITION Sequence 582 from Patent EPI281758. AX687850 AX687850.1 GI:29410548</p>			
<p>KEYWORDS Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p>			
<p>REFERENCE 1 Telerman,A., Amson,R. and Tuijnder,M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines Patent: WO 03025175-A 26 27-MAR-2003; Molecular Engines Laboratories (FR)</p>			
<p>FEATURES source 1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"</p>			
<p>Query Match 8.8%; Score 12.2; DB 1; Length 17; Best Local Similarity 82.4%; Pred. No. 1.8e+02; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>			
QY	1641 TGTAGCAGAGGCGACG 1657		
Db	17 TGTAGCAGATGCGATC 1		
<p>RESULT 149 AX734168 LOCUS DEFINITION Sequence 5802 from Patent WO03025175. AX734168 AX734168.1 GI:30513511</p>			
<p>KEYWORDS Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p>			
<p>REFERENCE 1 Telerman,A., Amson,R. and Tuijnder,M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines Patent: WO 03025175-A 5802 27-MAR-2003; Molecular Engines Laboratories (FR)</p>			
<p>FEATURES source 1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"</p>			
<p>Query Match 3.8%; Score 12.2; DB 1; Length 17; Best Local Similarity 82.4%; Pred. No. 1.8e+02; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>			
QY	1735 GCTCCCAACTCCTCCT 1751		
Db	1 GATCCCAACTGCTCCTT 17		
<p>RESULT 150 AX762563/c LOCUS DEFINITION Sequence 5884 from Patent WO03040369. AX762563 AX762563.1 GI:32257179</p>			
<p>KEYWORDS Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p>			
<p>REFERENCE 1 Telerman,A., Amson,R. and Tuijnder,M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines Patent: WO 03025175-A 5802 27-MAR-2003; Molecular Engines Laboratories (FR)</p>			
<p>FEATURES source 1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"</p>			
<p>Query Match 8.8%; Score 12.2; DB 1; Length 17; Best Local Similarity 82.4%; Pred. No. 1.8e+02; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>			
QY	1650 AGGCAAGCACCGCTC 1666		
Db	17 AGGCAAGAACCAAGGATC 1		



```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Telerman,A., Amson,R. and Tuijinder,M.
TITLE      Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL    Patent: WO 03040369-A 5884 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
            source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1641 TGTAGCAGAGCGCAGC 1657
Db 17 TGTAGCAGATGCGCATC 1

RESULT 151
AR106981/c
LOCUS      AR106981
DEFINITION Sequence 142 from patent US 6107092.
ACCESSION  AR106981
VERSION     AR106981.1 GI:12821511
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Cowser,L.M., Bennett,C.Frank. and O'Malley,B.W.
TITLE      Antisense modulation of SRA expression
JOURNAL    Patent: US 6107092-A 142 22-AUG-2000;
CONSIGLIO NAZIONALE RICERCH (IT)
COMMENT    Other publication AU 4944396 960923.
FEATURES   Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1658 ACCAGGCTCACGCTGG 1674
Db 17 ACCAGGCTTCAGCAGG 1

RESULT 152
A56874/c
LOCUS      A56874
DEFINITION Sequence 10 from Patent WO9627664.
ACCESSION  A56874
VERSION     A56874.1 GI:3712886
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE   1
AUTHORS    Morelli,S., Nicolin,A. and Quattrone,A.
TITLE      ANTISENSE TRANSCRIPT EXPRESSED IN B LYMPHOCYTES AND SYNTHETIC
OLIGONUCLEOTIDES USEFUL TO INHIBIT THE ACTIVITY THEREOF
JOURNAL    Patent: WO 9627664-A 10 12-SEP-1996;
CONSIGLIO NAZIONALE RICERCH (IT)
COMMENT    Other publication AU 4944396 960923.
FEATURES   Location/Qualifiers
            source
            1..18

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Telerman,A., Amson,R. and Tuijinder,M.
TITLE      Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL    Patent: WO 03040369-A 5884 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
            source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1641 TGTAGCAGAGCGCAGC 1657
Db 17 TGTAGCAGATGCGCATC 1

RESULT 151
AR106981/c
LOCUS      AR106981
DEFINITION Sequence 142 from patent US 6107092.
ACCESSION  AR106981
VERSION     AR106981.1 GI:12821511
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Cowser,L.M., Bennett,C.Frank. and O'Malley,B.W.
TITLE      Antisense modulation of SRA expression
JOURNAL    Patent: US 6107092-A 142 22-AUG-2000;
CONSIGLIO NAZIONALE RICERCH (IT)
COMMENT    Other publication AU 4944396 960923.
FEATURES   Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1658 ACCAGGCTCACGCTGG 1674
Db 17 ACCAGGCTTCAGCAGG 1

RESULT 152
A56874/c
LOCUS      A56874
DEFINITION Sequence 10 from Patent WO9627664.
ACCESSION  A56874
VERSION     A56874.1 GI:3712886
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE   1
AUTHORS    Morelli,S., Nicolin,A. and Quattrone,A.
TITLE      ANTISENSE TRANSCRIPT EXPRESSED IN B LYMPHOCYTES AND SYNTHETIC
OLIGONUCLEOTIDES USEFUL TO INHIBIT THE ACTIVITY THEREOF
JOURNAL    Patent: WO 9627664-A 10 12-SEP-1996;
CONSIGLIO NAZIONALE RICERCH (IT)
COMMENT    Other publication AU 4944396 960923.
FEATURES   Location/Qualifiers
            source
            1..18
```

```

/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1644 AGCAGAAGCGCAGCACC 1660
Db 17 AGCAGAAGCCACGCATC 1

RESULT 153
A56885
LOCUS      A56885
DEFINITION Sequence 21 from Patent WO9627664.
ACCESSION  A56885
VERSION     A56885.1 GI:3712897
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE   1
AUTHORS    Morelli,S., Nicolin,A. and Quattrone,A.
TITLE      ANTISENSE TRANSCRIPT EXPRESSED IN B LYMPHOCYTES AND SYNTHETIC
OLIGONUCLEOTIDES USEFUL TO INHIBIT THE ACTIVITY THEREOF
JOURNAL    Patent: WO 9627664-A 21 12-SEP-1996;
CONSIGLIO NAZIONALE RICERCH (IT)
COMMENT    Other publication AU 4944396 960923.
FEATURES   Location/Qualifiers
            source
            1..18
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1644 AGCAGAAGCGCAGCACC 1660
Db 2 AGCAGAAGCCACGCATC 18

RESULT 154
AR092022/c
LOCUS      AR092022
DEFINITION Sequence 46 from patent US 5998141.
ACCESSION  AR092022
VERSION     AR092022.1 GI:10018776
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Acton,S.Laurene.
TITLE      Intronic and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL    Patent: US 5998141-A 46 07-DEC-1999;
CONSIGLIO NAZIONALE RICERCH (IT)
COMMENT    Other publication AU 4944396 960923.
FEATURES   Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1682 GTGTCTCTCTCCAGCGTG 1698
Db 17 GTCTCTCTCTCCCGCTG 1
```

RESULT 155  
AR112157/c  
LOCUS AR112157 18 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 46 from patent US 6130041.  
ACCESSION AR112157  
VERSION AR112157.1 GI:14092057  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Acton,S.Laurene.  
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses therefor  
JOURNAL Patent: US 6130041-A 46 10-OCT-2000;  
FEATURES  
source Location/Qualifiers  
1. .18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 8.8%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1682 GTGTCCTCTCCAGCGTG 1698  
Db 17 GTCTCTCTCCGCGCTG 1  
RESULT 156  
AR118335/c  
LOCUS AR118335 18 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 10 from patent US 6140492.  
ACCESSION AR118335  
VERSION AR118335.1 GI:14099241  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Morelli,S., Nicolin,A. and Quattrone,A.  
TITLE Antisense transcript expressed in B lymphocytes and synthetic oligonucleotides useful to inhibit the activity thereof  
JOURNAL Patent: US 6140492-A 10 31-OCT-2000;  
FEATURES  
source Location/Qualifiers  
1. .18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 8.8%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1644 AGCAGAAGCGACGACC 1660  
Db 17 AGCAGAAGCGACGATC 1  
RESULT 157  
AR118346  
LOCUS AR118346 18 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 21 from patent US 6140492.  
ACCESSION AR118346  
VERSION AR118346.1 GI:14099252  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Morelli,S., Nicolin,A. and Quattrone,A.  
TITLE Antisense transcript expressed in B lymphocytes and synthetic oligonucleotides useful to inhibit the activity thereof  
JOURNAL Patent: US 6140492-A 21 31-OCT-2000;

FEATURES  
source Location/Qualifiers  
1. .18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 8.8%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1644 AGCAGAAGCGACGACC 1660  
Db 2 AGCAGAAGCGACGATC 18  
RESULT 158  
AR137364  
LOCUS AR137364 18 bp DNA linear PAT 16-JUN-2001  
DEFINITION Sequence 111 from patent US 6197505.  
ACCESSION AR137364  
VERSION AR137364.1 GI:14478873  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Norberg,L.Torbjorn., Andersson,M.Kristina. and Lindstrom,P.Harry.Rutger.  
TITLE Methods for assessing cardiovascular status and compositions for use thereof  
JOURNAL Patent: US 6197505-A 111 06-MAR-2001;  
FEATURES  
source Location/Qualifiers  
1. .18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 8.8%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1738 CCCACTCTCTCCCTATC 1754  
Db 2 CCAACCTCTCTCCCTC 18  
RESULT 159  
AR149199/c  
LOCUS AR149199 18 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 46 from patent US 6228581.  
ACCESSION AR149199  
VERSION AR149199.1 GI:15113790  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Acton,S.L. and Ordovas,J.M.  
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses therefor  
JOURNAL Patent: US 6228581-A 46 08-MAY-2001;  
FEATURES  
source Location/Qualifiers  
1. .18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 8.8%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1682 GTGTCCTCTCCAGCGTG 1698  
Db 17 GTCTCTCTCTCCGCGCTG 1

```
RESULT 160
AR160845/c
LOCUS      18 bp      DNA      linear      PAT 17-OCT-2001
DEFINITION Sequence 49 from patent US 6255111.
ACCESSION  AR160845
VERSION     AR160845.1  GI:16225674
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Bennett, C. Frank, and Cowse, L. M.
TITLE     Antisense modulation of Her-4 expression
JOURNAL   Patent: US 6255111-A 49 03-JUL-2001;
FEATURES   Location/Qualifiers
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1723 AGATGGAGATTGGCTCC 1739
Db 18 AGTTTGAGATGGCTCC 2

RESULT 161
BD231347
LOCUS      18 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Genes for assessing cardiovascular status and compositions for use
            thereof.
ACCESSION  BD231347
VERSION    BD231347.1  GI:33041117
KEYWORDS   JP 2002527079-A/111.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Norberg, L. T., Andersson, M. K., Lindstrom, P. H. R. and Jonsson, L.
TITLE     Genes for assessing cardiovascular status and compositions for use
            thereof
JOURNAL   Patent: JP 2002527079-A 111 27-AUG-2002;
            PAIROSEAKENSINGU AB
COMMENT    OS Artificial Sequence
            PN JP 2002527079-A/111
            PD 27-AUG-2002
            PF 13-OCT-1999 JP 2000576056
            PR 14-OCT-1998 US 60/104286,14-OCT-1998 US 60/104302 PI
            LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI
            RUTGER LINDSTROM,
            PI LENA JONSSON
            PC C12Q1/68,C12N15/09//G01N33/53,G01N33/566,C12N15/00 CC Genes
            for assessing cardiovascular status
            and compositions for
            CC use thereof
            FH Key Location/Qualifiers
            FT source 1..18
            FT /organism="Artificial Sequence".
            FT Location/Qualifiers
            source 1..18
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1738 CCCAACTCCTCCCTATC 1754
Db 2 CCAACTTCCTCCCTCTC 18

RESULT 162
E10022
LOCUS      18 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Antisense phosphorothioate DNA complementary to 2-7th codons of
            human amidophosphoribosyltransferase cDNA.
ACCESSION  E10022
VERSION    E10022.1  GI:22026644
KEYWORDS   JP 1995255487-A/1.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 18)
AUTHORS   Itakura, M.
TITLE     DNA AND ITS DERIVATIVE
JOURNAL   Patent: JP 1995255487-A 1 09-OCT-1995;
            OTSUKA PHARMACEUTICAL FACTORY INC
COMMENT    OS None
            OC Artificial sequences.
            PN JP 1995255487-A/1
            PD 09-OCT-1995
            PF 28-MAR-1994 JP 1994056879
            PI ITAKURA MITSUO
            PC C12N15/09,A61K35/12,C07H21/04//A61K31/70,A61K48/00,C12N9/10;
            CC strandedness: Single;
            CC topology: Linear;
            CC hypothetical: No;
            CC anti-sense: Yes;
            FH Key Location/Qualifiers
            FH source 1..18
            FT /organism="Artificial sequences" FT
            FT misc_feature 1..18
            FT /note="phosphorothioate DNA"
            FT misc_feature 1..18
            FT /note="complementary to 2-7th codons of human
            amidophosphoribosyltransferase cDNA".
FEATURES   Location/Qualifiers
            source 1..18
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1738 CCCAACTCCTCCCTATC 1754
Db 2 CCCAACTCCTCCAGCTC 18

RESULT 163
I14568/c
LOCUS      18 bp      DNA      linear      PAT 26-SEP-1995
DEFINITION Sequence 45 from patent US 5451512.
ACCESSION  I14568
VERSION    I14568.1  GI:997051
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Apple, R. J., Bugawan, T. L. and Erlich, H. A.
TITLE     Methods and reagents for HLA class I A locus DNA typing
JOURNAL   Patent: US 5451512-A 45 19-SEP-1995;
FEATURES   Location/Qualifiers
            source 1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.8%; Score 12.2; DB 1; Length 18;
```

```
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1732 TTGGCTCCCAACTCTC 1748
| | | | | | | | | | | | | | | |
Db 17 TAGGCTCTCAACTGCTC 1

RESULT 164
188615
LOCUS 188615 18 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 13 from patent US 5719021.
ACCESSION I88615
VERSION I88615.1 GI:3408555
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Inouye,M.
TITLE Protein activation
JOURNAL Patent: US 5719021-A 13 17-FEB-1998;
FEATURES
source
Location/Qualifiers
1..18
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1636 GGGCTTGTAGCAGAGG 1652
| | | | | | | | | | | | | | | |
Db 2 GGGTTGTTTCAGAGG 18

RESULT 165
AR350406/c
LOCUS AR350406 18 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 20 from patent US 6586411.
ACCESSION AR350406
VERSION AR350406.1 GI:33751525
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Russell,S.J. and Morris,J.
TITLE System for monitoring the location of transgenes
JOURNAL Patent: US 6586411-A 20 01-JUL-2003;
FEATURES
source
Location/Qualifiers
1..18
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match 8.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1717 GTACGAGATCGAGATT 1733
| | | | | | | | | | | | | | | |
Db 17 GTAGGCAGATGAAGATT 1

RESULT 166
AR409159/c
LOCUS AR409159 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 16 from patent US 6632800.
ACCESSION AR409159
VERSION AR409159.1 GI:40159778
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Best Local Similarity 82.4%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1738 CCCAACTCCTCCCTATC 1754
| | | | | | | | | | | | | | | |
Db 2 CCAACCTCCTCCCTCTC 18

RESULT 168
AX244626/c
LOCUS AX244626 18 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 10 from Patent WO0166129.
ACCESSION AX244626
VERSION AX244626.1 GI:15859527
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stamm,S., Wirth,B., Hofmann,Y., Androphy,E. and Lorson,C.
TITLE Substances for the treatment of spinal muscular atrophy
JOURNAL Patent: WO 0166129-A 10 13-SEP-2001;
FEATURES
source
Location/Qualifiers
1..18
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
```

Query Match	8.8%	Score 12.2;	DB 1;	Length 18;
Best Local Similarity	82.4%;	Pred. No. 2e+02;		
Matches	14;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
QY	1731	ATTGGCTCCCAACTCCT	1747	
DB	18	ATGGCTCCCATCTCCT	2	
RESULT 169				
AX7951173/c				
LOCUS	AX7951173	18 bp	DNA	linear
DEFINITION	Sequence 3 from Patent EPI323825.			
ACCESSION	AX7951173			
VERSION	AX7951173.1	GI:37515934		
KEYWORDS				
SOURCE	synthetic construct			
ORGANISM	artificial sequences.			
REFERENCE	1			
AUTHORS	Giuliano,G., Rosati,C., Dharmapuri,S., Pallara,P. and Camara,B.			
TITLE	Recombinant plants and dna constructs			
JOURNAL	Patent: Ep 1323825-A 3 02-JUL-2003;			
	ENEA ENTE PER LE NUOVE TECNOLOGIE, L'ENERGIA E L'AMBIENTE (IT) ;			
	Biogen S.r.l. (IT)			
FEATURES				
source	1. .18			
	Location/Qualifiers			
	/organism="synthetic construct"			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:32630"			
	/note="Upstream primer used to detect the expression of			
	the gene Capsicu m annum B-Chy by RT-PCR"			
primer_bind	1. .18			
	/note="Ca-Chy Upstream Primer"			
Query Match	8.8%	Score 12.2;	DB 1;	Length 18;
Best Local Similarity	82.4%;	Pred. No. 2e+02;		
Matches	14;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
QY	1644	AGCAGAGGCGACGACC	1660	
DB	17	AGCACAAAGCAGCAGC	1	
RESULT 170				
BD075238				
LOCUS	BD075238	18 bp	DNA	linear
DEFINITION	Methods for assessing cardiovascular status and compositions for			
	use thereof.			
ACCESSION	BD075238			
VERSION	BD075238.1	GI:22620841		
KEYWORDS	JP 2001519660-A/111.			
SOURCE	synthetic construct			
ORGANISM	artificial sequences.			
REFERENCE	1 (bases 1 to 18)			
AUTHORS	Norberg,J.T., Andersson,M.K. and Lindstrom,P.H.R.			
TITLE	Methods for assessing cardiovascular status and compositions for			
	use thereof			
JOURNAL	Patent: JP 2001519660-A 111 23-OCT-2001;			
	EURONA MEDICAL AB			
COMMENT	OS Artificial Sequence			
	PN JP 2001519660-A/111			
	ED 23-OCT-2001			
	PF 01-APR-1998 JP 1998542530			
	PR 04-APR-1997 US 60/042930			
	PI LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI			
	RUTGER LINDSTROM			
	PC C12Q1/68,C07K14/72,C07K14/575,C12N9/48			
	CC Description of Artificial Sequence: PCR PRIMER PH Key			

ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Guida,M. and Hall,J.  
TITLE Genetic typing of the human cytochrome P450 2A6 gene and related materials and methods  
JOURNAL Patent: US 6492115-A 5 10-DEC-2002;  
FEATURES  
source  
1..16  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 8.6%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1634 TGGGGCTGTAG 1645  
Db 1 TGGGGCTGTAG 12  
BD254997 17 bp DNA linear PAT 17-JUL-2003  
LOCUS Regulation of repressor genes using nucleic acid molecules.  
DEFINITION BD254997  
ACCESSION BD254997  
VERSION BD254997.1 GI:33064767  
KEYWORDS JP 2002541795-A/2790.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.  
TITLE Regulation of repressor genes using nucleic acid molecules  
JOURNAL Patent: JP 2002541795-A 2790 10-DEC-2002;  
COMMENT RIBOZYME PHARMACEUTICALS INC  
OS Eukaryote  
EN JP 2002541795-A/2790  
PD 10-DEC-2002  
PF 11-APR-2000 JP 2000611654  
PR 12-APR-1999 US 60/129390  
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC  
C12N15/09,A61K38/00,A61K48/00,A61P43/00,C12N5/10, PC  
C12P21/02,  
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC  
C12R1:91),  
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,  
PC A61K37/02,  
PC (C12N5/00,C12R1:91)  
CC Regulation of repressor genes using nucleic acid molecules FH  
Key Location/Qualifiers  
FT source 1..17  
FT /organism='Eukaryote'.  
FEATURES  
source  
1..17  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
Query Match 8.6%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1651 GGCAAGCACCAG 1662  
Db 12 GGCAAGCACCAG 1  
BD254997 17 bp DNA linear PAT 22-NOV-2002  
LOCUS Regulation of repressor genes using nucleic acid molecules.  
DEFINITION BD254997  
ACCESSION BD254997  
VERSION BD254997.1 GI:33064767  
KEYWORDS JP 2002541795-A/2790.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.  
TITLE Regulation of repressor genes using nucleic acid molecules  
JOURNAL Patent: JP 2002541795-A 2790 10-DEC-2002;  
COMMENT RIBOZYME PHARMACEUTICALS INC  
OS Eukaryote  
EN JP 2002541795-A/2790  
PD 10-DEC-2002  
PF 11-APR-2000 JP 2000611654  
PR 12-APR-1999 US 60/129390  
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC  
C12N15/09,A61K38/00,A61K48/00,A61P43/00,C12N5/10, PC  
C12P21/02,  
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC  
C12R1:91),  
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,  
PC A61K37/02,  
PC (C12N5/00,C12R1:91)  
CC Regulation of repressor genes using nucleic acid molecules FH  
Key Location/Qualifiers  
FT source 1..17  
FT /organism='Eukaryote'.  
FEATURES  
source  
1..17  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
Query Match 8.6%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1651 GGCAAGCACCAG 1662  
Db 12 GGCAAGCACCAG 1  
BD254997 17 bp DNA linear PAT 22-NOV-2002  
LOCUS Regulation of repressor genes using nucleic acid molecules.  
DEFINITION BD254997  
ACCESSION BD254997  
VERSION BD254997.1 GI:33064767  
KEYWORDS JP 2002541795-A/2790.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.  
TITLE Regulation of repressor genes using nucleic acid molecules  
JOURNAL Patent: JP 2002541795-A 2790 10-DEC-2002;  
COMMENT RIBOZYME PHARMACEUTICALS INC  
OS Eukaryote  
EN JP 2002541795-A/2790  
PD 10-DEC-2002  
PF 11-APR-2000 JP 2000611654  
PR 12-APR-1999 US 60/129390  
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC  
C12N15/09,A61K38/00,A61K48/00,A61P43/00,C12N5/10, PC  
C12P21/02,  
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC  
C12R1:91),  
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,  
PC A61K37/02,  
PC (C12N5/00,C12R1:91)  
CC Regulation of repressor genes using nucleic acid molecules FH  
Key Location/Qualifiers  
FT source 1..17  
FT /organism='Eukaryote'.  
FEATURES  
source  
1..17  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

ACCESSION AX531436  
VERSION AX531436.1 GI:25254650  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shannon,M.  
TITLE Human posh-like protein 1  
JOURNAL Patent: EP 1239051-A 945 11-SEP-2002;  
FEATURES  
source  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 8.6%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1645 GCAGAAGGCAAG 1656  
Db 6 GCAGAAGGCAAG 17  
BD254997 17 bp DNA linear PAT 22-NOV-2002  
LOCUS Sequence 946 from Patent EP1239051.  
DEFINITION AX531437  
ACCESSION AX531437  
VERSION AX531437.1 GI:25254652  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shannon,M.  
TITLE Human posh-like protein 1  
JOURNAL Patent: EP 1239051-A 946 11-SEP-2002;  
FEATURES  
source  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 8.6%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1645 GCAGAAGGCAAG 1656  
Db 5 GCAGAAGGCAAG 16  
BD254997 17 bp DNA linear PAT 22-NOV-2002  
LOCUS Sequence 947 from Patent EP1239051.  
DEFINITION AX531438  
ACCESSION AX531438  
VERSION AX531438.1 GI:25254654  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shannon,M.  
TITLE Human posh-like protein 1  
JOURNAL Patent: EP 1239051-A 947 11-SEP-2002;

```

FEATURES
  source
    Acemica, Inc. (US)
    Location/Qualifiers
      1..17
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 100.0%; Score 12; DB 1; Length 17;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1645 GCAGAGGCAAG 1656
Db 4 GCAGAGGCAAG 15

RESULT 177
AX531439
LOCUS
  AX531439 17 bp DNA linear PAT 22-NOV-2002
DEFINITION
  Sequence 948 from Patent EP1239051.
ACCESSION
  AX531439
VERSION
  AX531439.1 GI:25254656
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Shannon,M.
  TITLE
    Human posh-like protein 1
  JOURNAL
    Patent: EP 1239051-A 948 11-SEP-2002;
    Acemica, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      1..17
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 100.0%; Score 12; DB 1; Length 17;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1645 GCAGAGGCAAG 1656
Db 3 GCAGAGGCAAG 14

RESULT 178
AX531440
LOCUS
  AX531440 17 bp DNA linear PAT 22-NOV-2002
DEFINITION
  Sequence 949 from Patent EP1239051.
ACCESSION
  AX531440
VERSION
  AX531440.1 GI:25254658
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Shannon,M.
  TITLE
    Human posh-like protein 1
  JOURNAL
    Patent: EP 1239051-A 949 11-SEP-2002;
    Acemica, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      1..17
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 100.0%; Score 12; DB 1; Length 17;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1645 GCAGAGGCAAG 1656
Db 2 GCAGAGGCAAG 13

RESULT 179
AX531441
LOCUS
  AX531441 17 bp DNA linear PAT 22-NOV-2002
DEFINITION
  Sequence 950 from Patent EP1239051.
ACCESSION
  AX531441
VERSION
  AX531441.1 GI:25254660
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Shannon,M.
  TITLE
    Human posh-like protein 1
  JOURNAL
    Patent: EP 1239051-A 950 11-SEP-2002;
    Acemica, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      1..17
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 100.0%; Score 12; DB 1; Length 17;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1645 GCAGAGGCAAG 1656
Db 1 GCAGAGGCAAG 12

RESULT 180
AX723858
LOCUS
  AX723858 17 bp DNA linear PAT 08-MAY-2003
DEFINITION
  Sequence 1545 from Patent WO03025176.
ACCESSION
  AX723858
VERSION
  AX723858.1 GI:30503201
KEYWORDS
  Mus musculus (house mouse)
SOURCE
  Mus musculus
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1
  AUTHORS
    Teleman,A., Anson,R. and Tuijnder,M.
  TITLE
    Sequences involved in phenomena of tumour suppression, tumour
    reversion, apoptosis and/or virus resistance and their use as
    medicines
  JOURNAL
    Patent: WO 03025176-A 1545 27-MAR-2003;
    Molecular Engines Laboratories (FR)
FEATURES
  source
    Location/Qualifiers
      1..17
      /organism="Mus musculus"
      /mol_type="unassigned DNA"
      /db_xref="taxon:10090"

Query Match
  Best Local Similarity 100.0%; Score 12; DB 1; Length 17;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1659 CCAGGCTCACAG 1670
Db 4 CCAGGCTCACAG 15

RESULT 181
AR169593
LOCUS
  AR169593 18 bp DNA linear PAT 17-DEC-2001
DEFINITION
  Sequence 9 from patent US 6291176.

```

```

ACCESSION   AR169593
VERSION     AR169593.1  GI:17907465
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Harris,J.M. and You,Q.
TITLE       Identification of a DNA region potentially useful for the detection
            of mycobacterium kansasii
JOURNAL     Patent: US 6291176-A 9 18-SEP-2001;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.6%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1721 CGGAGATGGAGAT 1732
DB 4 GGAGATGGAGAT 15

RESULT 182
LOCUS       BD235157
DEFINITION  Oligonucleotide inhibitors of bcl-xL.
ACCESSION   BD235157
VERSION     BD235157.1  GI:33044927
KEYWORDS    JP 2002519048-A/9.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stein,C.A.
TITLE       Oligonucleotide inhibitors of bcl-xL.
JOURNAL     Patent: JP 2002519048-A 9 02-JUL-2002;
            THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT     OS Artificial Sequence
            PN JP 2002519048-A/9
            PD 02-JUL-2002
            PF 02-JUL-1999 JP 2000557839
            PR 02-JUL-1998 US 09/109614
            PI CY A STEIN
            PC C12N15/09,A61K9/127,A61K31/711,A61K31/712,A61K31/7125, PC
            A61K47/42.
            CC A61K47/48,A61K48/00,A61P35/00,C12N15/00
            CC ANTISENSE OLIGONUCLEOTIDE
            CC PHOSPHOROTHIATE LINKAGE
            CC PHOSPHOROTHIATE LINKAGE
            CC PHOSPHOROTHIATE LINKAGE
            CC PHOSPHOROTHIATE LINKAGE
            CC PHOSPHOROTHIATE LINKAGE
            CC PHOSPHOROTHIATE LINKAGE
            CC PROPENYL dt
            CC PROPENYL dc
            CC PROPENYL dc
            CC PROPENYL dt
            CC PROPENYL dt
            CC PROPENYL dt
            CC PROPENYL dc
            CC PROPENYL dt
            CC PROPENYL dt
            CC Key
            FT misc_binding (1)..(4)
            FT misc_binding (5)..(7)
            FT misc_binding (9)..(10)
            FT misc_binding (11)..(12)
            FT misc_binding (15)..(18)
            FT modified_base (3)..(3)
            FT modified_base (4)..(4)
            FT modified_base (6)..(7)
            FT modified_base (9)..(9)
            FT modified_base (10)..(10)
            FT modified_base (11)..(11)
            FT modified_base (12)..(13)
            FT modified_base (16)..(17).
FEATURES     Location/Qualifiers
            source
            1..18
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      8.6%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1720 CGGAGATGGAGA 1731
DB 14 CGGAGATGGAGA 3

RESULT 184
LOCUS       BD235176/c
DEFINITION  Oligonucleotide inhibitors of bcl-xL.
ACCESSION   BD235176
VERSION     BD235176.1  GI:33044946
KEYWORDS    JP 2002519048-A/28.

```



```

SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 18)
AUTHORS    Stein,C.A.
TITLE      Oligonucleotide inhibitors of bcl-xL
JOURNAL    THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK

COMMENT     OS Artificial Sequence
            PN JP 2002519048-A/28
            PD 02-JUL-2002
            PF 02-JUL-1999 JP 2000557839
            PR 02-JUL-1998 US 09/109614
            PI CY A STEIN
            PC

C12N15/09,A61K9/127,A61K9/51,A61K31/711,A61K31/712,A61K31/7125, PC
A61K47/42,
PC A61K47/48,A61K48/00,A61P35/00,C12N15/00
CC ANTISENSE OLIGONUCLEOTIDE
CC CC PHOSPHOROTHIOATE LINKAGE
CC CC PHOSPHOROTHIOATE LINKAGE
CC CC PHOSPHOROTHIOATE LINKAGE
CC CC PHOSPHOROTHIOATE LINKAGE
CC CC PHOSPHOROTHIOATE LINKAGE
CC CC PHOSPHOROTHIOATE LINKAGE
FH Key Location/Qualifiers
FT misc binding (1) . (4)
FT misc binding (5) . (7)
FT misc binding (9) . (10)
FT misc binding (11) . (12)
FT misc binding (15) . (18)

FEATURES             Location/Qualifiers
     source          1..18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

Query Match      8.6%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1720 CGGAGATGGAGA 1731
Db 14 CGGAGATGGAGA 3

RESULT 185
E33346
LOCUS      Identification of DNA region potentially efficacious in detecting
DEFINITION Mycobacterium kansaii.
ACCESSION  E33346.1 GI:13026956
VERSION     JP 199915589-A/9.
KEYWORDS    synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS    James,M.H. and Kimin,Y.
TITLE      Identification of DNA region potentially efficacious in detecting
JOURNAL    Mycobacterium kansaii
            Patent: JP 199915589-A 9 15-JUN-1999;
            BECTON DICKINSON & CO
COMMENT     OS Artificial Sequence
            PN JP 199915589-A/9
            PD 15-JUN-1999
            PF 22-SEP-1998 JP 1998267503
            PR 25-SEP-1997 US 08/937580
            PI JAMES M HARRIS,KIMIN YOU
            PC C12N15/09,C12Q1/04,C12Q1/68// (C12Q1/04,C12R1:32),C12N15/00 CC

FH Key Location/Qualifiers
FT source          1..18
                     /organism='Artificial Sequence'.

```

```

FEATURES             Location/Qualifiers
     source          1..18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

Query Match      8.6%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1721 GGAGATGGAGAT 1732
Db 4 GGAGATGGAGAT 15

RESULT 186
AX599639
LOCUS      Sequence 979 from Patent WO02077272.
DEFINITION 18 bp DNA
ACCESSION  AX599639
VERSION     AX599639.1 GI:28399787
KEYWORDS    synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,B., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pellet.C. and Ziebarth,H.
            Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
            Patent: WO 02077272-A 979 03-OCT-2002;
            Epigenomics AG (DE)
TITLE       Location/Qualifiers
JOURNAL     1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Detection oligonucleotide for PITX2"

FEATURES             Location/Qualifiers
     source          1..18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for PITX2"

Query Match      8.6%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1712 TAGGAGTACGGA 1723
Db 1 TAGGAGTACGGA 12

RESULT 187
A64217
LOCUS      Sequence 5 from Patent WO9727332.
DEFINITION 15 bp DNA
ACCESSION  A64217
VERSION     A64217.1 GI:3717648
KEYWORDS    unidentified
            SOURCE
            ORGANISM    unidentified
            unclassified.
REFERENCE   1
AUTHORS    Stuyver,L., Louwagie,J. and Rossau,R.
TITLE      METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE
            TRANSCRIPTASE GENE
            Patent: WO 9727332-A 5 31-JUL-1997;
            INNOGENETICS NV (BE)
COMMENT     Other publication AU 144397 19970820.
JOURNAL    Location/Qualifiers
FEATURES    1..15
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

```

```
Query Match      8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1717 GTACGGAGATGGAGA 1731
Db 1 GTACAGAGATGGAAA 15

RESULT 188
AR011805/c
LOCUS AR011805 15 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 18 from patent US 5763172.
ACCESSION AR011805
VERSION AR011805.1 GI:3969795
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Magda,D., Sessler,J.L., Wright,M., Miller,R.A. and Dow,W.C.
TITLE Method of phosphate ester hydrolysis
JOURNAL Patent: US 5763172-A 18 09-JUN-1998;
FEATURES
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1659 CCAGGCTCACAGCTG 1673
Db 15 CCCGGCTCACAGATG 1

RESULT 191
I36660/c
LOCUS I36660 15 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 4 from patent US 5607924.
ACCESSION I36660
VERSION I36660.1 GI:2086485
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Magda,D., Sessler,J.L., Iverson,B.L., Sansom,P.I. and Wright,M.
TITLE DNA photocleavage using texaphyrins
JOURNAL Patent: US 5607924-A 04-MAR-1997;
FEATURES
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1659 CCAGGCTCACAGCTG 1673
Db 15 CCCGGCTCACAGATG 1

RESULT 192
I83457/c
LOCUS I83457 15 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 1 from patent US 5714328.
ACCESSION I83457
VERSION I83457.1 GI:3406987
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Magda,D. and Sessler,J.L.
TITLE RNA photocleavage using texaphyrins
JOURNAL Patent: US 5714328-A 1 03-FEB-1998;
FEATURES
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1717 GTACGGAGATGGAGA 1731
Db 1 GTACAGAGATGGAAA 15

RESULT 190
I27821/c
LOCUS I27821 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 4 from patent US 5567687.
ACCESSION I27821
VERSION I27821.1 GI:1818597
KEYWORDS
```

AUTHORS	Lieven,S., Joost,L. and Rudi,R.
TITLE	Method for detection of drug-induced mutations in the reverse transcriptase gene
JOURNAL	Patent: US 631389-A 5 18-DEC-2001;
FEATURES	Location/Qualifiers source 1..15 /organism="unknown" /mol_type="genomic DNA"
Query Match	8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity	86.7%; Pred.No.1.8e+02;
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1717 GTACGGAGATGGAGA 1731 
Db	1 GTACAGAGATGGAA 15
RESULT 196	
BD057672/c	
LOCUS	BD057672 15 bp DNA linear PAT 27-AUG-2002
DEFINITION	Fusion proteins comprising bacteriophage coat protein and a single-chain T cell receptor.
ACCESSION	BD057672
VERSION	BD057672.1 GI:22603278
KEYWORDS	JP 2001514503-A/48.
SOURCE	Aspergillus tubingensis
ORGANISM	Aspergillus tubingensis Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE	1 (bases 1 to 15)
AUTHORS	Weidanz,J.A., Card,K.F. and Wong,H.C.
TITLE	Fusion proteins comprising bacteriophage coat protein and a single-chain T cell receptor
JOURNAL	Patent: JP 2001514503-A 48 11-SEP-2001;
COMMENT	SUNOL MOLECULAR CORP PN JP 2001514503-A/48 PD 11-SEP-2001 PF 05-MAR-1998 JP 1998537984 PR 07-MAR-1997 US 08/813781 PI JON A WEIDANZ,KIMBERLIN F CARD,HING C WONG PC Cl2Q1/68,Cl2N7/01,Cl2N15/70 CC Strandedness: Single; CC Topology: Linear; FH Key Location/Qualifiers. FEATURES source 1..15 /organism="Aspergillus tubingensis" /mol_type="genomic DNA" /db_xref="taxon:5068"
Query Match	8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity	86.7%; Pred.No.1.8e+02;
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1656 GCACCAGGCTCAG 1670 
Db	15 GAACCAGACTCACAG 1
RESULT 197	
BD081502/c	
LOCUS	BD081502 15 bp DNA linear PAT 27-AUG-2002
DEFINITION	Soluble single-chain T-cell receptor proteins.
ACCESSION	BD081502
VERSION	BD081502.1 GI:22627105
KEYWORDS	JP 2001519143-A/48.
SOURCE	synthetic construct
ORGANISM	synthetic construct artificial sequences. 1 (bases 1 to 15) Weidanz,J.A., Card,K.F. and Wong,H.C. Soluble single-chain T-cell receptor proteins
REFERENCE	1 (bases 1 to 15)
AUTHORS	Weidanz,J.A., Card,K.F. and Wong,H.C.
TITLE	Soluble single-chain T-cell receptor proteins

AUTHORS	Lieven,S., Joost,L. and Rudi,R.
TITLE	Method for detection of drug-induced mutations in the reverse transcriptase gene
JOURNAL	Patent: US 631389-A 5 18-DEC-2001;
FEATURES	Location/Qualifiers source 1..15 /organism="unknown" /mol_type="genomic DNA"
Query Match	8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity	86.7%; Pred.No.1.8e+02;
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1717 GTACGAGATGGAGA 1731 
Db	1 GTACAGAGTGGAA 15 
RESULT 196	
BD057672/c	
LOCUS	BD057672 15 bp DNA linear PAT 27-AUG-2002
DEFINITION	Fusion proteins comprising bacteriophage coat protein and a single-chain T cell receptor.
ACCESSION	BD057672
VERSION	BD057672.1 GI:22603278
KEYWORDS	JP 2001514503-A/48.
SOURCE	Aspergillus tubingensis
ORGANISM	Aspergillus tubingensis Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus. Weidanz,J.A., Card,K.F. and Wong,H.C. Fusion proteins comprising bacteriophage coat protein and a single-chain T cell receptor Patent: JP 2001514503-A 48 11-SEP-2001; SUNOL MOLECULAR CORP PN JP 2001514503-A/48 PD 11-SEP-2001 PF 05-MAR-1998 JP 1998537984 PR 07-MAR-1997 US 08/813781 PI JON A WEIDANZ,KIMBERLIN F CARD,HING C WONG PC Cl2Q1/68,Cl2N7/01,Cl2N15/70 CC Strandedness: Single; CC Topology: Linear; FH Key Location/Qualifiers.
REFERENCE	1 (bases 1 to 15)
AUTHORS	Weidanz,J.A., Card,K.F. and Wong,H.C.
TITLE	Fusion proteins comprising bacteriophage coat protein and a single-chain T cell receptor
JOURNAL	Patent: JP 2001514503-A 48 11-SEP-2001;
COMMENT	SUNOL MOLECULAR CORP PN JP 2001514503-A/48 PD 11-SEP-2001 PF 05-MAR-1998 JP 1998537984 PR 07-MAR-1997 US 08/813781 PI JON A WEIDANZ,KIMBERLIN F CARD,HING C WONG PC Cl2Q1/68,Cl2N7/01,Cl2N15/70 CC Strandedness: Single; CC Topology: Linear; FH Key Location/Qualifiers.
FEATURES	source 1..15 /organism="Aspergillus tubingensis" /mol_type="genomic DNA" /db_xref="taxon:5068"
Query Match	8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity	86.7%; Pred.No.1.8e+02;
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1656 GCACCAGGCTCAG 1670 
Db	15 GAACCACTCACAG 1 
RESULT 197	
BD081502/c	
LOCUS	BD081502 15 bp DNA linear PAT 27-AUG-2002
DEFINITION	Soluble single-chain T-cell receptor proteins.
ACCESSION	BD081502
VERSION	BD081502.1 GI:22627105
KEYWORDS	JP 2001519143-A/48.
SOURCE	synthetic construct
ORGANISM	synthetic construct artificial sequences. 1 (bases 1 to 15) Weidanz,J.A., Card,K.F. and Wong,H.C. Soluble single-chain T-cell receptor proteins
REFERENCE	1 (bases 1 to 15)
AUTHORS	Weidanz,J.A., Card,K.F. and Wong,H.C.
TITLE	Soluble single-chain T-cell receptor proteins

```
JOURNAL Patent: JP 2001519143-A 48 23-OCT-2001;
SUNOL MOLECULAR CORP
OS Artificial Sequence
COMMENT EN JP 2001519143-A/48
PD 23-OCT-2001
PF 28-SEP-1998 JP 2000514936
PI 02-OCT-1997 US 08/943086
PR JON A WEIDANZ, KIMBERLYN F CARD, HING C WONG
PC C12N15/09, A61K38/00, A61K39/395, A61P43/00, C07K14/725, C07K16/28,
PC C12P21/02//
PC C12P21/08, C12N15/00, A61K37/02
PC C12P21/02, C12N15/00, A61K37/02
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1..15
FT /organism='Artificial Sequence'.
FEATURES
source
1..15
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1656 GCACCGGCTCACAG 1670
Db 15 GAACCGACTCACAG 1
RESULT 198
BD090530/c
LOCUS 15 bp DNA linear PAT 27-AUG-2002
DEFINITION Photocleavage of RNA using texaphylline.
ACCESSION BD090530
VERSION JP 2001316270-A/1.
KEYWORDS synthetic construct
SOURCE artificial sequences.
ORGANISM 1 (bases 1 to 15)
AUTHORS Magda, D. and Sessler, J.L.
TITLE Photocleavage of RNA using texaphylline
JOURNAL Patent: JP 2001316270-A 1 13-NOV-2001;
PHARMACYCLICS INC. BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM
COMMENT OS Artificial Sequence
PN JP 2001316270-A/1
PD 13-NOV-2001
PF 07-JUN-1995 US 08/484551
PR DARREN MAGDA, JONATHAN L SESSLER
PC A61K31/7125, A61K31/7135, A61K41/00, A61P35/00//C07H21/00 PC
, C07H23/00, C12N15/09,
PC C12N15/00
CC Photocleavage of RNA using texaphylline
FH Key Location/Qualifiers
FT source 1..15
FT /organism='Artificial Sequence'.
FEATURES
source
1..15
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
Query Match 8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1659 CCAGGCTCACAGCTG 1673
Db 15 CCGGCTCACAGATG 1
RESULT 200
AR011801/c
LOCUS 16 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 14 from patent US 5763172.
ACCESSION AR011801
VERSION AR011801.1 GI:3969791
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Magda, D., Sessler, J.L., Wright, M., Miller, R.A. and Dow, W.C.
TITLE Method of phosphate ester hydrolysis
JOURNAL Patent: US 5763172-A 14 09-JUN-1998;
FEATURES
source
1..16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 8.5%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1655 AGCACCAGGCTCACA 1669
Db 15 AACACCCGGCTCACA 1
RESULT 201
BD233058
```

```

LOCUS      BD233058                      16 bp    DNA        linear        PAT 17-JUL-2003
DEFINITION Method of detecting mutation selected by drug in HIV protease gene.
ACCESSION  BD233058
VERSION    BD233058.1  GI:33042828
KEYWORDS   JP 2002518065-A/154.
SOURCE     Aids-associated retrovirus
ORGANISM   Aids-associated retrovirus
REFERENCE  1 (bases 1 to 16)
AUTHORS    Stuyver,L.
TITLE      Method of detecting mutation selected by drug in HIV protease gene
JOURNAL    INNOGENETICS NV
COMMENT    OS Aids-associated retrovirus
          PN JP 2002518065-A/154
          PD 25-JUN-2002
          PF 22-JUN-1999 JP 2000556068
          PR 24-JUN-1998 EP 98870143.9
          PT LIEVEN STUYVER
          PC C12N15/09, C12Q1/68, C12Q1/70, C12N15/00
          CC Method of detecting mutation selected by drug in HIV protease
          FH Key gene Location/Qualifiers
          FT source 1..16
          FT Location/Qualifiers
          source 1..16
          /organism='Aids-associated retrovirus'
          /mol_type='genomic DNA'
          /db_xref='taxon:11966'

Query Match      8.5%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1721 GGAGTGGAGATTGG 1735
      |||||
Db 2 GGAGTTGGAGGTGG 16

RESULT 202
AX007612
LOCUS      AX007612                      16 bp    DNA        linear        PAT 06-SEP-2000
DEFINITION Sequence 154 from Patent WO9967428.
ACCESSION  AX007612
VERSION    AX007612.1  GI:9995309
KEYWORDS   Aids-associated retrovirus
SOURCE     Aids-associated retrovirus
ORGANISM   Aids-associated retrovirus
REFERENCE  1
AUTHORS    Stuyver,L.
TITLE      Method for detection of drug-selected mutations in the hiv protease
JOURNAL    INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
FEATURES   source 1..16
          /organism='Aids-associated retrovirus'
          /mol_type='unassigned DNA'
          /db_xref='taxon:11966'

Query Match      8.5%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1721 GGAGTGGAGATTGG 1735
      |||||
Db 2 GGAGTTGGAGGTGG 16

RESULT 203
BD234600
LOCUS      BD234600                      17 bp    DNA        linear        PAT 17-JUL-2003
DEFINITION Thymidine kinase mutants and fusion proteins having thymidine
ACCESSION  BD234600
VERSION    BD234600.1  GI:33044370
KEYWORDS   JP 2002516061-A/4.
SOURCE     Unidentified
ORGANISM   Unidentified
REFERENCE  1 (bases 1 to 17)
AUTHORS    Black,M.E.
TITLE      Thymidine kinase mutants and fusion proteins having thymidine
JOURNAL    Patent: JP 2002516061-A 4 04-JUN-2002;
          DARWIN MOLECULAR CORP
COMMENT    OS Unidentified
          PN JP 2002516061-A/4
          PD 04-JUN-2002
          PF 14-OCT-1998 JP 2000516019
          PR 14-OCT-1997 US 60/061812
          PT MARGARET E BLACK
          PC C12N15/09, A61K31/711, A61K35/76, A61K38/45, A61K48/00, A61K49/00,
          A61P31/00,
          PC A61P35/00, C12N5/10, C12N9/12, C12N15/00, A61K37/52, C12N5/00 CC
          CC Strandedness: Single;
          CC Topology: Linear;
          CC Thymidine kinase mutants and fusion proteins having thymidine
          CC kinase and
          CC Guanylate kinase activities
          FH Key Location/Qualifiers
          FT source 1..17
          FT Location/Qualifiers
          source 1..17
          /organism='Unidentified'
          /mol_type='genomic DNA'
          /db_xref='taxon:32644'

Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCGTGGT 1700
      |||||
Db 1 CCCCTCCAGCGGT 15

RESULT 204
BD254104
LOCUS      BD254104                      17 bp    DNA        linear        PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION  BD254104
VERSION    BD254104.1  GI:33063874
KEYWORDS   JP 2002541795-A/1897.
SOURCE     Unidentified
ORGANISM   Unidentified
REFERENCE  1 (bases 1 to 17)
AUTHORS    Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE      Regulation of repressor genes using nucleic acid molecules
JOURNAL    Patent: JP 2002541795-A 1897 10-DEC-2002;
          RIBOZYME PHARMACEUTICALS INC
COMMENT    OS Eukaryote
          PN JP 2002541795-A/1897
          PD 10-DEC-2002
          PF 11-APR-2000 JP 2000611654
          PR 12-APR-1999 US 60/129390
          PT LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
          C12N15/09, A61K38/00, A61K48/00, A61P43/00, C12N5/10, PC
          C12P21/02,
          PC
          C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
          C12R1:91),

```

Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;

RESULT	209
AR286132/	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	

PAT 10-APR-2003

Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,  
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
TITLE Synthetic ribonucleic acids with RNase activity  
JOURNAL Patent: US 6528640-A 504 04-MAR-2003;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"  
  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1660 CAGGCTCACAGCTGG 1674  
Db 17 CAGTCACACAGCTGG 3  
  
RESULT 210  
LOCUS AR286133/c AR286133 17 bp RNA linear PAT 10-APR-2003  
DEFINITION Sequence 505 from patent US 6528640.  
ACCESSION AR286133  
VERSION AR286133.1 GI:29723729  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,  
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
TITLE Synthetic ribonucleic acids with RNase activity  
JOURNAL Patent: US 6528640-A 505 04-MAR-2003;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"  
  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1660 CAGGCTCACAGCTGG 1674  
Db 17 CAGTCACACAGCTGG 3  
  
RESULT 210  
LOCUS AR286133/c AR286133 17 bp RNA linear PAT 10-APR-2003  
DEFINITION Sequence 505 from patent US 6528640.  
ACCESSION AR286133  
VERSION AR286133.1 GI:29723729  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,  
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
TITLE Synthetic ribonucleic acids with RNase activity  
JOURNAL Patent: US 6528640-A 505 04-MAR-2003;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"  
  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1660 CAGGCTCACAGCTGG 1674  
Db 15 CAGTCACACAGCTGG 1  
  
RESULT 211  
LOCUS AR286141/c AR286141 17 bp RNA linear PAT 10-APR-2003  
DEFINITION Sequence 513 from patent US 6528640.  
ACCESSION AR286141  
VERSION AR286141.1 GI:29723737  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,  
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
TITLE Synthetic ribonucleic acids with RNase activity  
JOURNAL Patent: US 6528640-A 513 04-MAR-2003;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"  
  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1660 CAGGCTCACAGCTGG 1674  
Db 17 CGGGCGCACAGCTGG 3  
  
RESULT 212  
LOCUS AR286177 AR286177 17 bp RNA linear PAT 10-APR-2003  
DEFINITION Sequence 549 from patent US 6528640.  
ACCESSION AR286177  
VERSION AR286177.1 GI:29723773  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,  
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
TITLE Synthetic ribonucleic acids with RNase activity  
JOURNAL Patent: US 6528640-A 549 04-MAR-2003;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"  
  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1677 CCCTGCTCTCTCTC 1691  
Db 2 CCCTGATGTCTCTC 16  
  
RESULT 213  
LOCUS AR323019 AR323019 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 421 from patent US 6566127.  
ACCESSION AR323019  
VERSION AR323019.1 GI:33708827  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions  
related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 421 20-MAY-2003;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"  
  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1745 CCTCCTATCTCTAA 1759  
Db 3 CCTCCTATCTCGAA 17  
  
RESULT 214  
LOCUS AR323020 AR323020 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 422 from patent US 6566127.  
ACCESSION AR323020  
VERSION AR323020.1 GI:33708828  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions  
related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 421 20-MAY-2003;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

QY 1660 CAGGCTCACAGCTGG 1674



AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,  
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
TITLE Oligoribonucleotides with enzymatic activity  
JOURNAL Patent: US 6617438-A 548 09-SEP-2003;  
FEATURES Location/Qualifiers  
1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1677 CCTGCTGCTCTCTC 1691  
||||| |||||  
Db 2 CCTGATGCTCTC 16

RESULT 220  
AR401998  
LOCUS AR401998 17 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 338 from patent US 6623962.  
ACCESSION AR401998  
VERSION AR401998.1 GI:40149448  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.  
TITLE Enzymatic nucleic acid treatment of diseases of conditions related  
to levels of epidermal growth factor receptors  
JOURNAL Patent: US 6623962-A 338 23-SEP-2003;  
FEATURES Location/Qualifiers  
1. .17  
source /organism="unknown"  
/mol\_type="genomic DNA"

Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1685 TCTCTCCAGCGTGG 1699  
||||| |||||  
Db 3 TCTCTCCATCTCTG 17

RESULT 221  
AX039622  
LOCUS AX039622 17 bp DNA linear PAT 18-NOV-2000  
DEFINITION Sequence 11 from Patent WO0063441.  
ACCESSION AX039622  
VERSION AX039622.1 GI:11229651  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE 1  
AUTHORS Herrnstadt,C. and Davis,R.E.  
TITLE Single nucleotide polymorphisms in mitochondrial genes that segreg  
ate with alzheimer's disease  
JOURNAL Patent: WO 0063441-A 11 26-OCT-2000;  
MITOKOR (US)

FEATURES Location/Qualifiers  
1. .17  
source /organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="PCR primer"

Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1652 GCAAGCACCAGGCTC 1666  
||||| |||||  
Db 1 GCTATCACCAGGCTC 15

RESULT 222  
AX039652  
LOCUS AX039652 17 bp DNA linear PAT 18-NOV-2000  
DEFINITION Sequence 41 from Patent WO0063441.  
ACCESSION AX039652  
VERSION AX039652.1 GI:11229681  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Herrnstadt,C. and Davis,R.E.  
TITLE Single nucleotide polymorphisms in mitochondrial genes that segreg  
ate with alzheimer's disease  
JOURNAL Patent: WO 0063441-A 41 26-OCT-2000;  
MITOKOR (US)

FEATURES Location/Qualifiers  
1. .17  
source /organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="PCR primer"

Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1652 GCAAGCACCAGGCTC 1666  
||||| |||||  
Db 1 GCTATCACCAGGCTC 15

RESULT 223  
AX263012  
LOCUS AX263012 17 bp DNA linear PAT 26-OCT-2001  
DEFINITION Sequence 403 from Patent WO0173002.  
ACCESSION AX263012  
VERSION AX263012.1 GI:16511811  
KEYWORDS  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.  
TITLE Targeted chromosomal genomic alterations with modified single  
stranded oligonucleotides  
JOURNAL Patent: WO 0173002-A 403 04-OCT-2001;  
UNIVERSITY OF DELAWARE (US)

FEATURES Location/Qualifiers  
1. .17  
source /organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1695 CGTGGTGAAGTTGG 1709  
||||| |||||  
Db 1 CGTGGATGAAGTTGG 15

RESULT 224  
AX263013/c  
LOCUS AX263013 17 bp DNA linear PAT 26-OCT-2001

```

DEFINITION Sequence 404 from Patent WO0173002.
ACCESSION AX263013
VERSION AX263013.1 GI:16511812
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 404 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1695 CGTGGTGAAGTTGG 1709
||||| |||||||
Db 17 CGTGGATGAAGTTGG 3

RESULT 225
AX263016
LOCUS AX263016 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 407 from Patent WO0173002.
ACCESSION AX263016
VERSION AX263016.1 GI:16511815
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 407 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1695 CGTGGTGAAGTTGG 1709
||||| |||||||
Db 17 CGTGGATGAAGTTGG 3

RESULT 226
AX263017/c
LOCUS AX263017 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 408 from Patent WO0173002.
ACCESSION AX263017
VERSION AX263017.1 GI:16511816
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 408 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1695 CGTGGTGAAGTTGG 1709
||||| |||||||
Db 2 CGTGGATGAAGTTGG 16

RESULT 227
AX266567
LOCUS AX266567 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 3958 from Patent WO0173002.
ACCESSION AX266567
VERSION AX266567.1 GI:16515366
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 3958 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1695 CGTGGTGAAGTTGG 1709
||||| |||||||
Db 16 CGTGGATGAAGTTGG 2

RESULT 228
AX266568/c
LOCUS AX266568 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 3959 from Patent WO0173002.
ACCESSION AX266568
VERSION AX266568.1 GI:16515367
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 3959 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"

```

```
/db_xref="taxon:9606"

Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1661 AGGCTCACAGCTGGA 1675
      ||||| |||||
Db 16 AGGCTCCAGCTGGA 2

RESULT 229
AX422716/c
LOCUS      AX422716      17 bp      RNA      linear      PAT 18-JUN-2002
DEFINITION Sequence 1052 from Patent WO0188124.
ACCESSION  AX422716
VERSION     AX422716.1 GI:21526098
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
TITLE       Randi,A.M.
JOURNAL     Patent: WO 0188124-A 1052 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
  source
    Location/Qualifiers
      1..17
        /organism="Homo sapiens"
        /mol_type="unassigned RNA"
        /db_xref="taxon:9606"

Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1675 AACCTCGTGTCTCC 1689
      ||||| |||||
Db 17 AACCTCGAGTCTCC 3

RESULT 230
AX498904
LOCUS      AX498904      17 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 211 from Patent EP1229046.
ACCESSION  AX498904
VERSION     AX498904.1 GI:23381197
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan,J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 211 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      1..17
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAAGCGCAGCACC 1660
      ||||| |||||
Db 3 CGGAAGGCGAGCAGC 17

RESULT 231
AX498905
LOCUS      AX498905      17 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 212 from Patent EP1229046.
ACCESSION  AX498905
VERSION     AX498905.1 GI:23381198
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan,J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 212 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      1..17
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAAGCGCAGCACC 1660
      ||||| |||||
Db 2 CGGAAGGCGAGCAGC 16

RESULT 232
AX498906
LOCUS      AX498906      17 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 213 from Patent EP1229046.
ACCESSION  AX498906
VERSION     AX498906.1 GI:23381199
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan,J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 213 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      1..17
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match      8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAAGCGCAGCACC 1660
      ||||| |||||
Db 1 CGGAAGGCGAGCAGC 15

RESULT 233
AX499446
LOCUS      AX499446      17 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 753 from Patent EP1229046.
ACCESSION  AX499446
VERSION     AX499446.1 GI:23381739
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
1									
Zhan, J.									
Human testis expressed patched like protein									
Patent: EP 1229046-A 753 07-AUG-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1664 CTCACAGCTGGAACC 1678									
17 bp DNA linear PAT 27-SEP-2002									
2 CTCACAGCTGGAACC 16									
RESULT 234									
AX499447									
LOCUS									
AX499447									
DEFINITION									
Sequence 754 from Patent EP1229046.									
ACCESSION									
AX499447									
VERSION									
AX499447.1 GI:23381740									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Zhan, J.									
TITLE									
Human testis expressed patched like protein									
JOURNAL									
Patent: EP 1229046-A 754 07-AUG-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1664 CTCACAGCTGGAACC 1678									
17 bp DNA linear PAT 22-NOV-2002									
1 CTCACAGCTGGAACC 15									
RESULT 235									
AX532098									
LOCUS									
AX532098									
DEFINITION									
Sequence 1607 from Patent EP1239051.									
ACCESSION									
AX532098									
VERSION									
AX532098.1 GI:25255958									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Shannon, M.									
TITLE									
Human posh-like protein 1									
JOURNAL									
Patent: EP 1239051-A 1607 11-SEP-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1751 TATCCTAAAGGCCCA 1765									
17 bp DNA linear PAT 22-NOV-2002									
17 TGTCCTAAAGTCCCA 3									
RESULT 237									
AX532252/c									
LOCUS									
AX532252									
DEFINITION									
Sequence 1761 from Patent EP1239051.									
ACCESSION									
AX532252									
VERSION									
AX532252.1 GI:25256289									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Shannon, M.									
TITLE									
Human posh-like protein 1									
JOURNAL									
Patent: EP 1239051-A 1761 11-SEP-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1751 TATCCTAAAGGCCCA 1765									
17 bp DNA linear PAT 22-NOV-2002									
16 TGTCCTAAAGTCCCA 2									
RESULT 238									
AX532251/c									
LOCUS									
AX532251									
DEFINITION									
Sequence 1760 from Patent EP1239051.									
ACCESSION									
AX532251									
VERSION									
AX532251.1 GI:25256287									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Shannon, M.									
TITLE									
Human posh-like protein 1									
JOURNAL									
Patent: EP 1239051-A 1760 11-SEP-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1751 TATCCTAAAGGCCCA 1765									
17 bp DNA linear PAT 22-NOV-2002									
16 TGTCCTAAAGTCCCA 2									
RESULT 239									
AX532251/c									
LOCUS									
AX532251									
DEFINITION									
Sequence 1760 from Patent EP1239051.									
ACCESSION									
AX532251									
VERSION									
AX532251.1 GI:25256287									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Shannon, M.									
TITLE									
Human posh-like protein 1									
JOURNAL									
Patent: EP 1239051-A 1760 11-SEP-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1751 TATCCTAAAGGCCCA 1765									
17 bp DNA linear PAT 22-NOV-2002									
16 TGTCCTAAAGTCCCA 2									
RESULT 240									
AX532251/c									
LOCUS									
AX532251									
DEFINITION									
Sequence 1760 from Patent EP1239051.									
ACCESSION									
AX532251									
VERSION									
AX532251.1 GI:25256287									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Shannon, M.									
TITLE									
Human posh-like protein 1									
JOURNAL									
Patent: EP 1239051-A 1760 11-SEP-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1751 TATCCTAAAGGCCCA 1765									
17 bp DNA linear PAT 22-NOV-2002									
16 TGTCCTAAAGTCCCA 2									
RESULT 241									
AX532251/c									
LOCUS									
AX532251									
DEFINITION									
Sequence 1760 from Patent EP1239051.									
ACCESSION									
AX532251									
VERSION									
AX532251.1 GI:25256287									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Shannon, M.									
TITLE									
Human posh-like protein 1									
JOURNAL									
Patent: EP 1239051-A 1760 11-SEP-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1751 TATCCTAAAGGCCCA 1765									
17 bp DNA linear PAT 22-NOV-2002									
16 TGTCCTAAAGTCCCA 2									
RESULT 242									
AX532251/c									
LOCUS									
AX532251									
DEFINITION									
Sequence 1760 from Patent EP1239051.									
ACCESSION									
AX532251									
VERSION									
AX532251.1 GI:25256287									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Shannon, M.									
TITLE									
Human posh-like protein 1									
JOURNAL									
Patent: EP 1239051-A 1760 11-SEP-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1751 TATCCTAAAGGCCCA 1765									
17 bp DNA linear PAT 22-NOV-2002									
16 TGTCCTAAAGTCCCA 2									
RESULT 243									
AX532251/c									
LOCUS									
AX532251									
DEFINITION									
Sequence 1760 from Patent EP1239051.									
ACCESSION									
AX532251									
VERSION									
AX532251.1 GI:25256287									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Shannon, M.									
TITLE									
Human posh-like protein 1									
JOURNAL									
Patent: EP 1239051-A 1760 11-SEP-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1751 TATCCTAAAGGCCCA 1765									
17 bp DNA linear PAT 22-NOV-2002									
16 TGTCCTAAAGTCCCA 2									
RESULT 244									
AX532251/c									
LOCUS									
AX532251									
DEFINITION									
Sequence 1760 from Patent EP1239051.									
ACCESSION									
AX532251									
VERSION									
AX532251.1 GI:25256287									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Shannon, M.									
TITLE									
Human posh-like protein 1									
JOURNAL									
Patent: EP 1239051-A 1760 11-SEP-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1751 TATCCTAAAGGCCCA 1765									
17 bp DNA linear PAT 22-NOV-2002									
16 TGTCCTAAAGTCCCA 2									
RESULT 245									
AX532251/c									
LOCUS									
AX532251									
DEFINITION									
Sequence 1760 from Patent EP1239051.									
ACCESSION									
AX532251									
VERSION									
AX532251.1 GI:25256287									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Shannon, M.									
TITLE									
Human posh-like protein 1									
JOURNAL									
Patent: EP 1239051-A 1760 11-SEP-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1751 TATCCTAAAGGCCCA 1765									
17 bp DNA linear PAT 22-NOV-2002									
16 TGTCCTAAAGTCCCA 2									
RESULT 246									
AX532251/c									
LOCUS									
AX532251									
DEFINITION									
Sequence 1760 from Patent EP1239051.									
ACCESSION									
AX532251									
VERSION									
AX532251.1 GI:25256287									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Shannon, M.									
TITLE									
Human posh-like protein 1									
JOURNAL									
Patent: EP 1239051-A 1760 11-SEP-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1751 TATCCTAAAGGCCCA 1765									
17 bp DNA linear PAT 22-NOV-2002									
16 TGTCCTAAAGTCCCA 2									
RESULT 247									
AX532251/c									
LOCUS									
AX532251									
DEFINITION									
Sequence 1760 from Patent EP1239051.									
ACCESSION									
AX532251									
VERSION									
AX532251.1 GI:25256287									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Shannon, M.									
TITLE									
Human posh-like protein 1									
JOURNAL									
Patent: EP 1239051-A 1760 11-SEP-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1751 TATCCTAAAGGCCCA 1765									
17 bp DNA linear PAT 22-NOV-2002									
16 TGTCCTAAAGTCCCA 2									
RESULT 248									
AX532251/c									
LOCUS									
AX532251									
DEFINITION									
Sequence 1760 from Patent EP1239051.									
ACCESSION									
AX532251									
VERSION									
AX532251.1 GI:25256287									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE									
1									
AUTHORS									
Shannon, M.									
TITLE									
Human posh-like protein 1									
JOURNAL									
Patent: EP 1239051-A 1760 11-SEP-2002;									
Aeomica, Inc. (US)									
Location/Qualifiers									
1..17									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match									
8.5%; Score 11.8; DB 1; Length 17;									
Best Local Similarity									
86.7%; Pred. No. 2.2e+02;									
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY 1751 TATCCTAAAGGCCCA 1765									
17 bp DNA linear PAT 22-NOV-2002									
16 TGTCCTAAAGTCCCA 2									
RESULT 249									
AX532251/c									
LOCUS									
AX532251									
DEFINITION									
Sequence 1760 from Patent EP1239051.									
ACCESSION									
AX532251									
VERSION									
AX532251.1 GI:25256287									
KEYWORDS									
Homo sapiens (human)									
SOURCE									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria									

```
AX672921
LOCUS AX672921 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 1366 from Patent WO0304526.
ACCESSION AX672921
VERSION AX672921.1 GI:29331269
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 0304526-A 1366 16-JAN-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1735 GCTCCCAACTCTCTCC 1749
Db 1 GATCCCAACTGTCTCC 15

RESULT 239
AX687558
LOCUS AX687558 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 290 from Patent EP1281758.
ACCESSION AX687558
VERSION AX687558.1 GI:29410254
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 290 05-FEB-2003;
FEATURES Aeomica, Inc. (US)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCTCTGG 1682
Db 3 CAGCTGGACCCAGG 17

RESULT 240
AX687559
LOCUS AX687559 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 291 from Patent EP1281758.
ACCESSION AX687559
VERSION AX687559.1 GI:29410255
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 580 05-FEB-2003;
FEATURES Aeomica, Inc. (US)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 291 05-FEB-2003;
FEATURES Aeomica, Inc. (US)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCTCTGG 1682
Db 2 CAGCTGGACCCAGG 16

RESULT 241
AX687560
LOCUS AX687560 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 292 from Patent EP1281758.
ACCESSION AX687560
VERSION AX687560.1 GI:29410256
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 292 05-FEB-2003;
FEATURES Aeomica, Inc. (US)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCTCTGG 1682
Db 1 CAGCTGGACCCAGG 15

RESULT 242
AX687848
LOCUS AX687848 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 580 from Patent EP1281758.
ACCESSION AX687848
VERSION AX687848.1 GI:29410544
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 580 05-FEB-2003;
FEATURES Aeomica, Inc. (US)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
```

```

source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.5%; Score 11.8; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAAACCTGG 1682
Db 17 CAGCTGGATGCTGG 3

RESULT 243
AX723249/c
LOCUS
DEFINITION
Sequence 936 from Patent WO03025176.
ACCESSION
AX723249
VERSION
AX723249.1 GI:30423750
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1
Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL
Patent: WO 03025176-A 936 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.5%; Score 11.8; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAAACCTGG 1682
Db 16 CAGCTGGATGCTGG 2

RESULT 244
AX723249/c
LOCUS
DEFINITION
Sequence 936 from Patent WO03025176.
ACCESSION
AX723249
VERSION
AX723249.1 GI:30423750
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1
Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL
Patent: WO 03025176-A 936 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.5%; Score 11.8; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAAACCTGG 1682
Db 16 CAGCTGGATGCTGG 2

RESULT 245
AX723448/c
LOCUS
DEFINITION
Sequence 1135 from Patent WO03025176.
ACCESSION
AX723448
VERSION
AX723448.1 GI:30423949
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1
Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL
Patent: WO 03025176-A 1135 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match
Best Local Similarity 8.5%; Score 11.8; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1635 GGGGCTGTGACGAGA 1649
Db 17 GGGGTTGTATCAGA 3

RESULT 246
AX725456/c
LOCUS
DEFINITION
Sequence 3143 from Patent WO03025176.
ACCESSION
AX725456
VERSION
AX725456.1 GI:30504799
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1
Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL
Patent: WO 03025176-A 3143 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match
Best Local Similarity 8.5%; Score 11.8; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1663 GCTCACAGCTGGAAC 1677
Db 15 GCTCACAGTTGGATC 1

RESULT 247

```

AX727005  
LOCUS AX727005 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 4692 from Patent WO03025176.  
ACCESSION AX727005  
VERSION AX727005.1 GI:30506348  
KEYWORDS Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines  
JOURNAL Patent: WO 03025176-A 4692 27-MAR-2003;  
FEATURES Molecular Engines Laboratories (FR)  
source Location/Qualifiers  
1..17  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1687 TCCTCCAGCGTGGTG 1701  
Db 3 TCCTCCTGGTGGTG 17  
RESULT 248  
AX730367/c  
LOCUS AX730367 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 2001 from Patent WO03025175.  
ACCESSION AX730367  
VERSION AX730367.1 GI:30509710  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines  
JOURNAL Patent: WO 03025175-A 2001 27-MAR-2003;  
FEATURES Molecular Engines Laboratories (FR)  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1712 TAGGAGTACGGAGAT 1726  
Db 16 TAGGAGGAAGGAGAT 2  
RESULT 249  
AX732114/c  
LOCUS AX732114 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 3748 from Patent WO03025175.  
ACCESSION AX732114  
VERSION AX732114.1 GI:30511457  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines  
JOURNAL Patent: WO 03025175-A 3748 27-MAR-2003;  
FEATURES Molecular Engines Laboratories (FR)  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1702 GAAGTTGGGTTAGGA 1716  
Db 17 GAAGATGTTAGGA 3  
RESULT 250  
AX734174  
LOCUS AX734174 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 5808 from Patent WO03025175.  
ACCESSION AX734174  
VERSION AX734174.1 GI:30513517  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines  
JOURNAL Patent: WO 03025175-A 5808 27-MAR-2003;  
FEATURES Molecular Engines Laboratories (FR)  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 2.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1735 GCTCCCAACTCTCC 1749  
Db 1 GATCCCAACTCTCC 15  
RESULT 251  
AX734182  
LOCUS AX734182 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 5816 from Patent WO03025175.  
ACCESSION AX734182  
VERSION AX734182.1 GI:30513525  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as





```

LOCUS AX783897 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2228 from Patent WO03050284.
ACCESSION AX783897
VERSION AX783897.1 GI:32951746
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2228 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1696 GTGTGGAGTTGGG 1710
Dn 15 GAGCTGGAGTTGGG 1
RESULT 257
BD067498
LOCUS BD067498 17 bp RNA linear PAT 27-AUG-2002
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors.
ACCESSION BD067498
VERSION BD067498.1 GI:22613101
KEYWORDS JP 2001511003-A/338.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 338 07-AUG-2001;
RIBOZYME PHARMACEUTICALS INC.ASTON UNIV
COMMENT OS Unidentified
PN JP 2001511003-A/338
PD 07-AUG-2001
PR 31-JAN-1997 US 60/036476.04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: single;
CC Topology: linear;
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC levels of epidermal growth factor receptors
FH Key Location/Qualifiers
FT source 1..17
/organism="Unidentified".
FEATURES
source
1..17
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1685 TCTCCTCCAGCTGG 1699
|||||||

```

```

Db 3 TCTCCTCCATCTCTGG 17
RESULT 258
BD197619
LOCUS BD197619 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION BD197619
VERSION BD197619.1 GI:33007389
KEYWORDS JP 2002509721-A/645.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 645 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/645
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
/organism="Homo sapiens (human)".
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1681 GGTGTCTCTCTCCAGC 1695
Dn 2 GGCATCTCTCTCCAGC 16
|||||||
RESULT 259
BD198720
LOCUS BD198720 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION BD198720
VERSION BD198720.1 GI:33008490
KEYWORDS JP 2002509721-A/1746.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 17)
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
METHOD and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 1746 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)

```

```

PN JP 2002509721-A/1746
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC
C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Homo sapiens (human)'.
FEATURES
    source
    1..17
    /organism='Homo sapiens'
    /mol_type='genomic RNA'
    /db_xref='taxon:9606'
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1714 GGAGTACGGAGATGG 1728
Db 17 GCAGTACAGAGATGG 3

RESULT 260
BD202828
LOCUS
DEFINITION
    Method and reagent for treating diseases or conditions concerning
    molecule participating in vasculogenic response.
ACCESSION
    BD202828
VERSION
    BD202828.1 GI:33012598
KEYWORDS
    JP 2002509721-A/5854.
SOURCE
    Homo sapiens (human)
ORGANISM
    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 17)
    Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
    Method and reagent for treating diseases or conditions concerning
    molecule participating in vasculogenic response
    Patent: JP 2002509721-A 5854 02-APR-2002;
    RIBOPYME PHARMACEUTICALS INC
COMMENT
    OS Homo sapiens (human)
    PN JP 2002509721-A/5854
    PD 02-APR-2002
    PF 24-MAR-1999 JP 2000541291
    PR 27-MAR-1998 US 60/079678
    PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
    PI JAMES A MCSWIGGEN
    PC
    C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
    A61P29/00,
    PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
    C12N5/00
    CC Method and reagent for treating diseases or conditions CC
    CC participating in vasculogenic response
    FH Key Location/Qualifiers
    FT source 1..17
    FT /organism='Homo sapiens (human)'.
    FT Location/Qualifiers
    1..17
    /organism='Homo sapiens'
    /mol_type='genomic RNA'
    /db_xref='taxon:9606'
FEATURES
    source
    1..17
    /organism='Homo sapiens'
    /mol_type='genomic RNA'
    /db_xref='taxon:9606'

```

```

Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1683 TGTCTCTCTCCAGCGT 1697
Db 1 TGCCTCTCTCCAGTGT 15

RESULT 261
AL7920
LOCUS
DEFINITION
    oligonucleotide primer.
ACCESSION
    AL7920
VERSION
    AL7920.1 GI:513115
KEYWORDS
    .
SOURCE
    synthetic construct
    synthetic construct
    artificial sequences.
ORGANISM
    Meyer, U.A.
REFERENCE
    1 (bases 1 to 18)
    Detection of pocr metabolizers of drugs
    Patent: EP 0463395-A 11 02-JAN-1992;
    F. HOFFMANN-LA ROCHE AG
FEATURES
    Location/Qualifiers
    source
    1..18
    /organism='synthetic construct'
    /mol_type='unassigned DNA'
    /db_xref='taxon:32630'
Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1665 TCACAGCTGGACCC 1679
Db 4 TCCACAGCTGGATCC 18

RESULT 262
A87622/c
LOCUS
DEFINITION
    Sequence 19 from Patent WO9836089.
ACCESSION
    A87622
VERSION
    A87622.1 GI:6736262
KEYWORDS
    .
SOURCE
    unidentified
    unidentified
    unclassified.
ORGANISM
    Flohe, L. and Singh, M.
REFERENCE
    1 (bases 1 to 18)
    TEST KIT FOR TUBERCULOSIS DIAGNOSIS OR THE LIKE
    Patent: WO 9836089-A 19 20-AUG-1998;
    FLOHE LEOPOLD (DE); SINGH MAHAVIR (DE)
FEATURES
    Location/Qualifiers
    source
    1..18
    /organism='unidentified'
    /mol_type='unassigned DNA'
    /db_xref='taxon:32644'
Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1688 CCTCCAGCTGGTGG 1702
Db 17 CCGCCAGCTGGTGG 3

RESULT 263
AR063222
LOCUS

```

PR	04-DEC-1998 US	09/205995
PI	minzhen kusu,gang qiu,robert hunfrees	
CC	Description of Artificial Sequence: antisense oligonucleotide	
CC	corresponding	
CC	to a specific region of the mouse li gene.	
FH	Key Location/Qualifiers.	
FEATURES		
source	1..18	
	/organism="synthetic construct"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:32630"	
Query Match	8.5%; Score 11.8; DB 1; Length 18;	
Best Local Similarity	86.7%; Pred. No. 2.4e+02;	
Matches 13; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
QY	1656 GCACCGCTCACAG 1670	
Dd		
	3 GCATCTGGCTCACAG 17	
RESULT 266		
I56123		
LOCUS	I56123 18 bp DNA linear PAT 07-OCT-1997	
DEFINITION	Sequence 1 from patent US 5648482.	
ACCESSION	I56123	
VERSION	I56123.1 GI:2476917	
KEYWORDS	.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 18)	
AUTHORS	Meyer,J.Albert.	
TITLE	Primers targeted to CYP2D6 gene for detecting poor metabolizers of drugs	
JOURNAL	Patent: US 5648482-A 1 15-JUL-1997;	
FEATURES		
source	Location/Qualifiers	
	1..18	
	/organism="unknown"	
	/mol_type="unassigned DNA"	
Query Match	8.5%; Score 11.8; DB 1; Length 18;	
Best Local Similarity	86.7%; Pred. No. 2.4e+02;	
Matches 13; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
QY	1665 TCACAGCTGGAACC 1679	
Dd		
	4 TCCAGCTGGAATCC 18	
RESULT 267		
AR205250		
LOCUS	AR205250 18 bp DNA linear PAT 20-JUN-2002	
DEFINITION	Sequence 10 from patent US 6368855.	
ACCESSION	AR205250	
VERSION	AR205250.1 GI:21502786	
KEYWORDS	.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 18)	
AUTHORS	Xu,M., Qiu,G. and Humphreys,R.	
TITLE	MHC class II antigen presenting cells containing oligonucleotides which inhibit Ii protein expression	
JOURNAL	Patent: US 6368855-A 10 09-APR-2002;	
FEATURES		
source	Location/Qualifiers	
	1..18	
	/organism="unknown"	
	/mol_type="unassigned DNA"	
Query Match	8.5%; Score 11.8; DB 1; Length 18;	
Best Local Similarity	86.7%; Pred. No. 2.4e+02;	
Matches 13; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	

```

QY 1656 GCACGAGGCTACAG 1670
Db 3 GCATCTGGCTACAG 17

RESULT 268
AR294317/c
LOCUS AR294317 linear PAT 12-JUN-2003
DEFINITION Sequence 6052 from patent US 6537751.
ACCESSION AR294317
VERSION AR294317.1 GI:31681601
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
PATENT: US 6537751-A 6052 25-MAR-2003;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1721 GGAGTGGAGATTGG 1735
Db 18 GAAGTGGAGATTGG 4

RESULT 269
AX022481
LOCUS AX022481 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 8 from Patent WO9937763.
ACCESSION AX022481
VERSION AX022481.1 GI:10046078
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Flegel, W.A. and Wagner, F.F.
TITLE Novel nucleic acid molecules correlated with the rhesus weak d
JOURNAL phenotype
PATENT: WO 9937763-A 8 29-JUL-1999;
FLEGEL WILLY A (DE) ; WAGNER FRANZ F (DE) ; DRK BLUTSPENDEDIENST
BADEN WUE (DE)
FEATURES
Location/Qualifiers
1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1681 GGTGTCCTCCACG 1695
Db 2 GGTCCCTCCCTCCACG 16

RESULT 270
AX103735
LOCUS AX103735 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 52 from Patent WO0125458.
ACCESSION AX103735
VERSION AX103735.1 GI:13919945

QY 1649 AAGCGAAGCACCAGG 1663
Db 17 ATGGGAAGCACCAGG 3

RESULT 272
AX342470/c
LOCUS AX342470 18 bp DNA linear PAT 12-JAN-2002
DEFINITION Sequence 4 from Patent WO0198475.
ACCESSION AX342470
VERSION AX342470.1 GI:18151913
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Melms, A., Wienhold, W. and Tolosa, E.
TITLE Method for the detection of cathepsins, asparaginyl endopeptidases
and isozymes thereof and leukocystatin

```

```

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Olivier, J., Deslandes, L. and Marco, Y.
TITLE Novel class of proteins and uses thereof for plant resistance to
JOURNAL various pathogenic agents
PATENT: WO 0125458-A 52 12-APR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (I.N.R.A.) (FR) ;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
Location/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1741 AACTCTCTCCTATCC 1755
Db 1 AACTCTCTCATGTCC 15

RESULT 271
AX326967/c
LOCUS AX326967 18 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 163 from Patent WO0178894.
ACCESSION AX326967
VERSION AX326967.1 GI:18097678
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Keith, T.
TITLE Novel human gene relating to respiratory diseases, obesity, and
JOURNAL inflammatory bowel disease
PATENT: WO 0178894-A 163 25-OCT-2001;
Genome Therapeutics Corp. (US)
FEATURES
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1649 AAGCGAAGCACCAGG 1663
Db 17 ATGGGAAGCACCAGG 3

RESULT 272
AX342470/c
LOCUS AX342470 18 bp DNA linear PAT 12-JAN-2002
DEFINITION Sequence 4 from Patent WO0198475.
ACCESSION AX342470
VERSION AX342470.1 GI:18151913
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Melms, A., Wienhold, W. and Tolosa, E.
TITLE Method for the detection of cathepsins, asparaginyl endopeptidases
and isozymes thereof and leukocystatin

```

JOURNAL Patent: WO 0198475-A 4 27-DEC-2001;  
Eberhard-Karls-Universitaet Tuebingen Universitaetsklinikum (DE)  
FEATURES  
source  
Location/Qualifiers

1. .18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Beschreibung der kunstlichen Sequenz:  
Nukleotidsequenz"

Query Match 8.5%; Score 11.8; DB 1; Length 18;  
Best Local Similarity 86.7%; Pred. No. 2.4e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1733 TGGCTCCCACTCT 1747  
| | | | | | | | | |  
Db 17 TGGTGCCTCACTCT 3

RESULT 273  
AX352805  
LOCUS AX352805 18 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 11 from Patent EP1174518.  
ACCESSION AX352805  
VERSION AX352805.1 GI:18617887  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Loukachov, V.V., van Gemen, B. and Goudsmit, J.  
TITLE Collection of binding molecules  
JOURNAL Patent: EP 1174518-A 11 23-JAN-2002;  
Amsterdam Support Diagnostics B.V. (NL)

FEATURES  
source  
Location/Qualifiers  
1. .18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="position 41"

Query Match 8.5%; Score 11.8; DB 1; Length 18;  
Best Local Similarity 86.7%; Pred. No. 2.4e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1717 GTACGGAGATGGAGA 1731  
| | | | | | | | | |  
Db 1 GTACAGAGATGGAAA 15

RESULT 274  
AX352808  
LOCUS AX352808 18 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 14 from Patent EP1174518.  
ACCESSION AX352808  
VERSION AX352808.1 GI:18617890  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Loukachov, V.V., van Gemen, B. and Goudsmit, J.  
TITLE Collection of binding molecules  
JOURNAL Patent: EP 1174518-A 14 23-JAN-2002;  
Amsterdam Support Diagnostics B.V. (NL)

FEATURES  
source  
Location/Qualifiers  
1. .18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="position 41"

Query Match 8.5%; Score 11.8; DB 1; Length 18;

Best Local Similarity 86.7%; Pred. No. 2.4e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1717 GTACGGAGATGGAGA 1731  
| | | | | | | | | |  
Db 1 GTACAGAAATGGAGA 15

RESULT 275  
AX362650  
LOCUS AX362650 18 bp DNA linear PAT 15-FEB-2002  
DEFINITION Sequence 11 from Patent WO0208463.  
ACCESSION AX362650  
VERSION AX362650.1 GI:18694790  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Loukachov, V.V., Goudsmit, J. and van Gemen, B.  
TITLE Collection of binding molecules  
JOURNAL Patent: WO 0208463-A 11 31-JAN-2002;  
Amsterdam Support Diagnostics B.V. (NL)

FEATURES  
source  
Location/Qualifiers  
1. .18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="position 41"

Query Match 8.5%; Score 11.8; DB 1; Length 18;  
Best Local Similarity 86.7%; Pred. No. 2.4e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1717 GTACGGAGATGGAGA 1731  
| | | | | | | | | |  
Db 1 GTACAGAGATGGAAA 15

RESULT 276  
AX362653  
LOCUS AX362653 18 bp DNA linear PAT 15-FEB-2002  
DEFINITION Sequence 14 from Patent WO0208463.  
ACCESSION AX362653  
VERSION AX362653.1 GI:18694793  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Loukachov, V.V., Goudsmit, J. and van Gemen, B.  
TITLE Collection of binding molecules  
JOURNAL Patent: WO 0208463-A 14 31-JAN-2002;  
Amsterdam Support Diagnostics B.V. (NL)

FEATURES  
source  
Location/Qualifiers  
1. .18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="position 41"

Query Match 8.5%; Score 11.8; DB 1; Length 18;  
Best Local Similarity 86.7%; Pred. No. 2.4e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1717 GTACGGAGATGGAGA 1731  
| | | | | | | | | |  
Db 1 GTACAGAAATGGAGA 15

RESULT 277  
BD006224/c  
LOCUS BD006224 18 bp DNA linear PAT 31-JAN-2002

```

FEATURES
    source
        1. .18
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match
Best Local Similarity 8.5%; Score 11.8; DB 1; Length 18;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1689 CTCACGGCTGGTGA 1703
DB 2 CTCACGGCTCATGA 16

RESULT 279
BD103926/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
    Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
    Nishida,M.
TITLE
JOURNAL
COMMENT
    OS Artificial Sequence
    PN WO 0192572-A/30
    PD 06-DEC-2001
    PF 01-JUN-2001 WO 2001JP004662
    PR 01-JUN-2000 JP 00P 164798
    PT HIDEOTOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIOYUKI
    MATSUMURA,
    PI SHOGO MORIYA,MICHIHO NISHIDA
    PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
    CC Description of Artificial Sequence:capture
    FH Key Location/Qualifiers
    FT source
    FT /organism='Artificial Sequence'.

FEATURES
    source
        1. .18
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match
Best Local Similarity 8.5%; Score 11.8; DB 1; Length 18;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1650 AGGCAGCACCGGC 1664
DB 18 AGGCAGCACCGAGC 4

RESULT 280
BD124069
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
    Fregel,V.A. and Wagner,F.F.

```

```

TITLE Novel nucleic acid molecule correlating to Rhesus weak D phenotype
JOURNAL Patent: JP 2002500884-A 8 15-JAN-2002;
COMMENT DRK BLUOTSPENDEDIENST BADEN WUERTTEMBERG G3MBH
Unidentified
PN JP 2002500884-A/8
PD 15-JAN-2002
PF 18-DEC-1998 JP 2000528671
PR 23-JAN-1998 EP 98101203.2
PI VILLY A FREGEL, FRANZ F WAGNER
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12P21/08, C12Q1/02, C12Q1/68, G01N33/566, C12N15/00, PC
C12N5/00
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'oligonucleotide',
FH Key Location/Qualifiers
FT source 1..18
FEATURES
source Location/Qualifiers
1..18 /organism='Unidentified'.
1..18 /organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 8.5%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1681 GGTGCTCTCTCCAGC 1695
DB 2 GGTCTCTCTCTCCAGC 16

RESULT 281
AB067849
LOCUS AB067849 18 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-D1S243 at
lp36.
ACCESSION AB067849
VERSION AB067849.1 GI:15128653
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.
and Soeda, E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human
chromosome 1p35-p36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE 2 (bases 1 to 18)
AUTHORS Horii, A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES
source Location/Qualifiers
1..18 /organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

misc_feature 1..18
/note='reverse primer for human STS sts-D1S243 at lp36
sts-D1S243 obtained from clones B83K22, B47P3, B43E2,
B123D13, B290B2 and B82D16, B226P2, Human BAC library
RPC1-11'

Novel nucleic acid molecule correlating to Rhesus weak D phenotype
Patent: JP 2002500884-A 8 15-JAN-2002;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1689 CTCGAGCGTGGTGA 1703
DB 2 CTCGAGCGTGGTGA 16

RESULT 282
AX250715/c
LOCUS AX250715 20 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 7 from Patent WO0168670.
ACCESSION AX250715
VERSION AX250715.1 GI:15984453
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lazdunski, M., Lesage, F. and Maindret, F.
TITLE Novel family of mechanically sensitive human potassium channels
activated by polyunsaturated fatty acids and use thereof
JOURNAL Patent: WO 0168670-A 7 20-SEP-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
source Location/Qualifiers
1..20 /organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'
misc_feature 1..20
/note='Oligonucleotide utilise pour l'analyse des blots,
marque au P32'

Query Match 8.5%; Score 11.8; DB 1; Length 20;
Best Local Similarity 86.7%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACTCCG 1682
DB 15 CAGCTGGAGCCTCG 1

RESULT 283
AX007253
LOCUS AX007253 15 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 15 from Patent WO0000593.
ACCESSION AX007253
VERSION AX007253.1 GI:9995109
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Zaehringer, U., Heinz, E., Schmidt, H. and Sperling, P.
TITLE Sphingolipid-desaturase
JOURNAL Patent: WO 0000593-A 15 06-JAN-2000;
ZAEHRINGER ULRICH (DE); HEINZ ERNST (DE); SCHMIDT HERMANN (DE);
SPERLING PETRA (DE); GVS GES FUER ERWERB UND VERWER (DE)
FEATURES
source Location/Qualifiers
1..15 /organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/note='degenerierter forward Primer aus Hilianthus annuus'

Query Match 8.3%; Score 11.6; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2e+02;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1694 GCGTGGTGAAGTTG 1708

```

```

Db      1  |||||:|:|
        1  GSNTGCTGGAAATGG 15

RESULT 284
LOCUS   AR175362                13 bp    DNA          linear    PAT 17-DEC-2001
DEFINITION   Sequence 85 from patent US 6309823.
ACCESSION   AR175362
VERSION     AR175362.1  GI:17916661
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 13)
AUTHORS    Cronin,M.T., Miyada,C.G., Hubbell,E.A., Chee,M., Fodor,S.P.A.,
            Huang,X.C., Lipshutz,R.J., Lobban,P.E., Morris,M.S. and
            Sheldon,E.L.
TITLE      Arrays of nucleic acid probes for analyzing biotransformation genes
            and methods of using the same
JOURNAL    Patent: US 6309823-A 85 30-OCT-2001;
FEATURES    Location/Qualifiers
            source
            1..13
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1649 AAGGCAAGCACCA 1661
Db      13 AGGGCAAGCACCA 1

RESULT 285
LOCUS   AR285094/c              13 bp    DNA          linear    PAT 10-APR-2003
DEFINITION   Sequence 17 from patent US 6528268.
ACCESSION   AR285094
VERSION     AR285094.1  GI:29722011
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 13)
AUTHORS    Andersson,M.K., Berglund,L.G.T., Reneland,R.H. and Adam,G.I.R.
TITLE      Reagents and methods for detection of heart failure
JOURNAL    Patent: US 6528268-A 17 04-MAR-2003;
FEATURES    Location/Qualifiers
            source
            1..13
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1662 GGCTCAGCTGG 1674
Db      13 GGCTCAGCTGG 1

RESULT 286
LOCUS   AR285104                13 bp    DNA          linear    PAT 10-APR-2003
DEFINITION   Sequence 27 from patent US 6528268.
ACCESSION   AR285104
VERSION     AR285104.1  GI:29722021
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 13)
AUTHORS    Andersson,M.K., Berglund,L.G.T., Reneland,R.H. and Adam,G.I.R.
TITLE      Reagents and methods for detection of heart failure
JOURNAL    Patent: US 6528268-A 17 04-MAR-2003;
FEATURES    Location/Qualifiers
            source
            1..13
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1662 GGCTCAGCTGG 1674
Db      13 GGCTCAGCTGG 1

RESULT 287
LOCUS   A64221                  14 bp    DNA          linear    PAT 29-MAR-1999
DEFINITION   Sequence 9 from Patent WO9727332.
ACCESSION   A64221
VERSION     A64221.1  GI:3717652
KEYWORDS    .
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1
AUTHORS    Stuyver,L., Louwagie,J. and Rossau,R.
TITLE      METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE
            TRANSCRIPTASE GENE
JOURNAL    Patent: WO 9727332-A 9 31-JUL-1997;
            INNOGENETICS NV (BE)
COMMENT    Other publication AU 144397 19970820.
FEATURES    Location/Qualifiers
            source
            1..14
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      8.2%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1717 GTACGAGATGGA 1729
Db      1  GTACGAGATGGA 13

RESULT 288
LOCUS   AR102520                14 bp    DNA          linear    PAT 14-FEB-2001
DEFINITION   Sequence 9 from patent US 6087093.
ACCESSION   AR102520
VERSION     AR102520.1  GI:12814108
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 14)
AUTHORS    Lieven,S., Joost,L. and Rudi,R.
TITLE      Method for detection of drug-induced mutations in the reverse
            transcriptase gene
JOURNAL    Patent: US 6087093-A 9 11-JUL-2000;
FEATURES    Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.2%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1662 GGCTCAGCTGG 1674
Db      13 GGCTCAGCTGG 1
```



Qy 1717 GTACGGAGATGGA 1729  
 Db 1 GTACAGAGATGGA 13

RESULT 289  
 AR262823  
 LOCUS AR262823 14 bp DNA linear PAT 29-JAN-2003  
 DEFINITION Sequence 9 from patent US 6331389.  
 ACCESSION AR262823  
 VERSION AR262823.1 GI:28074526  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 14)  
 AUTHORS Lieven, S., Joost, L. and Rudi, R.  
 TITLE Method for detection of drug-induced mutations in the reverse transcriptase gene  
 JOURNAL Patent: US 6331389-A 9 18-DEC-2001;  
 FEATURES Location/Qualifiers  
 source 1..14  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 8.2%; Score 11.4; DB 1; Length 14;  
 Best Local Similarity 92.3%; Pred. No. 1.9e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1717 GTACGGAGATGGA 1729  
 Db 1 GTACAGAGATGGA 13

RESULT 290  
 AX802880/c  
 LOCUS AX802880 14 bp DNA linear PAT 24-NOV-2003  
 DEFINITION Sequence 11 from Patent WO03057909.  
 ACCESSION AX802880  
 VERSION AX802880.1 GI:38501577  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1  
 AUTHORS Berlin, K.  
 TITLE Method for detecting cytosine-methylation patterns by exponential ligation of hybridised probe oligo-nucleotides (mla)  
 JOURNAL Patent: WO 03057909-A 11 17-JUL-2003;  
 FEATURES Epigenomics AG (DE)  
 source Location/Qualifiers  
 1..14  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="oligonucleotide"

Query Match 8.2%; Score 11.4; DB 1; Length 14;  
 Best Local Similarity 92.3%; Pred. No. 1.9e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1634 TGGGGCTTGAC 1646  
 Db 14 TGGGGCTTGACG 2

RESULT 291  
 BD061635/c  
 LOCUS BD061635 14 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Human Lafora type epilepsy causal gene full-length sequence and use of mutation thereof.  
 ACCESSION BD061635

VERSION BD061635.1 GI:22607240  
 KEYWORDS JP 2001299350-A/26.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 14)  
 AUTHORS Yamakawa, K. and Excweta, A.D.  
 TITLE Human Lafora type epilepsy causal gene full-length sequence and use of mutation thereof  
 JOURNAL Patent: JP 2001299350-A 26 30-OCT-2001;  
 COMMENT THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH  
 OS Homo sapiens (human)  
 PN JP 2001299350-A/26  
 PD 30-OCT-2001  
 PF 19-APR-2000 JP 2000118361  
 PI KAZUHIRO YAMAKAWA, ANTONIO DELGARD EXCWETA  
 PC C12N15/09, C12M1/00, C12M1/34, C12Q1/68, C12N15/00 CC  
 FH Key Location/Qualifiers

FEATURES  
 source 1..14  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 14;  
 Best Local Similarity 92.3%; Pred. No. 1.9e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1746 CTCCTATCTTAA 1758  
 Db 14 CTCCTATCTTAA 2

RESULT 292  
 AR000458/c  
 LOCUS AR000458 15 bp DNA linear PAT 04-DEC-1998  
 DEFINITION Sequence 17 from patent US 5736365.  
 ACCESSION AR000458  
 VERSION AR000458.1 GI:3962989  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Walker, G. Terrance., Nadeau, J. G., Spears, P. Anne., Nycz, C. M., Shank, D. Dee., Schram, J. L. and Jurgensen, S. Russel.  
 TITLE Multiplex nucleic acid amplification  
 JOURNAL Patent: US 5736365-A 17 07-APR-1998;  
 FEATURES Location/Qualifiers  
 source 1..15  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 92.3%; Pred. No. 2.2e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1658 ACCAGGCTCACAG 1670  
 Db 14 ACCAGGCTCACAG 2

RESULT 293  
 AR008358  
 LOCUS AR008358 15 bp DNA linear PAT 04-DEC-1998  
 DEFINITION Sequence 16 from patent US 5753481.  
 ACCESSION AR008358  
 VERSION AR008358.1 GI:3967467  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Walker, G. Terrance., Nadeau, J. G., Spears, P. Anne., Nycz, C. M., Shank, D. Dee., Schram, J. L. and Jurgensen, S. Russel.  
 TITLE Multiplex nucleic acid amplification  
 JOURNAL Patent: US 5736365-A 17 07-APR-1998;  
 FEATURES Location/Qualifiers  
 source 1..15  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

```
REFERENCE 1 (bases 1 to 15)
AUTHORS Niwa,M., Saito,Y., Ishii,Y., Yoshida,M. and Suzuki,H.
TITLE L-sorbose dehydrogenase and novel L-sorbose dehydrogenase
JOURNAL obtained from gluconobacter oxydans T-100
FEATURES Patent: US 5753481-A 16 19-MAY-1998;
source Location/Qualifiers
      1..15
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1724 GATGGAGATTGGC 1736
Db      2 GATGGAGAATGGC 14

RESULT 294
AR030667 LOCUS 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 16 from patent US 5861292.
ACCESSION AR030667
VERSION AR030667.1 GI:5943881
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Niwa,M., Saito,Y., Ishii,Y., Yoshida,M. and Suzuki,H.
TITLE L-sorbose dehydrogenase and novel L-sorbose dehydrogenase
JOURNAL obtained from Gluconobacter oxydans T-100
FEATURES Patent: US 5861292-A 16 19-JAN-1999;
source Location/Qualifiers
      1..15
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1724 GATGGAGATTGGC 1736
Db      2 GATGGAGAATGGC 14

RESULT 295
AR033686 LOCUS 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 452 from patent US 5869253.
ACCESSION AR033686
VERSION AR033686.1 GI:5949291
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 452 09-FEB-1999;
FEATURES Location/Qualifiers
      1..15
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1724 GATGGAGATTGGC 1736
Db      2 GATGGAGAATGGC 14

RESULT 295
AR033686 LOCUS 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 452 from patent US 5869253.
ACCESSION AR033686
VERSION AR033686.1 GI:5949291
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 452 09-FEB-1999;
FEATURES Location/Qualifiers
      1..15
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1686 CTCCTCCAGCGTG 1698
Db      CTCCTCCAGCGTG 15

RESULT 298
AR137837 LOCUS 15 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 16 from patent US 6197562.
ACCESSION AR137837
VERSION AR137837.1 GI:14479346
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Niwa,M., Saito,Y., Ishii,Y., Yoshida,M. and Suzuki,H.
TITLE L-sorbose dehydrogenase and novel L-sorbose dehydrogenase
obtained from gluconobacter oxydans T-100
```

```
Db      3 CTCCTCCAACGTG 15

RESULT 296
AR053773 LOCUS 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 17 from patent US 5834263.
ACCESSION AR053773
VERSION AR053773.1 GI:5978635
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Niwa,M., Saito,Y., Ishii,Y., Yoshida,M. and Hayashi,H.
TITLE Method for producing 2-keto-L-gulonic acid
JOURNAL Patent: US 5834263-A 17 10-NOV-1998;
FEATURES Location/Qualifiers
      1..15
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1724 GATGGAGATTGGC 1736
Db      2 GATGGAGAATGGC 14

RESULT 297
AR113508 LOCUS 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 452 from patent US 6132966.
ACCESSION AR113508
VERSION AR113508.1 GI:14093830
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 6132966-A 452 17-OCT-2000;
FEATURES Location/Qualifiers
      1..15
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1686 CTCCTCCAGCGTG 1698
Db      3 CTCCTCCAACGTG 15

RESULT 298
AR137837 LOCUS 15 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 16 from patent US 6197562.
ACCESSION AR137837
VERSION AR137837.1 GI:14479346
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Niwa,M., Saito,Y., Ishii,Y., Yoshida,M. and Suzuki,H.
TITLE L-sorbose dehydrogenase and novel L-sorbose dehydrogenase
obtained from gluconobacter oxydans T-100
```

QY 1658 ACCAGGCTCACAG 1670  
DB 14 ACCAGGCTCACAG 2

[illegible]

Query Match 8.2%; Score 11.4; DB 1; Length 15;  
Best Local Similarity 92.3%; Pred. No. 2.2e+02;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCGTG 1698  
|||||||  
3 CTCCTCCACGCTG 15

RESULT 303  
A26037 16 bp DNA linear PAT 14-MAR-1995  
LOCUS polynucleotide 16C17.  
DEFINITION A26037  
ACCESSION A26037  
VERSION A26037.1 GI:904809  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 16)  
AUTHORS  
JOURNAL Patent: FR 2680520-A 32 26-FEB-1993;  
FEATURES Location/Qualifiers  
source 1..16  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 8.2%; Score 11.4; DB 1; Length 16;  
Best Local Similarity 92.3%; Pred. No. 2.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1655 AGCACCAGGCTCA 1667  
|||||||  
1 AGACACAGGCTCA 13

RESULT 304  
I26247 16 bp DNA linear PAT 07-OCT-1996  
LOCUS Sequence 32 from patent US 5558955.  
DEFINITION I26247  
ACCESSION I26247  
VERSION I26247.1 GI:1606117  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS Vernaud,G.  
TITLE Process for detection of new polymorphic loci in a DNA sequence,  
nucleotide sequences forming hybridization probes and their  
applications  
JOURNAL Patent: US 5556955-A 32 17-SEP-1996;  
FEATURES Location/Qualifiers  
source 1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 8.2%; Score 11.4; DB 1; Length 16;  
Best Local Similarity 92.3%; Pred. No. 2.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1655 AGCACCAGGCTCA 1667  
|||||||  
1 AGACACAGGCTCA 13

RESULT 305  
AX266567/c 17 bp DNA linear PAT 26-OCT-2001  
LOCUS Sequence 3958 from Patent WO0173002.  
DEFINITION AX266567  
ACCESSION AX266567  
VERSION AX266567.1 GI:16515366  
KEYWORDS  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.  
TITLE Targeted chromosomal genomic alterations with modified single  
stranded oligonucleotides  
JOURNAL Patent: WO 0173002-A 3958 04-OCT-2001;  
UNIVERSITY OF DELAWARE (US)  
FEATURES Location/Qualifiers  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 2.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1668 CAGCTGGAGCCCT 1680  
|||||||  
14 CAGCTGGAGCCCT 2

RESULT 306  
AX266568 17 bp DNA linear PAT 26-OCT-2001  
LOCUS Sequence 3959 from Patent WO0173002.  
DEFINITION AX266568  
ACCESSION AX266568  
VERSION AX266568.1 GI:16515367  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.  
TITLE Targeted chromosomal genomic alterations with modified single  
stranded oligonucleotides  
JOURNAL Patent: WO 0173002-A 3959 04-OCT-2001;  
UNIVERSITY OF DELAWARE (US)  
FEATURES Location/Qualifiers  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 2.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1668 CAGCTGGAGCCCT 1680  
|||||||  
4 CAGCTGGAGCCCT 16

RESULT 307  
AR019338/c 17 bp DNA linear PAT 05-DEC-1998  
LOCUS Sequence 5 from patent US 5783416.  
DEFINITION AR019338  
ACCESSION AR019338  
VERSION AR019338.1 GI:3974452  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Thim,L., Norris,K., Norris,F., Bj.o slashedren,Erik.,  
Christensen,M. and Nielsen,P.Franklin.  
TITLE Human epasmolytic polypeptide in glycosylated form  
JOURNAL Patent: US 5783416-A 5 21-JUL-1998;  
FEATURES Location/Qualifiers  
source 1..17

```

/organism="unknown"
/mol_type="unassigned DNA"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1677 CCCTGGTGTCTCC 1698
    |||||
Db 14 CCCTGGTGTCTCC 2

RESULT 308
AR161494/c
LOCUS AR161494 17 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 16 from patent US 6255467.
ACCESSION AR161494
VERSION AR161494.1 GI:16227404
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Lindner,L.E. and MacPhee,K.
TITLE Human blood bacterium
JOURNAL Patent: US 6255467-A 16 03-JUL-2001;
FEATURES
    source
        1. .17
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1698 GGTGGAGAGTTGGG 1710
    |||||
Db 16 GGTGGAGAGTTGGG 4

RESULT 309
BD231535/c
LOCUS BD231535 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Chromosome 17q-linked prostate cancer susceptibility gene.
ACCESSION BD231535
VERSION BD231535.1 GI:33041305
KEYWORDS JP 2002529065-A/87.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 17)
AUTHORS Tavtigian,S.V., Teng,D.H.F., Simard,J. and Rommens,J.M.
TITLE Chromosome 17q-linked prostate cancer susceptibility gene
JOURNAL Patent: JP 2002529065-A 87 10-SEP-2002;
COMMENT MYRIAD GENETICS INC,THE HOSPITAL FOR SICK CHILDREN
OS Homo sapiens (human)
PN JP 2002529065-A/87
PD 10-SEP-2002
PF 05-NOV-1998 JP 2000581041
PR 06-NOV-1998 US 60/107468
PI SEAN V TAVTIGIAN,DAVID H F TENG,JACQUES SIMARD,JOHANNA M PI ROMMENS
PC C12N15/09,A61K31/713,A61K38/00,A61K39/395,A61K45/00,A61K48/00,
PC A61P35/00,
PC C07K14/47,C07K16/18,C07K16/44,C12N1/15,C12N1/19,C12N1/21,C12N5/10,
PC C12N1/02,C12N1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566,
PC G01N33/577,
PC G01N37/00,C12N15/00,A61K37/02,C12N5/00
CC Chromosome 17q-linked prostate cancer susceptibility gene FH
KEY Location/Qualifiers

/organism="Homo sapiens (human)"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1657 CACCAGGCTCACA 1669
    |||||
Db 17 CACCAGGCTGACA 5

RESULT 310
BD254457/c
LOCUS BD254457 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254457
VERSION BD254457.1 GI:33064227
KEYWORDS JP 2002541795-A/2250.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2250 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2250
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC C12P21/02,
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00, PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
KEY Location/Qualifiers
FT source
    1. .17
    /organism="Eukaryote".
    Location/Qualifiers
        1. .17
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1686 CTCCTCCAGCGTG 1698
    |||||
Db 17 CTCCTCCAGAGTG 5

RESULT 311
AR187364
LOCUS AR187364 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2852 from patent US 6346398.
ACCESSION AR187364
VERSION AR187364.1 GI:20233329
KEYWORDS Unknown.
SOURCE

```

```

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
        related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2852 12-FEB-2002;
FEATURES
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"
    Query Match
        Best Local Similarity 8.2%; Score 11.4; DB 1; Length 17;
        Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1725 ATGGATATTGGCT 1737
Db 3 ATGGATATTGGCT 15

RESULT 312
LOCUS AR187365 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2853 from patent US 6346398.
ACCESSION AR187365
VERSION AR187365.1 GI:20233330
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
        related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2853 12-FEB-2002;
FEATURES
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"
    Query Match
        Best Local Similarity 8.2%; Score 11.4; DB 1; Length 17;
        Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1725 ATGGATATTGGCT 1737
Db 1 ATGGATATTGGCT 13

RESULT 313
LOCUS AR195588/c 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 53 from patent US 6350934.
ACCESSION AR195588
VERSION AR195588.1 GI:20245025
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
        Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 53 26-FEB-2002;
FEATURES
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"
    Query Match
        Best Local Similarity 8.2%; Score 11.4; DB 1; Length 17;
        Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
        related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2853 12-FEB-2002;
FEATURES
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"
    Query Match
        Best Local Similarity 8.2%; Score 11.4; DB 1; Length 17;
        Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1725 ATGGATATTGGCT 1737
Db 1 ATGGATATTGGCT 13

RESULT 314
LOCUS AR286088 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 460 from patent US 6528640.
ACCESSION AR286088
VERSION AR286088.1 GI:29723684
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
        Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 460 04-MAR-2003;
FEATURES
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned RNA"
    Query Match
        Best Local Similarity 8.2%; Score 11.4; DB 1; Length 17;
        Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1663 GTCACAGCTGGA 1675
Db 2 GTCACAGCTGGA 14

RESULT 315
LOCUS AR323974 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1376 from patent US 6566127.
ACCESSION AR323974
VERSION AR323974.1 GI:33709782
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
        related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1376 20-MAY-2003;
FEATURES
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned RNA"
    Query Match
        Best Local Similarity 8.2%; Score 11.4; DB 1; Length 17;
        Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1725 ATGGATATTGGCT 1737
Db 3 ATGGATATTGGCT 15

RESULT 316
LOCUS AR323975 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1377 from patent US 6566127.
ACCESSION AR323975
VERSION AR323975.1 GI:33709783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

```

Unclassified.  
1 (bases 1 to 17)  
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
Method and reagent for the treatment of diseases or conditions  
related to levels of vascular endothelial growth factor receptor  
Patent: US 6566127-A 1377 20-MAY-2003;  
Location/Qualifiers  
source  
1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 2.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1725 ATGGAGATTGGCT 1737  
||||| |||||  
Db 1 ATGGATATTGGCT 13

RESULT 317  
AR327590/C  
LOCUS AR327590 17 bp RNA  
DEFINITION Sequence 4992 from patent US 6566127.  
ACCESSION AR327590  
VERSION AR327590.1 GI:33713398  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions  
related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 4992 20-MAY-2003;  
FEATURES Location/Qualifiers  
source  
1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 2.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGA 1676  
||||| |||||  
Db 17 CCCACAGCTGGA 5

RESULT 318  
AR398078  
LOCUS AR398078 17 bp RNA  
DEFINITION Sequence 459 from patent US 6617438.  
ACCESSION AR398078  
VERSION AR398078.1 GI:40135598  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,  
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
TITLE Oligoribonucleotides with enzymatic activity  
JOURNAL Patent: US 6617438-A 459 09-SEP-2003;  
FEATURES Location/Qualifiers  
source  
1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 2.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1663 GCTCACAGCTGGA 1675  
||||| |||||  
Db 2 GCTCACTGCTGGA 14

RESULT 319  
AR401959  
LOCUS AR401959 17 bp DNA  
DEFINITION Sequence 299 from patent US 6623962.  
ACCESSION AR401959  
VERSION AR401959.1 GI:40149409  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.  
TITLE Enzymatic nucleic acid treatment of diseases of conditions related  
to levels of epidermal growth factor receptors  
JOURNAL Patent: US 6623962-A 299 23-SEP-2003;  
FEATURES Location/Qualifiers  
source  
1. .17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 2.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1729 AGATTGGCTCCCA 1741  
||||| |||||  
Db 5 ATATTGGCTCCCA 17

RESULT 320  
AX272527/C  
LOCUS AX272527 17 bp RNA  
DEFINITION Sequence 96 from Patent WO0162911.  
ACCESSION AX272527  
VERSION AX272527.1 GI:16545264  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Jarvis,T., von Carlowitz,I., McSwiggen,J.A., Hamblin,P.A. and  
Ellis,J.H.  
TITLE Method and reagent for the inhibition of grid  
JOURNAL Patent: WO 0162911-A 96 30-AUG-2001;  
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)  
Location/Qualifiers  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 2.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1719 ACGGAGATGGAGA 1731  
||||| |||||  
Db 14 ACAGAGATGGAGA 2

RESULT 321  
AX272713/C  
LOCUS AX272713 17 bp RNA  
DEFINITION Sequence 282 from Patent WO0162911.  
ACCESSION AX272713  
VERSION AX272713.1 GI:16545450  
KEYWORDS





```

Qy 1646 CAGAAGGCAAGCA 1658
Db 5 CGGAAGGCAAGCA 17

RESULT 326
LOCUS AX498903 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 210 from Patent EP1229046.
ACCESSION AX498903
VERSION AX498903.1 GI:23381196
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 210 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1648 GAAGGCAAGCACC 1660
Db 1 GAAGGCAAGCAGC 13

RESULT 329
LOCUS AX499429 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 736 from Patent EP1229046.
ACCESSION AX499429
VERSION AX499429.1 GI:23381722
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 736 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1684 GTCTCCTCCAGCG 1696
Db 5 GTCTCCTACAGCG 17

RESULT 330
LOCUS AX499430 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 737 from Patent EP1229046.
ACCESSION AX499430
VERSION AX499430.1 GI:23381723
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 737 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1684 GTCTCCTCCAGCG 1696
Db 5 GTCTCCTACAGCG 17

RESULT 330
LOCUS AX499430 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 737 from Patent EP1229046.
ACCESSION AX499430
VERSION AX499430.1 GI:23381723
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 737 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1646 CAGAAGGCAAGCA 1658
Db 4 CGGAAGGCAAGCA 16

RESULT 327
LOCUS AX498907 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 214 from Patent EP1229046.
ACCESSION AX498907
VERSION AX498907.1 GI:23381200
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 214 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1648 CAGAAGGCAAGCA 1658
Db 4 CGGAAGGCAAGCA 16

RESULT 327
LOCUS AX498907 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 214 from Patent EP1229046.
ACCESSION AX498907
VERSION AX498907.1 GI:23381200
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 214 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1648 GAAGGCAAGCACC 1660
Db 2 GAAGGCAAGCAGC 14

RESULT 328
LOCUS AX498908 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 215 from Patent EP1229046.
ACCESSION AX498908
VERSION AX498908.1 GI:23381201

```

```

source      1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1684 GTCTCTCCAGCG 1696
|||||
Db 4 GTCTCTACAGCG 16

RESULT 331
AX499431
LOCUS      17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 738 from Patent EP1229046.
ACCESSION AX499431
VERSION AX499431.1 GI:23381724
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 738 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1684 GTCTCTCCAGCG 1696
|||||
Db 3 GTCTCTACAGCG 15

RESULT 332
AX499432
LOCUS      17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 739 from Patent EP1229046.
ACCESSION AX499432
VERSION AX499432.1 GI:23381725
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 739 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1684 GTCTCTCCAGCG 1696
|||||
Db 3 GTCTCTACAGCG 15

RESULT 333
AX499433
LOCUS      17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 740 from Patent EP1229046.
ACCESSION AX499433
VERSION AX499433.1 GI:23381726
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 740 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1684 GTCTCTCCAGCG 1696
|||||
Db 1 GTCTCTACAGCG 13

RESULT 334
AX531787/c
LOCUS      17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1296 from Patent EP1239051.
ACCESSION AX531787
VERSION AX531787.1 GI:25255351
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1296 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGAA 1676
|||||
Db 17 CACACAGCTGGAA 5

RESULT 335
AX531788/c
LOCUS      17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1297 from Patent EP1239051.
ACCESSION AX531788
VERSION AX531788.1 GI:25255353
KEYWORDS
SOURCE Homo sapiens (human)

```

```
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1297 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1664 CTCACAGCTGGAA 1676
Db 16 CACACAGCTGGAA 4
RESULT 336
AX531789/c
LOCUS AX531789 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1298 from Patent EP1239051.
ACCESSION AX531789
VERSION AX531789.1 GI:25255355
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1298 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1664 CTCACAGCTGGAA 1676
Db 15 CACACAGCTGGAA 3
RESULT 337
AX531790/c
LOCUS AX531790 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1299 from Patent EP1239051.
ACCESSION AX531790
VERSION AX531790.1 GI:25255357
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1299 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
```

```
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1664 CTCACAGCTGGAA 1676
Db 14 CACACAGCTGGAA 2
RESULT 338
AX531791/c
LOCUS AX531791 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1300 from Patent EP1239051.
ACCESSION AX531791
VERSION AX531791.1 GI:25255359
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1300 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1664 CTCACAGCTGGAA 1676
Db 13 CACACAGCTGGAA 1
RESULT 339
AX532249/c
LOCUS AX532249 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1758 from Patent EP1239051.
ACCESSION AX532249
VERSION AX532249.1 GI:25256283
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1758 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1753 TCCTAAAGGCCCA 1765
Db 17 TCCTAAAGTCCCA 5
```

```

RESULT 340
AX532250/c
LOCUS          17 bp      DNA          linear          PAT 22-NOV-2002
DEFINITION     Sequence 1759 from Patent EP1239051.
ACCESSION      AX532250
VERSION        AX532250.1  GI:25256285
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS       Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE         Human posh-like protein 1
JOURNAL       Patent: EP 1239051-A 1759 11-SEP-2002;
              Aeomica, Inc. (US)
FEATURES      1..17
               Location/Qualifiers
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1753 TCCTAAGGCCCA 1765
Db 16 TCCTAAGGCCCA 4

RESULT 341
AX616595
LOCUS          17 bp      DNA          linear          PAT 20-FEB-2003
DEFINITION     Sequence 4 from Patent EP1262534.
ACCESSION      AX616595
VERSION        AX616595.1  GI:28447578
KEYWORDS       synthetic construct
               synthetic construct
               artificial sequences.
SOURCE         Lever,A.M. and Hunter,E.
ORGANISM       Defective packaging non-oncoviral vectors based on mpmv and hiv
               Patent: EP 1262534-A 4 04-DEC-2002;
               SYNGENIX LIMITED (GB)
REFERENCE      1
AUTHORS       Lever,A.M. and Hunter,E.
TITLE         Defective packaging non-oncoviral vectors based on mpmv and hiv
JOURNAL       Patent: EP 1262534-A 4 04-DEC-2002;
              SYNGENIX LIMITED (GB)
FEATURES      1..17
               Location/Qualifiers
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Plasmid sequence"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1715 GACTACGGAGATG 1727
Db 5 GAGTACTGAGATG 17

RESULT 342
AX687668
LOCUS          17 bp      DNA          linear          PAT 31-MAR-2003
DEFINITION     Sequence 400 from Patent EP1281758.
ACCESSION      AX687668
VERSION        AX687668.1  GI:29410364
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS       Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE         Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL       Patent: EP 1281758-A 402 05-FEB-2003;
              Aeomica, Inc. (US)
FEATURES      1..17
               Location/Qualifiers

```

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS       Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE         Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL       Patent: EP 1281758-A 400 05-FEB-2003;
              Aeomica, Inc. (US)
FEATURES      1..17
               Location/Qualifiers
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1744 TCCTCCCTATCCT 1756
Db 4 TCCTCACTATCCT 16

RESULT 343
AX687669
LOCUS          17 bp      DNA          linear          PAT 31-MAR-2003
DEFINITION     Sequence 401 from Patent EP1281758.
ACCESSION      AX687669
VERSION        AX687669.1  GI:29410365
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS       Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE         Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL       Patent: EP 1281758-A 401 05-FEB-2003;
              Aeomica, Inc. (US)
FEATURES      1..17
               Location/Qualifiers
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1744 TCCTCCCTATCCT 1756
Db 3 TCCTCACTATCCT 15

RESULT 344
AX687670
LOCUS          17 bp      DNA          linear          PAT 31-MAR-2003
DEFINITION     Sequence 402 from Patent EP1281758.
ACCESSION      AX687670
VERSION        AX687670.1  GI:29410366
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS       Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE         Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL       Patent: EP 1281758-A 402 05-FEB-2003;
              Aeomica, Inc. (US)
FEATURES      1..17
               Location/Qualifiers

```

```
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1744 TCCTCCCTATCCT 1756
      ||||| |||||
Db 2 TCCTCACTATCCT 14

RESULT 345
AX691854
LOCUS AX691854 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 403 from Patent EP1281758.
ACCESSION AX687671
VERSION AX687671.1 GI:29410367
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 403 05-FEB-2003;
FEATURES
source Location/Qualifiers
      1..17
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1744 TCCTCCCTATCCT 1756
      ||||| |||||
Db 1 TCCTCACTATCCT 13

RESULT 346
AX691853
LOCUS AX691853 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 4585 from Patent EP1281758.
ACCESSION AX691853
VERSION AX691853.1 GI:29414794
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 4585 05-FEB-2003;
FEATURES
source Location/Qualifiers
      1..17
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1642 GTAGCAGAGGCA 1654
      ||||| |||||
Db 3 GTAGCAGAGGAA 15

RESULT 349
AX691856
LOCUS AX691856 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 4588 from Patent EP1281758.
ACCESSION AX691856
```



```

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1685 TCTCCTCAGCGT 1697
Db      ||||| |||||
14 CGAGTACGAGAT 2

RESULT 356
AX735391
LOCUS      17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 981 from Patent WO03025177.
ACCESSION AX735391
VERSION AX735391.1 GI:30514668
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 981 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1659 CCAGGCTCACAGC 1671
Db      ||||| |||||
5 CCAGCCTCACAGC 17

RESULT 357
AX752612
LOCUS      17 bp DNA linear PAT 20-JUN-2003
DEFINITION Sequence 7 from Patent WO03035884.
ACCESSION AX752612
VERSION AX752612.1 GI:32134550
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Kueper,J.H., Meyer,R., Meyer-Ficca,M. and Kuhn,A.
TITLE Transient immortalization
JOURNAL Patent: WO 03035884-A 7 01-MAY-2003;
Heart Biosystems GmbH (DE)
FEATURES
source Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer zur Gewinnung von ueberlappenden
PCR-Fragmenten"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1679 CTGGTGTCTCCTC 1691
Db      ||||| |||||
2 CTGGTGTCTCCTC 14

RESULT 358
AX753719
LOCUS      17 bp DNA linear PAT 23-JUN-2003

```

---

```

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1685 TCTCCTCAGCGT 1697
Db      ||||| |||||
3 TCTCCTCAGCGT 15

RESULT 354
AX730112
LOCUS      17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1746 from Patent WO03025175.
ACCESSION AX730112
VERSION AX730112.1 GI:30509455
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 1746 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1679 CTGGTGTCTCCTC 1691
Db      ||||| |||||
4 CTGGTGTCTCCTC 16

RESULT 355
AX732381/c
LOCUS      17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4015 from Patent WO03025175.
ACCESSION AX732381
VERSION AX732381.1 GI:30511724
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 4015 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1679 CTGGTGTCTCCTC 1691
Db      ||||| |||||
4 CTGGTGTCTCCTC 16

```





```

source      1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1665 TCACAGCTGGGAAAC 1677
Db 13 TCACAGCTGGGATC 1

RESULT 363
AX783893/c
LOCUS      AX783893      17 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Sequence 2224 from Patent WO03050284.
ACCESSION  AX783893
VERSION     AX783893.1 GI:32951742
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Guo,J.
TITLE       Human prostate cancer candidate protein 1
JOURNAL     Patent: WO 03050284-A 2224 19-JUN-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES    source
            1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1698 GGTGGAAAGTTGGG 1710
Db 17 GGTGGAAAGTTGGG 5

RESULT 364
AX783894/c
LOCUS      AX783894      17 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Sequence 2225 from Patent WO03050284.
ACCESSION  AX783894
VERSION     AX783894.1 GI:32951743
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Guo,J.
TITLE       Human prostate cancer candidate protein 1
JOURNAL     Patent: WO 03050284-A 2225 19-JUN-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES    source
            1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1698 GGTGGAAAGTTGGG 1710
Db 17 GGTGGAAAGTTGGG 5

RESULT 365
BD067459
LOCUS      BD067459      17 bp      RNA      linear      PAT 27-AUG-2002
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors.
ACCESSION  BD067459
VERSION     BD067459.1 GI:22613062
KEYWORDS    JP 2001511003-A/299.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE       Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors
JOURNAL     Patent: JP 2001511003-A 299 07-AUG-2001;
            RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT     OS Unidentified
            PN JP 2001511003-A/299
            PD 07-AUG-2001
            PF 14-JAN-1998 JP 1998532913
            PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
            SAGHR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
            C12N9/00,C07K14/71
            CC Strandedness: Single;
            CC Topology: Linear;
            CC Enzymatic nucleic acid treatment of diseases or conditions CC
            related to
            CC levels of epidermal growth factor receptors
            FH Key Location/Qualifiers
            FT source 1. .17
            /organism='Unidentified'.

FEATURES    source
            1. .17
            Location/Qualifiers
            /organism="unidentified"
            /mol_type="genomic RNA"
            /db_xref="taxon:32644"

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1729 AGATTGGCTCCCA 1741
Db 5 ATATTGGCTCCCA 17

RESULT 366
BD104949/c
LOCUS      BD104949      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION  BD104949
VERSION     BD104949.1 GI:22650523
KEYWORDS    WO 0192572-A/1053.
SOURCE      synthetic construct
            ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
TITLE       Kit and method for determining HLA type
JOURNAL     Patent: WO 0192572-A 1053 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAeko
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS Artificial Sequence
            PN WO 0192572-A/1053
            PD 06-DEC-2001
            PE 01-JUN-2001 WO 2001JP004662
            PR 01-JUN-2000 JP 00P 164798

```

```

PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
MATSUMURA,
PI SHOGO MORIYA,MICHIO NISHIDA
PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
CC Description of Artificial Sequence:capture
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
FEATURES
    source
        1..17
            /organism='Artificial Sequence'.
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match
Best Local Similarity 8.2%; Score 11.4; DB 1; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1661 AGGCTCAGCTG 1673
Db 17 AGGCTCAGCTG 5

RESULT 367
BD105056/c
LOCUS BD105056 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD105056
VERSION BD105056.1 GI:22650630
KEYWORDS WO 0192572-A/1160.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 1160 06-DEC-2001;
NISHINEO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO NISHIDA
COMMENT OS Artificial Sequence
PN WO 0192572-A/1160
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
MATSUMURA,
PI SHOGO MORIYA,MICHIO NISHIDA
PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
CC Description of Artificial Sequence:capture
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
FEATURES
    source
        1..17
            /organism='Artificial Sequence'.
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match
Best Local Similarity 8.2%; Score 11.4; DB 1; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1661 AGGCTCAGCTG 1673
Db 17 AGGCTCAGCTG 5

RESULT 368
BD132027/c
LOCUS BD132027 17 bp DNA linear PAT 18-SEP-2002
DEFINITION Human blood bacterium.

```

```

ACCESSION BD132027
VERSION BD132027.1 GI:23226972
KEYWORDS JP 2002502583-A/16.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Lindner,L. and Macphree,K.
TITLE Human blood bacterium
JOURNAL Patent: JP 2002502583-A 16 29-JAN-2002;
COMMENT PATHBIOTEK INC
OS Artificial Sequence
PN JP 2002502583-A/16
PD 29-JAN-2002
PF 06-NOV-1998 JP 2000519605
PR 06-NOV-1997 US 60/064472
PI LUTHER LINDNER,KATHLEEN MACPHEE
PC C12N15/09,A61K31/18,A61K31/395,A61K31/424,A61K31/431 PC
,A61K31/47,A61K31/4709.
PC A61K31/65,A61K31/7036,A61K31/704,A61K31/7048,A61K31/7052, PC
A61K39/00.
PC A61P31/04,C07H21/04,C12N1/20,C12Q1/06,C12Q1/69,C12N15/00 CC
primer specific for intergenic spacer region
(IGS) sequence of
CC a new human
CC blood bacterium
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
FEATURES
    source
        1..17
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match
Best Local Similarity 8.2%; Score 11.4; DB 1; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1698 GGTGGAAGTTGGG 1710
Db 16 GGTGGAAGTTGGG 4

RESULT 369
BD198719/c
LOCUS BD198719 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.
ACCESSION BD198719
VERSION BD198719.1 GI:33008489
KEYWORDS JP 2002509721-A/1745.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 1745 02-APR-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
PN JP 2002509721-A/1745
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT, JAMES A MCSWIGGEN
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00.
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC

```

C12N5/00  
CC Method and reagent for treating diseases or conditions CC  
concerning molecule  
CC participating in vasculogenic response  
FH Key Location/Qualifiers  
FT source 1..17  
/organism='Homo sapiens (human)'.  
FT Location/Qualifiers  
FEATURES  
source  
1..17  
/organism='Homo sapiens'  
/mol\_type='genomic RNA'  
/db\_xref='taxon:9606'  
Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 2.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1716 AGTACGGAGATGG 1728  
||||| |||||  
Db 17 AGTACAGATGG 5  
RESULT 370  
BD198825/c  
LOCUS  
DEFINITION  
Method and reagent for treating diseases or conditions concerning  
molecule participating in vasculogenic response.  
ACCESSION  
BD198825  
VERSION  
BD198825.1 GI:33008595  
KEYWORDS  
JP 2002509721-A/1851.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 17)  
AUTHORS  
Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.  
TITLE  
Method and reagent for treating diseases or conditions concerning  
molecule participating in vasculogenic response  
JOURNAL  
Patent: JP 2002509721-A 1851 02-APR-2002;  
RIBOZYME PHARMACEUTICALS INC  
COMMENT  
OS Homo sapiens (human)  
PN JP 2002509721-A/1851  
PD 02-APR-2002  
PF 24-MAR-1999 JP 2000541291  
PR 27-MAR-1998 US 60/079678  
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,  
PJ JAMES A MCSWIGGEN  
PC  
C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC  
A61P29/00  
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC  
C12N5/00  
CC Method and reagent for treating diseases or conditions CC  
concerning molecule  
CC participating in vasculogenic response  
FH Key Location/Qualifiers  
FT source 1..17  
/organism='Homo sapiens (human)'.  
FT Location/Qualifiers  
FEATURES  
source  
1..17  
/organism='Homo sapiens'  
/mol\_type='genomic RNA'  
/db\_xref='taxon:9606'  
Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 2.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1661 AGGCTCAGCTG 1673  
||||| |||||  
Db 16 AGGCTCAGAGCTG 4

RESULT 371  
I31522/c  
LOCUS  
DEFINITION  
Sequence 434 from patent US 5582979.  
ACCESSION  
I31522  
VERSION  
I31522.1 GI:1822313  
KEYWORDS  
Unknown.  
SOURCE  
Unknown.  
ORGANISM  
Unclassified.  
REFERENCE  
1 (bases 1 to 20)  
AUTHORS  
Weber, J.L.  
TITLE  
Length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and  
method of using the same  
JOURNAL  
Patent: US 5582979-A 434 10-DEC-1996;  
FEATURES  
Location/Qualifiers  
source  
1..20  
/organism='unknown'  
/mol\_type='unassigned DNA'  
Query Match 8.2%; Score 11.4; DB 1; Length 20;  
Best Local Similarity 92.3%; Pred. No. 3.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1735 GCTCCCACTCCT 1747  
||||| |||||  
Db 13 GCTCCTAACTCCT 1  
RESULT 372  
A09974  
LOCUS  
DEFINITION  
Probe HBV.  
ACCESSION  
A09974  
VERSION  
A09974.1 GI:490630  
KEYWORDS  
synthetic construct  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.  
REFERENCE  
1 (bases 1 to 16)  
AUTHORS  
Vijg, J. and Uitterlinden, A.G.  
TITLE  
A method for the simultaneous determination of DNA sequence  
variations at a large number of sites, and a kit therefor  
JOURNAL  
Patent: EP 0349024-A 9 03-JAN-1990;  
NEDERLANDSE ORGANISATIE VOOR TOEGEPAST-NATUURWETENSCHAPPELIJK  
ONDERZOEK TWO  
FEATURES  
Location/Qualifiers  
source  
1..16  
/organism='synthetic construct'  
/mol\_type='unassigned DNA'  
/db\_xref='taxon:32630'  
Query Match 8.1%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 2.6e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1702 GAAGTTGGGTAGGAG 1717  
||||| |||||  
Db 1 GGAGTTGGGGGAGGAG 16  
RESULT 373  
AR105448/c  
LOCUS  
DEFINITION  
Sequence 11 from patent US 6096549.  
ACCESSION  
AR105448  
VERSION  
AR105448.1 GI:12819045  
KEYWORDS  
Unknown.  
SOURCE  
Unknown.  
ORGANISM  
Unclassified.  
REFERENCE  
1 (bases 1 to 16)  
AUTHORS  
Pellicic, V., Reyrat, J.-M., Gicquel, B., Guilhot, C. and Jackson, M.

```

TITLE      Method of selection of allelic exchange mutants
JOURNAL    Patent: US 6096549-A 11 01-AUG-2000;
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.1%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1754 CCTAAGGCCCACTGG 1769
Db 16 CCTATGGCCTAATGG 1

RESULT 374
LOCUS      AR328255                16 bp    RNA
DEFINITION Sequence 5657 from patent US 6566127.
ACCESSION  AR328255
VERSION     AR328255.1 GI:33714063
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unassigned.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 5657 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      8.1%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1661 AGGCTCACAGCTGGAA 1676
Db 16 AGGTCACAGCTGGAA 1

RESULT 377
LOCUS      AR435895                16 bp    RNA
DEFINITION Sequence 154 from patent US 6656731.
ACCESSION  AR435895
VERSION     AR435895.1 GI:40198979
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unassigned.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Eckstein, F., Ludwig, J. and Beigelman, L.
TITLE     Nucleic acid catalysts with endonuclease activity
JOURNAL    Patent: US 6656731-A 154 02-DEC-2003;
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      8.1%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1654 AAGCACACAGGCTCACA 1669
Db 16 AAGCTCAAGGTTTACA 1

RESULT 378
LOCUS      AX255727                16 bp    DNA
DEFINITION Sequence 148 from Patent WO0170982.
ACCESSION  AX255727
VERSION     AX255727.1 GI:16074782
KEYWORDS   .
SOURCE     synthetic construct
          synthetic construct
          artificial sequences.
REFERENCE  1
AUTHORS   Beger, C., Barber, J. and Wong-Staal, F.
TITLE     Brca-1 regulators and methods of use
JOURNAL    Patent: WO 0170982-A 148 27-SEP-2001;
          Immusol Incorporated (US); Beger, Carmela (DE)

TITLE      Method of selection of allelic exchange mutants
JOURNAL    Patent: US 6096549-A 11 01-AUG-2000;
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      8.1%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1754 CCTAAGGCCCACTGG 1769
Db 16 CCTATGGCCTAATGG 1

RESULT 374
LOCUS      AR328255                16 bp    RNA
DEFINITION Sequence 5657 from patent US 6566127.
ACCESSION  AR328255
VERSION     AR328255.1 GI:33714063
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unassigned.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 5657 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      8.1%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1666 CACAGCTGGACCCCTG 1681
Db 16 CACAGCAGGACCCCG 1

RESULT 375
LOCUS      AR328256                16 bp    RNA
DEFINITION Sequence 5658 from patent US 6566127.
ACCESSION  AR328256
VERSION     AR328256.1 GI:33714064
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unassigned.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 5658 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      8.1%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCACAGCTGGACCC 1678
Db 16 GCGCACAGCAGGACCC 1
```

```

FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic oligonucleotide"

Query Match
  Best Local Similarity 8.1%; Score 11.2; DB 1; Length 16;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1679 CTGGTGTCTCTCCAG 1694
Db 1 CTGGTGTCTACTACAG 16

RESULT 379
AX284046/c
LOCUS AX284046 16 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 11 from Patent WO0179487.
ACCESSION AX284046
VERSION AX284046.1 GI:17044756
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Degitz, K.K. and Besch, R.
  TITLE
    Polydesoxyribonucleotides for inhibiting the expression of the
    icam-1-gene
  JOURNAL
    Patent: WO 0179487-A 11 25-OCT-2001;
    Degitz, Klaus Karl (DE); Besch, Robert (DE)
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Beschreibung der kunstlichen
      Sequenz: Polydesoxyribonukleotid"

Query Match
  Best Local Similarity 8.1%; Score 11.2; DB 1; Length 16;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1736 CTCCCACTCTCCCT 1751
Db 16 CCCCCACCTCTCCCT 1

RESULT 380
AX572221/c
LOCUS AX572221 16 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 261 from Patent WO02055741.
ACCESSION AX572221
VERSION AX572221.1 GI:26004311
KEYWORDS
  Human immunodeficiency virus
SOURCE
  ORGANISM
    Human immunodeficiency virus
    Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
    lentivirus group.
REFERENCE
  1
  AUTHORS
    de Smet, K. and Stuyver, L.
  TITLE
    Method for detection of drug-induced mutations in the hiv reverse
    transcriptase gene
  JOURNAL
    Patent: WO 02055741-A 261 18-JUL-2002;
    INNOGENETICS N.V. (BE)
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="Human immunodeficiency virus"
      /mol_type="unassigned DNA"
      /db_xref="taxon:12721"

Query Match
  Best Local Similarity 8.1%; Score 11.2; DB 1; Length 16;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1690 TCCAGCGTGGTGAAG 1705
Db 16 TCCATCCTGTGGAG 1

RESULT 381
AX687850
LOCUS AX687850 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 582 from Patent EP1281758.
ACCESSION AX687850
VERSION AX687850.1 GI:29410548
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Shannon, M., Gu, Y. and Nguyen, C.T.
  TITLE
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    mdz12
  JOURNAL
    Patent: EP 1281758-A 582 05-FEB-2003;
    Acomica, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      1..17
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1659 CCAGGCTCACAGCTGG 1674
Db 1 CCAGGCATCCAGCTGG 16

RESULT 382
AX687849
LOCUS AX687849 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 581 from Patent EP1281758.
ACCESSION AX687849
VERSION AX687849.1 GI:29410547
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
    Shannon, M., Gu, Y. and Nguyen, C.T.
  TITLE
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    mdz12
  JOURNAL
    Patent: EP 1281758-A 581 05-FEB-2003;
    Acomica, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      1..17
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1659 CCAGGCTCACAGCTGG 1674
Db 2 CCAGGCATCCAGCTGG 17

RESULT 383

```

A66875/c  
LOCUS A66875 17 bp DNA  
DEFINITION Sequence 42 from Patent WO9740193.  
ACCESSION A66875  
KEYWORDS A66875.1 GI:4538246  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Stuyver, L., Rossau, R. and Maertens, G.  
TITLE METHOD FOR TYPING AND DETECTING HBV  
JOURNAL Patent: WO 9740193-A 42 30-OCT-1997;  
INNOGENETICS NV (BE)  
FEATURES  
source location/Qualifiers  
1..17  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1747 TCCCTATCCTCTAAAGCC 1762  
|||||  
Db 17 TCAATGCTCTAAAGCC 2  
RESULT 384  
A87652/c  
LOCUS A87652 17 bp DNA  
DEFINITION Sequence 3 from Patent EP0860445.  
ACCESSION A87652  
KEYWORDS A87652.1 GI:6736286  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Liu, N. and Mueller, R. P.  
TITLE New nucleotide sequences for the cell cycle regulated expression of structural genes  
JOURNAL Patent: EP 0860445-A 3 26-AUG-1998;  
HOECHST AG (DE)  
FEATURES  
source location/Qualifiers  
1..17  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1734 GGCTCCCACTCTCTCC 1749  
|||||  
Db 17 GCCTCCCACTCTCTC 2  
RESULT 385  
A95622/c  
LOCUS A95622 17 bp DNA  
DEFINITION Sequence 24 from Patent WO9925815.  
ACCESSION A95622  
KEYWORDS A95622.1 GI:6779559  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Herrmann, B. and Kispert, A.  
TITLE NUCLEIC ACIDS INVOLVED IN THE RESPONDER PHENOTYPE AND APPLICATIONS  
THEREOF  
Patent: WO 9925815-A 24 27-MAY-1999;  
HERRMANN BERNHARD (DE); MAX PLANCK GESELLSCHAFT (DE)  
FEATURES  
source location/Qualifiers  
1..17  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1690 TCCAGCGTGTGGAG 1705  
|||||  
Db 16 TCCAGCCAGGGGAG 1  
RESULT 386  
AR022370  
LOCUS AR022370 17 bp DNA  
DEFINITION Sequence 16 from patent US 5792833.  
ACCESSION AR022370  
KEYWORDS AR022370.1 GI:3976432  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Androphy, E. J. and Breiding, D. E.  
TITLE E2 binding proteins  
JOURNAL Patent: US 5792833-A 16 11-AUG-1998;  
FEATURES  
source location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1691 CCAGCGTGTGGAGT 1706  
|||||  
Db 1 CCAGGCGGTAGAGT 16  
RESULT 387  
AR046570/c  
LOCUS AR046570 17 bp DNA  
DEFINITION Sequence 1363 from patent US 5817796.  
ACCESSION AR046570  
KEYWORDS AR046570.1 GI:5968035  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb, D. T., Draper, K., McSwiggen, J. and Jarvis, T.  
TITLE C-myb ribozymes having 2'-5'-linked adenylate residues  
JOURNAL Patent: US 5817796-A 1363 06-OCT-1998;  
FEATURES  
source location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1715 GAGTACGGAGATGAG 1730  
|||||  
Db 16 GAGAGCTGAGATGAG 1

```

RESULT 388
AR057466/c
LOCUS AR057466 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1670 from patent US 5837542.
ACCESSION AR057466
VERSION AR057466.1 GI:5983043
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1670 17-NOV-1998;
FEATURES
Location/Qualifiers
1..17
/mol_type="unassigned DNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1704 AGTTGGGTTAGGAGTA 1719
Db 17 AGGTGGGTGAGGGGTA 2

RESULT 389
AR057770/c
LOCUS AR057770 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1974 from patent US 5837542.
ACCESSION AR057770
VERSION AR057770.1 GI:5983347
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1974 17-NOV-1998;
FEATURES
Location/Qualifiers
1..17
/mol_type="unassigned DNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1704 AGTTGGGTTAGGAGTA 1719
Db 17 AGGTGGGTGAGGGGTA 2

RESULT 390
AR099617/c
LOCUS AR099617 17 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 28 from patent US 6077934.
ACCESSION AR099617
VERSION AR099617.1 GI:12809383
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Jacobsen,R., Jimenez,E., Cruz,L.J., Olivera,B.M., Gray,W.R., Grilley,M., Watkins,M. and Hillyard,D.R.
TITLE Contryphan peptides

```

```

JOURNAL Patent: US 6077934-A 28 20-JUN-2000;
FEATURES
Location/Qualifiers
1..17
/mol_type="unassigned DNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 76.9%; Pred. No. 2.9e+02;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1673 GGAACCCCTGGTCT 1685
Db 15 GGARCCNTGGTGY 3

RESULT 391
AR100616
LOCUS AR100616 17 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 12 from patent US 6080727.
ACCESSION AR100616
VERSION AR100616.1 GI:12811064
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zupi,G.
TITLE Oligonucleotide treatments and compositions for human melanoma
JOURNAL Patent: US 6080727-A 12 27-JUN-2000;
FEATURES
Location/Qualifiers
1..17
/mol_type="unassigned DNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1731 ATTGGCTCCCAACTCC 1746
Db 2 ATTGTTTCCCACTCC 17

RESULT 392
AR115224/c
LOCUS AR115224 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1670 from patent US 6132967.
ACCESSION AR115224
VERSION AR115224.1 GI:14095546
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1670 17-OCT-2000;
FEATURES
Location/Qualifiers
1..17
/mol_type="unassigned DNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1704 AGTTGGGTTAGGAGTA 1719
Db 17 AGGTGGGTGAGGGGTA 2

```

```

RESULT 393
AR115528/c
LOCUS      17 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 1974 from patent US 6132967.
ACCESSION AR115528
VERSION    AR115528.1 GI:14095850
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
TITLE      Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
JOURNAL    Patent: US 6132967-A 1974 17-OCT-2000;
FEATURES   Location/Qualifiers
            source          1..17
                        /organism="unknown"
                        /mol_type="unassigned DNA"
            Query Match      8.1%; Score 11.2; DB 1; Length 17;
            Best Local Similarity 81.2%; Pred. No. 2.9e+02;
            Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1704 AGTTGGGTAGAGTA 1719
      ||||| |||||
Db 17 AGTGGGTGAGGGTA 2

RESULT 394
AR120130/c
LOCUS      17 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 28 from patent US 6153738.
ACCESSION AR120130
VERSION    AR120130.1 GI:14102829
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Jacobsen,R., Jimenez,E., Cruz,L.J., Olivera,B.M., Gray,W.R.,
            Grilley,M., Watkins,M. and Hillyard,D.R.
TITLE      Contryphan peptides
JOURNAL    Patent: US 6153738-A 28 NOV-2000;
FEATURES   Location/Qualifiers
            source          1..17
                        /organism="unknown"
                        /mol_type="unassigned DNA"
            Query Match      8.1%; Score 11.2; DB 1; Length 17;
            Best Local Similarity 76.9%; Pred. No. 2.9e+02;
            Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1673 GGAACCTGGTGT 1685
      ||||| |||||
Db 15 GGARCCNTGGTG 3

RESULT 395
BD240770/c
LOCUS      17 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Expression systems comprising chimeric promoters with binding sites
            for recombinant transcription factors.
ACCESSION BD240770
VERSION    BD240770.1 GI:33050540
KEYWORDS   Saccharomyces cerevisiae (baker's yeast)
SOURCE     Saccharomyces cerevisiae
ORGANISM   Saccharomycetes
REFERENCE  1 (bases 1 to 17)
AUTHORS    Mueller,R., Nettelbeck,D. and Sedlacek,H.H.

```

```

TITLE      Expression systems comprising chimeric promoters with binding sites
            for recombinant transcription factors
JOURNAL    Patent: JP 2002538759-A 4 19-NOV-2002;
            AVENTIS PHARMA DEUTSCHLAND GMBH
COMMENT    OS Saccharomyces cerevisiae (yeast)
            PN JP 2002538759-A/4
            PD 19-NOV-2002
            PF 01-JUL-1999 JP 2000560275
            PR 14-JUL-1998 DE 198 31 420.5
            PI ROLF MUELLER,DIRK NETTELBECK,HANS HARALD SEDLACEK PC
            C12N15/09,C12Q1/68//C12N15/09,C12R1/92,C12N15/00,C12N15/00,PC
            C12R1/92
            CC Expression systems comprising chimeric promoters with binding
            CC sites for
            CC recombinant transcription factors
            FH Key      Location/Qualifiers
            FT source    1..17
                        /organism='Saccharomyces cerevisiae (yeast)'
            FEATURES     Location/Qualifiers
                        1..17
                        /organism='Saccharomyces cerevisiae'
                        /mol_type='genomic DNA'
                        /db_xref='taxon:4932'
            Query Match      8.1%; Score 11.2; DB 1; Length 17;
            Best Local Similarity 81.2%; Pred. No. 2.9e+02;
            Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GGCTCCCAACTCTCTC 1749
      ||||| |||||
Db 17 GGCTCCCAACAGCTGC 2

RESULT 396
BD244486/c
LOCUS      17 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION New triplex forming oligonucleotides and their use in anti-HBV.
ACCESSION BD244486
VERSION    BD244486.1 GI:33054256
KEYWORDS   JP 2002511384-A/4.
SOURCE     synthetic construct
            ORGANISM      artificial sequences.
            REFERENCE     1 (bases 1 to 17)
            AUTHORS       Lu,C.
            TITLE         New triplex forming oligonucleotides and their use in anti-HBV
            JOURNAL       Patent: JP 2002511384-A 4 16-APR-2002;
            COMMENT        SHANGHAI INSTITUTE OF BIOCHEMISTRY CHINESE ACADEMY OF SCIENCES
            OS Artificial Sequence
            PN JP 2002511384-A/4
            PD 16-APR-2002
            PF 19-OCT-1998 JP 2000516982
            PR 21-OCT-1997 CN 97 1 06667.1
            PI CHANGDE LU
            PC A61K31/711,A61K48/00,A61P31/20,C12N15/09,C12N15/00 CC
            Description of Artificial Sequence: Triplex forming CC
            CC This oligo may or may not be 3'-monophosphorylated FH Key
            FT source      1..17
                        Location/Qualifiers
            FEATURES     Location/Qualifiers
                        1..17
                        /organism='Artificial Sequence'
                        /mol_type='synthetic construct'
                        /db_xref='taxon:32630'
            Query Match      8.1%; Score 11.2; DB 1; Length 17;
            Best Local Similarity 81.2%; Pred. No. 2.9e+02;
            Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 CTCCCAACTCTCTCCT 1751
      ||||| |||||

```



```
Db 16 CTCCTCTCTCTCTCT 1

RESULT 397
BD254012/c
LOCUS BD254012 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254012
VERSION BD254012.1 GI:33063782
KEYWORDS JP 2002541795-A/1805.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 1805 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/1805
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
/organism='Eukaryote'.
FEATURES
source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1647 AGAAGCGCAAGCACCAG 1662
|||||
Db 16 AGCAGGCAAGCCCG 1

RESULT 399
E07498/c
LOCUS E07498 17 bp DNA linear PAT 29-SEP-1997
DEFINITION Synthetic DNA for probe.
ACCESSION E07498
VERSION E07498.1 GI:2175636
KEYWORDS JP 1994133799-A/7.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Yamanishi,K., Yamamoto,T. and Mori,H.
TITLE ANALYSIS OF HUMAN HERPES VIRUS 6 TYPE @ (3754/24) HHV-6) DNA AND
DISCRIMINATION OF SUB-TYPE
JOURNAL Patent: JP 1994133799-A 7 17-MAY-1994;
INTERNAIL REAGENTS CORP
COMMENT OS None
OC Artificial sequences.
PN JP 1994133799-A/7
PD 17-MAY-1994
PF 27-OCT-1992 JP 1992311416
PI YAMANISHI KOICHI, YAMAMOTO TAKESHI, MORI HIROYUKI PC
C12Q1/68, C12Q1/68, C12N15/11, C12N15/38;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
Key Location/Qualifiers
FT source 1..17
/organism='Artificial sequences'.
FEATURES
source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1665 TCACAGCTGGAACCCCT 1680
|||||
Db 16 TCACAGATGGAAGACT 1

RESULT 400

Db 16 CTCCTCTCTCTCTCT 1

RESULT 397
BD254012/c
LOCUS BD254012 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254012
VERSION BD254012.1 GI:33063782
KEYWORDS JP 2002541795-A/1805.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 1805 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/1805
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
/organism='Eukaryote'.
FEATURES
source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1638 GCTTGTAGCAGAGGC 1653
|||||
Db 17 GCTTGTAGTAGAGGCC 2

RESULT 398
BD255189/c
LOCUS BD255189 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255189
VERSION BD255189.1 GI:33064959
KEYWORDS JP 2002541795-A/2982.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2982 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/2982
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
```

E24413/c	E24413	17 bp	DNA	linear	PAT 18-JUN-2001
LOCUS	Pharmacologically controllable self-accelerating expression system.				
DEFINITION	E24413				
ACCESSION	E24413.1	GI:13024640			
VERSION	JP 1999000176-A/7.				
KEYWORDS	unidentified				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Rolf,M. and Hansharald,S.				
TITLE	Pharmacologically controllable self-accelerating expression system				
JOURNAL	Patent: JP 1999000176-A 7 06-JAN-1999;				
COMMENT	HOECHST AG				
OS	Unidentified				
PN	JP 1999000176-A/7				
PD	06-JAN-1999				
PF	11-DEC-1997	JP 1997341728			
PR	11-DEC-1996	DE			
PI	ROLF MUELLER,HANS-HARALD SEDLACEK				
PC	C12N15/09,A61K31/70,A61K31/70,A61K31/70,A61K31/70,A61K31/70,				
PC	A61K31/70,				
PC	A61K31/70,A61K31/70,A61K31/70,A61K38/00,A61K48/00,C07K16/18,				
PC	C07K19/00,				
PC	C12N5/10,C12P21/02,C12N15/00,A61K37/02,C12N5/00	CC			
Strandedness:	Single;				
CC	Topology: Linear;				
FH	Key	Location/Qualifiers			
FT	source	1..17			
FEATURES	source	Location/Qualifiers			
		1..17			
	/organism="unidentified"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:32644"				
Query Match	8.1%;	Score 11.2;	DB 1;	Length 17;	
Best Local Similarity	81.2%;	Pred. No. 2.9e+02;			
Matches	13;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
QY	1734	GGCTCCCAACTCTCC	1749		
Db	17	GGCTCCCAACCTGC	2		
RESULT 402					
E39008/c					
LOCUS					
DEFINITION	E39008	17 bp	DNA	linear	PAT 18-JUN-2001
ACCESSION	E39008				
VERSION	E39008.1	GI:13017670			
KEYWORDS	JP 1999308997-A/7.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Martin,A., Andrea,B. and Hansharald,S.				
TITLE	Nucleic acid construction for gene therapy affected in activity by				
JOURNAL	Patent: JP 1999308997-A 7 09-NOV-1999;				
COMMENT	HOECHST MARION ROUSSEL DEUTSCHLAND GMBH				
OS	Homo sapiens (human)				
PN	JP 1999308997-A/7				
PD	09-NOV-1999				
PF	21-DEC-1998	JP 1998376131			
PR	20-DEC-1997	DE 197 56 975.7			
PI	MARTIN AIRASU,ANDREA BUAGIN,HANS-HARALD SEDLACEK	PC			
C12N15/09,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,					
A61K31/00,					
PC	A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K38/00,A61K38/22,				
PC	A61K38/43,				
PC	A61K39/395,A61K48/00,C12N15/00,A61K37/02,A61K37/24,A61K37/465				
CC					
FH	Key	Location/Qualifiers			
FT	source	1..17			
FEATURES	source	Location/Qualifiers			
		1..17			
	/organism="Homo sapiens"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				
Query Match	8.1%;	Score 11.2;	DB 1;	Length 17;	
Best Local Similarity	81.2%;	Pred. No. 2.9e+02;			
Matches	13;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
QY	1734	GGCTCCCAACTCTCC	1749		
Db	17	GGCTCCCAACCTGC	2		
RESULT 403					
E64351/c					
LOCUS					
DEFINITION	E64351	17 bp	DNA	linear	PAT 31-JAN-2002
ACCESSION	E64351				
VERSION	E64351.1	GI:18628512			
KEYWORDS	JP 2000201678-A/2.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Kathryn,K., Rolf,M. and Hansharald,S.				
TITLE	cdc25B Gene promoter, preparation thereof and utilization of the				
JOURNAL	Patent: JP 1999000181-A 1 06-JAN-1999;				
COMMENT	HOECHST AG				
OS	Unidentified				
PN	JP 1999000181-A/1				
PD	06-JAN-1999				
PF	16-MAR-1998	JP 1998084995			
PR	14-MAR-1997	DE			
PI	KATHRYN KERUNA,ROLF MUELLER,HANS-HARALD SEDLACEK	PC			
C12N15/09,A61K48/00,C12P21/02,C12P21/02,C12N5/10,					
C12R1:91),					
PC	(C12N9/12,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00,				
PC	(C12N5/00,C12R1:91)				
CC	Strandedness: Single;				
CC	Topology: Linear;				

SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE artificial sequences.  
1 (bases 1 to 17)  
AUTHORS Kontaman,R., Sedlacek,H.H. and Mueller,R.  
TITLE Single-stranded multiple antigen-binding molecule and method for producing it and use  
JOURNAL Patent: JP 2000201678-A 2 25-JUL-2000;  
COMMENT HORCHST MARION ROUSSEL DEUTSCHLAND GMBH  
OS Artificial Sequence  
PN JP 2000201678-A/2  
PD 25-JUL-2000  
PF 09-APR-1999 JP 1999102595  
PR  
PI ROLAND KONTAMAN, HANS HARALD SEDLACEK, ROLF MUELLER PC  
C12N15/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00, PC  
A61K35/74,  
PC A61K35/76,A61K38/00,C07K16/46,C12N1/19,C12N1/21,C12N5/10, PC  
C12N15/00,  
PC A61K37/02,C12N5/00  
CC  
FH Key Location/Qualifiers  
FT source 1..17  
/organism='Artificial Sequence'.  
FEATURES  
source  
1..17  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1734 GGCTCCCACTCTCC 1749  
| | | | | | | | | |  
Db 17 GCCTCCCACTCTGC 2  
RESULT 404  
150743  
LOCUS 17 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 25 from patent US 5643724.  
ACCESSION I50743  
VERSION I50743.1 GI:2472446  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Fildes,N.Jane. and Reynolds,R.Lynne.  
TITLE Methods and reagents for Glycophorin A typing  
JOURNAL Patent: US 5643724-A 25 01-JUL-1997;  
FEATURES  
source  
1..17  
/organism='unknown'  
/mol\_type='unassigned DNA'  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1670 GCTGGAACCTGGGT 1685  
| | | | | | | | | |  
Db 1 GGTGGAATCTTGGGT 16  
RESULT 405  
I53622/c  
LOCUS 17 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 1363 from patent US 5646042.  
ACCESSION I53622  
VERSION I53622.1 GI:2474825

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.  
TITLE C-myb targeted ribozymes  
JOURNAL Patent: US 5646042-A 1363 08-JUL-1997;  
FEATURES  
source  
1..17  
/organism='unknown'  
/mol\_type='unassigned DNA'  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1715 GAGTACCGAGATGGAG 1730  
| | | | | | | | | |  
Db 16 GAGAGCTGAGATGGAG 1  
RESULT 406  
AR185989/c  
LOCUS 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 1477 from patent US 6346398.  
ACCESSION AR185989  
VERSION AR185989.1 GI:20231954  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Payco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 1477 12-FEB-2002;  
FEATURES  
source  
1..17  
/organism='unknown'  
/mol\_type='unassigned DNA'  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1666 CACAGCTGGAACCTG 1681  
| | | | | | | | | |  
Db 17 CACAGCAGGACCCCG 2  
RESULT 407  
AR186749/c  
LOCUS 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 2237 from patent US 6346398.  
ACCESSION AR186749  
VERSION AR186749.1 GI:20232714  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Payco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 2237 12-FEB-2002;  
FEATURES  
source  
1..17  
/organism='unknown'  
/mol\_type='unassigned DNA'  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;



```
QY 1733 TGGCTCCCAACTCTCC 1748
Db 17 TGGCTGCCAACACTTC 2

RESULT 413
AR209224/c
LOCUS AR208224 17 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 3 from patent US 6380170.
ACCESSION AR208224
VERSION AR208224.1 GI:21508185
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Muller,R., Liu,N., Zwicker,J. and Sedlacek,H.-H.
TITLE Nucleic acid construct for the cell cycle regulated expression of
structural genes
JOURNAL Patent: US 6380170-A 3 30-APR-2002;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GCCTCCCAACTCTCC 1749
Db 17 GCCTCCCAACACTTC 2

RESULT 414
AR262374
LOCUS AR262374 17 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 10 from patent US 6323184.
ACCESSION AR262374
VERSION AR262374.1 GI:28073805
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zalewski,A. and Shi,Y.
TITLE Arteriovenous and venous graft treatments: methods and compositions
JOURNAL Patent: US 6323184-A 10 27-NOV-2001;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1731 ATTGGCTCCCAACTCC 1746
Db 2 ATTGTTTCCAACTCC 17

RESULT 415
AR286208
LOCUS AR286208 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 580 from patent US 6528640.
ACCESSION AR286208
VERSION AR286208.1 GI:29723804
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 580 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1677 CCTCGTGTCTCTCC 1692
Db 1 CGCTGGGGCTCTCTCC 16

RESULT 416
AR322620/c
LOCUS AR322620 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 22 from patent US 6566127.
ACCESSION AR322620
VERSION AR322620.1 GI:33708428
KEYWORDS
SOURCE
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 22 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAACTCTG 1681
Db 17 CACAGCAGGACCCCG 2

RESULT 417
AR323380/c
LOCUS AR323380 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 782 from patent US 6566127.
ACCESSION AR323380
VERSION AR323380.1 GI:33709188
KEYWORDS
SOURCE
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 782 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1661 AGGCTCACAGCTGGAA 1676
```

```
Db      16 AGGCTCAGAGTGGGA 1
|||||
RESULT 418
LOCUS   AR325180          17 bp  RNA          PAT 17-AUG-2003
DEFINITION Sequence 2582 from patent US 6566127.
ACCESSION AR325180
VERSION   AR325180.1  GI:33710988
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6566127-A 2582 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1642 GTAGCAGAAGGCAAGC 1657
|||||
Db      16 GCATCATAGGCAAGC 1

RESULT 419
LOCUS   AR325490          17 bp  RNA          PAT 17-AUG-2003
DEFINITION Sequence 2892 from patent US 6566127.
ACCESSION AR325490
VERSION   AR325490.1  GI:33711298
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6566127-A 2892 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1642 GTAGCAGAAGGCAAGC 1657
|||||
Db      16 GCATCATAGGCAAGC 1

RESULT 420
LOCUS   AR325491          17 bp  RNA          PAT 17-AUG-2003
DEFINITION Sequence 2893 from patent US 6566127.
ACCESSION AR325491
VERSION   AR325491.1  GI:33711299
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)

AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6566127-A 2893 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1666 CACAGCTGGAAACCTG 1681
|||||
Db      17 CCCAGCAGAAACCTG 2

RESULT 421
LOCUS   AR325509          17 bp  RNA          PAT 17-AUG-2003
DEFINITION Sequence 2911 from patent US 6566127.
ACCESSION AR325509
VERSION   AR325509.1  GI:33711317
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6566127-A 2911 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1666 CACAGCTGGAAACCTG 1681
|||||
Db      16 CCCAGCAGAAACCTG 1

RESULT 422
LOCUS   AR326802/c        17 bp  RNA          PAT 17-AUG-2003
DEFINITION Sequence 4204 from patent US 6566127.
ACCESSION AR326802
VERSION   AR326802.1  GI:33712610
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6566127-A 4204 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1738 CCCAAGCTCTCCTAT 1753
|||||
Db      2 CCCAAGCTCTCAGTAT 17

RESULT 423
LOCUS   AR326802/c        17 bp  RNA          PAT 17-AUG-2003
DEFINITION Sequence 4204 from patent US 6566127.
ACCESSION AR326802
VERSION   AR326802.1  GI:33712610
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
          related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6566127-A 4204 20-MAY-2003;
FEATURES   Location/Qualifiers
            source
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1666 CACAGCTGGAAACCTG 1681
|||||
```

Db 16 CACAGCAGGACCCGG 1

RESULT 423  
AR326803/c  
LOCUS 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 4205 from patent US 6566127.  
ACCESSION AR326803  
VERSION AR326803.1 GI:33712611  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 4205 20-MAY-2003;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGACCC 1679  
Db 17 CGCAGCAGGACCC 2

RESULT 424  
AR327651/c  
LOCUS 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 5053 from patent US 6566127.  
ACCESSION AR327651  
VERSION AR327651.1 GI:33713459  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 5053 20-MAY-2003;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGACCC 1679  
Db 17 CGCAGCAGGACCC 2

RESULT 425  
AR327652/c  
LOCUS 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 5054 from patent US 6566127.  
ACCESSION AR327652  
VERSION AR327652.1 GI:33713460  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.

TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 5054 20-MAY-2003;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1654 AAGCACCAGGCTCACA 1669  
Db 16 AAGCAGCTGGCTCCCA 1

RESULT 426  
AR327765/c  
LOCUS 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 5167 from patent US 6566127.  
ACCESSION AR327765  
VERSION AR327765.1 GI:33713573  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 5167 20-MAY-2003;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1661 AGGCTCAGCTGGAA 1676  
Db 17 AGGCTCAGCTGGGA 2

RESULT 427  
AR398198  
LOCUS 17 bp RNA linear PAT 18-DEC-2003  
DEFINITION Sequence 579 from patent US 6617438.  
ACCESSION AR398198  
VERSION AR398198.1 GI:40135816  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
TITLE Oligoribonucleotides with enzymatic activity  
JOURNAL Patent: US 6617438-A 579 09-SEP-2003;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1677 CCCTGGGTCTCTCC 1692  
Db 1 CGCTGGGGCTCTCC 16

```

thereof
JOURNAL Patent: US 6642339-A 24 04-NOV-2003;
FEATURES Location/Qualifiers
source
1..17
/mol_type="genomic DNA"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1690 TCCAGCGTGTGGGAG 1705
Db 16 TCCAGCGCGGGGGAAG 1

RESULT 431
AR432062 17 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 4 from patent US 6653119.
ACCESSION AR432062
VERSION AR432062.1 GI:40194267
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kondo,R., Sakai,K. and Wakao,K.
TITLE White rot fungi and method for decomposing dioxins using them
JOURNAL Patent: US 6653119-A 4 25-NOV-2003;
FEATURES Location/Qualifiers
source
1..17
/mol_type="genomic DNA"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1648 GAAGGCGACCCAGG 1663
Db 16 GAAGGCGACCCAGG 1

RESULT 432
AR432063 17 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 5 from patent US 6653119.
ACCESSION AR432063
VERSION AR432063.1 GI:40194268
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kondo,R., Sakai,K. and Wakao,K.
TITLE White rot fungi and method for decomposing dioxins using them
JOURNAL Patent: US 6653119-A 5 25-NOV-2003;
FEATURES Location/Qualifiers
source
1..17
/mol_type="genomic DNA"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1648 GAAGGCGACCCAGG 1663
Db 2 GAAGGCGACCCAGG 17

RESULT 433
AR432063 17 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 5 from patent US 6653119.
ACCESSION AR432063
VERSION AR432063.1 GI:40194268
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kondo,R., Sakai,K. and Wakao,K.
TITLE White rot fungi and method for decomposing dioxins using them
JOURNAL Patent: US 6653119-A 5 25-NOV-2003;
FEATURES Location/Qualifiers
source
1..17
/mol_type="genomic DNA"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1648 GAAGGCGACCCAGG 1663
Db 2 GAAGGCGACCCAGG 17

RESULT 433

```



AUTHORS	Mueller,R., Nettelbeck,D. and Sedlacek,H.H.
TITLE	Expression system containing chimeric promoters with binding sites for recombinant transcription factors
JOURNAL	Patent: WO 0004178-A 4 27-JAN-2000; HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES	Location/Qualifiers
source	1..17
Query Match	/organism="Saccharomyces cerevisiae"
Best Local Similarity	8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative	0; Mismatches 3; Indels 0; Gaps 0
QY	1734 GGCTCCCAACTCCTCC 1749
DB	17 GCCTCCCAACCTGC 2
RESULT 436	
AX015204/c	
LOCUS	AX015204 17 bp DNA linear PAT 07-SEP-2000
DEFINITION	Sequence 4 from Patent EP0952218.
ACCESSION	AX015204
VERSION	AX015204.1 GI:10041245
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Kontermann,R.D., Mueller,R.P. and Sedlacek,H.H.
TITLE	Single chain, multiple antigen-binding molecule, its preparation and use
JOURNAL	Patent: EP 0952218-A 4 27-OCT-1999; HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES	Location/Qualifiers
source	1..17
Query Match	/organism="synthetic construct"
Best Local Similarity	8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative	0; Mismatches 3; Indels 0; Gaps 0
QY	1734 GGCTCCCAACTCCTCC 1749
DB	17 GCCTCCCAACCTGC 2
RESULT 437	
AX022637/c	
LOCUS	AX022637 17 bp DNA linear PAT 07-SEP-2000
DEFINITION	Sequence 7 from Patent EP0926237.
ACCESSION	AX022637
VERSION	AX022637.1 GI:10046194
KEYWORDS	unidentified
SOURCE	unidentified
ORGANISM	unclassified.
REFERENCE	1
AUTHORS	Eilers,M.P., Buergin,A. and Sedlacek,H.H.
TITLE	Nucleic acid constructs for gene therapy, whose activity is influenced by inhibitors of cyclin-dependent kinases
JOURNAL	Patent: EP 0926237-A 7 30-JUN-1999; HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES	Location/Qualifiers
source	1..17
Query Match	/organism="unidentified"
Best Local Similarity	8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative	0; Mismatches 3; Indels 0; Gaps 0
QY	1734 GGCTCCCAACTCCTCC 1749
DB	17 GCCTCCCAACCTGC 2
RESULT 438	
AX022637/c	
LOCUS	AX022637 17 bp DNA linear PAT 07-SEP-2000
DEFINITION	Sequence 7 from Patent EP0926237.
ACCESSION	AX022637
VERSION	AX022637.1 GI:10046194
KEYWORDS	unidentified
SOURCE	unidentified
ORGANISM	unclassified.
REFERENCE	1
AUTHORS	Eilers,M.P., Buergin,A. and Sedlacek,H.H.
TITLE	Nucleic acid constructs for gene therapy, whose activity is influenced by inhibitors of cyclin-dependent kinases
JOURNAL	Patent: EP 0926237-A 7 30-JUN-1999; HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES	Location/Qualifiers
source	1..17
Query Match	/organism="unassigned DNA"
Best Local Similarity	8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative	0; Mismatches 3; Indels 0; Gaps 0
QY	1734 GGCTCCCAACTCCTCC 1749
DB	17 GCCTCCCAACCTGC 2
RESULT 439	
AX022637/c	
LOCUS	AX022637 17 bp DNA linear PAT 07-SEP-2000
DEFINITION	Sequence 7 from Patent EP0926237.
ACCESSION	AX022637
VERSION	AX022637.1 GI:10046194
KEYWORDS	unidentified
SOURCE	unidentified
ORGANISM	unclassified.
REFERENCE	1
AUTHORS	Eilers,M.P., Buergin,A. and Sedlacek,H.H.
TITLE	Nucleic acid constructs for gene therapy, whose activity is influenced by inhibitors of cyclin-dependent kinases
JOURNAL	Patent: EP 0926237-A 7 30-JUN-1999; HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES	Location/Qualifiers
source	1..17
Query Match	/note="E-Box (Myo D binding site)"
Best Local Similarity	8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative	0; Mismatches 3; Indels 0; Gaps 0
QY	1734 GGCTCCCAACTCCTCC 1749
DB	17 GCCTCCCAACCTGC 2

```

exon      1. 17
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GCCTCCCACTCTCC 1749
Db 17 GCCTCCCACTCTCC 1749

RESULT 438
LOCUS AX215133 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 575 from Patent WO0159103.
ACCESSION AX215133
VERSION AX215133.1 GI:15525176
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
        nogo gene expression
JOURNAL Patent: WO 0159103-A 575 16-AUG-2001;
        RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
        McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
    source
        1. .17
            Location/Qualifiers
                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"
                /note="Nucleic Acid"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1704 AGTTGGTTAGGAGTA 1719
Db 2 AGTTGGTTAGGAGTA 1719

RESULT 439
LOCUS AX216004 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1446 from Patent WO0159103.
ACCESSION AX216004
VERSION AX216004.1 GI:15526047
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
        nogo gene expression
JOURNAL Patent: WO 0159103-A 1446 16-AUG-2001;
        RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
        McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
    source
        1. .17
            Location/Qualifiers
                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"
                /note="Nucleic Acid"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1705 GTTGGTTAGGAGTAC 1720
Db 17 GTTGGTTAGGAGTAC 1720

exon      1. 17
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GCCTCCCACTCTCC 1749
Db 17 GCCTCCCACTCTCC 1749

RESULT 440
LOCUS AX217394 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2836 from Patent WO0159103.
ACCESSION AX217394
VERSION AX217394.1 GI:15527455
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
        nogo gene expression
JOURNAL Patent: WO 0159103-A 2836 16-AUG-2001;
        RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
        McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
    source
        1. .17
            Location/Qualifiers
                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"
                /note="Nucleic Acid"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1647 AGAAGGCAAGCACCAG 1662
Db 17 AGAAGGCAAGCACCAG 1662

RESULT 441
LOCUS AX217395 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2837 from Patent WO0159103.
ACCESSION AX217395
VERSION AX217395.1 GI:15527456
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
        nogo gene expression
JOURNAL Patent: WO 0159103-A 2837 16-AUG-2001;
        RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
        McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
    source
        1. .17
            Location/Qualifiers
                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"
                /note="Nucleic Acid"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1647 AGAAGGCAAGCACCAG 1662
Db 16 AGAAGGCAAGCACCAG 1662

RESULT 442
LOCUS AX217770 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2837 from Patent WO0159103.
ACCESSION AX217770
VERSION AX217770.1 GI:15527456
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
        nogo gene expression
JOURNAL Patent: WO 0159103-A 2837 16-AUG-2001;
        RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
        McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
    source
        1. .17
            Location/Qualifiers
                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"
                /note="Nucleic Acid"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1705 GTTGGTTAGGAGTAC 1720
Db 17 GTTGGTTAGGAGTAC 1720
```

```

DEFINITION Sequence 3212 from Patent WO0159103.
ACCESSION AX217770
VERSION AX217770.1 GI:15527831
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 3212 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1706 TTGGGTTAGGAGTAGC 1721
Db 17 TTGGGCTGGAGCAGC 2

RESULT 443
AX217771/c
LOCUS AX217771 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 3213 from Patent WO0159103.
ACCESSION AX217771
VERSION AX217771.1 GI:15527832
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 3213 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1706 TTGGGTTAGGAGTAGC 1721
Db 16 TTGGGCTGGAGCAGC 1

RESULT 444
AX264312/c
LOCUS AX264312 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 1703 from Patent WO0173002.
ACCESSION AX264312
VERSION AX264312.1 GI:16513111
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE 1
AUTHORS Kmiec, E.B., Gamper, H.B. and Rice, M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 1703 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1674 GAACCCCTGGTCTCC 1689
Db 16 GAACCCCTGCAGTCTGC 1

RESULT 445
AX264313
LOCUS AX264313 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 1704 from Patent WO0173002.
ACCESSION AX264313
VERSION AX264313.1 GI:16513112
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kmiec, E.B., Gamper, H.B. and Rice, M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 1704 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1674 GAACCCCTGGTCTCC 1689
Db 2 GAACCCCTGCAGTCTGC 17

RESULT 446
AX272550/c
LOCUS AX272550 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 119 from Patent WO0162911.
ACCESSION AX272550
VERSION AX272550.1 GI:16545287
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and
Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 119 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
Location/Qualifiers

```

```
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGGC 1736
|||||
Db 17 GGAGATGGAATTGTC 2

RESULT 447
AX272551/c
LOCUS AX272551 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 120 from Patent WO0162911.
ACCESSION AX272551
VERSION AX272551.1 GI:16545288
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 120 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGGC 1736
|||||
Db 16 GGAGATGGAATTGTC 1

RESULT 448
AX272840
LOCUS AX272840 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 409 from Patent WO0162911.
ACCESSION AX272840
VERSION AX272840.1 GI:16545577
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 409 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1632 GATGGGCTTGATGCA 1647
|||||
Db 1632 GATGGGCTTGATGCA 1647

/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1632 GATGGGCTTGATGCA 1647
|||||
Db 2 GGAGATGGAATTGTC 2

RESULT 449
AX273034/c
LOCUS AX273034 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 603 from Patent WO0162911.
ACCESSION AX273034
VERSION AX273034.1 GI:16545771
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 603 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1753 TCCTAAAGGCCCACTG 1768
|||||
Db 17 TCCACAGCCCACTG 2

RESULT 450
AX326513
LOCUS AX326513 17 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 2651 from Patent WO0192512.
ACCESSION AX326513
VERSION AX326513.1 GI:18097277
KEYWORDS Triticum aestivum (bread wheat)
SOURCE Triticum aestivum
ORGANISM Triticum aestivum
REFERENCE 1
AUTHORS Kniec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 2651 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
Location/Qualifiers
1..17
/organism="Triticum aestivum"
/mol_type="unassigned DNA"
/db_xref="taxon:4565"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1642 GTAGCAGAGCGCAGC 1657
|||||
Db 2 GGAGATGGAATTGTC 17

RESULT 451
AX326514/c
LOCUS AX326514 17 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 2652 from Patent WO0192512.
|||||
Db 2 GGAGATGGAATTGTC 17
```

```

ACCESSION   AX326514
VERSION     AX326514.1  GI:18097278
KEYWORDS
SOURCE      Triticum aestivum (bread wheat)
ORGANISM    Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooidae; Triticeae; Triticum.
REFERENCE   1
AUTHORS    Kmiec,B.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE      Targeted chromosomal genomic alterations in plants using modified
            single stranded oligonucleotides
JOURNAL    Patent: WO 0192512-A 2652 06-DEC-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES
source     Location/Qualifiers
            1..17
            /organism="Triticum aestivum"
            /mol_type="unassigned DNA"
            /db_xref="taxon:4565"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1642 GTAGCAGAGGCAAGC 1657
      |||||
Db 16 GGACAGTAGGCGGAC 1

RESULT 452
AX393401
LOCUS       AX393401 17 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 331 from Patent WO0210217.
ACCESSION   AX393401
VERSION     AX393401.1  GI:19701383
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    St Croix,B., Kinzler,K.W. and Vogelstein,B.
TITLE      Endothelial cell expression patterns
JOURNAL    Patent: WO 0210217-A 331 07-FEB-2002;
            The Johns Hopkins University (US)
FEATURES
source     Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1741 AACTCCTCCCTATCCT 1756
      |||||
Db 2 ACCACCTCCCTTCCT 17

RESULT 453
AX423730
LOCUS       AX423730 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 2066 from Patent WO0188124.
ACCESSION   AX423730
VERSION     AX423730.1  GI:21527112
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and

```

```

Randi,A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 2066 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source     Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned RNA"
            /db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1708 GGGTTAGGAGTACGGA 1723
      |||||
Db 2 GTGTAGGAGAAAGGA 17

RESULT 454
AX423731
LOCUS       AX423731 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 2067 from Patent WO0188124.
ACCESSION   AX423731
VERSION     AX423731.1  GI:21527113
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
            Randi,A.M.
TITLE      Method and reagent for the inhibition of erg
JOURNAL    Patent: WO 0188124-A 2067 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source     Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned RNA"
            /db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1710 GTTAGGAGTAGGAGA 1725
      |||||
Db 2 GTTAGGAGAAAGGACA 17

RESULT 455
AX475293
LOCUS       AX475293 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 514 from Patent WO0224750.
ACCESSION   AX475293
VERSION     AX475293.1  GI:22214578
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Zhang,J.
TITLE      Human kidney tumor overexpressed membrane protein 1
JOURNAL    Patent: WO 0224750-A 514 28-MAR-2002;
            Acomica, Inc. (US)
FEATURES
source     Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

```

```
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGGAACCC 1679
Db 2 CTCACAGCTGGGAGACC 17

RESULT 456
AX475294
LOCUS AX475294 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 515 from Patent WO0224750.
ACCESSION AX475294
VERSION AX475294.1 GI:22214579
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 515 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGGAACCC 1679
Db 1 CTCACAGCTGGGAGACC 16

RESULT 457
AX498962
LOCUS AX498962 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 269 from Patent EPI229046.
ACCESSION AX498962
VERSION AX498962.1 GI:23381255
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 269 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1671 CTGGAACCTGGTGTC 1686
Db 2 CAGGACCCCTGGCGTC 17

RESULT 458
AX498963
LOCUS AX498963 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 270 from Patent EPI229046.
ACCESSION AX498963
VERSION AX498963.1 GI:23381256
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 270 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1671 CTGGAACCTGGTGTC 1686
Db 1 CAGGACCCCTGGCGTC 16

RESULT 459
AX499444
LOCUS AX499444 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 751 from Patent EPI229046.
ACCESSION AX499444
VERSION AX499444.1 GI:23381737
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 751 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCAGCTGGGAAC 1677
Db 2 GACTCACTGCTGGACC 17

RESULT 460
AX531276
LOCUS AX531276 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 785 from Patent EPI239051.
ACCESSION AX531276
VERSION AX531276.1 GI:25254340
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M.
```

```

TITLE      Human posh-like protein 1
JOURNAL    Patent: EP 1239051-A 785 11-SEP-2002;
           Aeomica, Inc. (US)
FEATURES   source
           1..17
           Location/Qualifiers
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1691 CCAGCTCGTGGAGT 1706
Db 2 CCAGCTCCGTGGAGT 17

RESULT 461
AX531277
LOCUS      AX531277
DEFINITION Sequence 786 from Patent EP1239051.
ACCESSION AX531277
VERSION    AX531277.1 GI:25254341
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Shannon,M.
TITLE     Human posh-like protein 1
JOURNAL   Patent: EP 1239051-A 786 11-SEP-2002;
           Aeomica, Inc. (US)
FEATURES   source
           1..17
           Location/Qualifiers
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1691 CCAGCTCGTGGAGT 1706
Db 1 CCAGCTCCGTGGAGT 16

RESULT 462
AX532096
LOCUS      AX532096
DEFINITION Sequence 1605 from Patent EP1239051.
ACCESSION AX532096
VERSION    AX532096.1 GI:25255955
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Shannon,M.
TITLE     Human posh-like protein 1
JOURNAL   Patent: EP 1239051-A 1605 11-SEP-2002;
           Aeomica, Inc. (US)
FEATURES   source
           1..17
           Location/Qualifiers
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1691 CCAGCTCGTGGAGT 1706
Db 1 CCAGCTCCGTGGAGT 16

RESULT 463
AX532100
LOCUS      AX532100
DEFINITION Sequence 1609 from Patent EP1239051.
ACCESSION AX532100
VERSION    AX532100.1 GI:25255987
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Shannon,M.
TITLE     Human posh-like protein 1
JOURNAL   Patent: EP 1239051-A 1609 11-SEP-2002;
           Aeomica, Inc. (US)
FEATURES   source
           1..17
           Location/Qualifiers
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTCGTGTCTCC 1689
Db 1 GAGCCCTCGTGTCTAC 16

RESULT 464
AX532102
LOCUS      AX532102
DEFINITION Sequence 1611 from Patent EP1239051.
ACCESSION AX532102
VERSION    AX532102.1 GI:25255991
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Shannon,M.
TITLE     Human posh-like protein 1
JOURNAL   Patent: EP 1239051-A 1611 11-SEP-2002;
           Aeomica, Inc. (US)
FEATURES   source
           1..17
           Location/Qualifiers
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 CCCTGGTGTCTCTCC 1692
Db 2 CCCTGGTGTCTCTAC 17

RESULT 465
AX532104
LOCUS      AX532104
DEFINITION Sequence 1613 from Patent EP1239051.

```





```
QY 1696 GTGGTGAAGTTGGGT 1711
|||||
Db 2 GTGGTGAAGTTGGGT 17

RESULT 470
AX532449
LOCUS AX532449 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1958 from Patent EP1239051.
ACCESSION AX532449
VERSION AX532449.1 GI:25256672
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1958 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1696 GTGGTGAAGTTGGGT 1711
|||||
Db 1 GTGGTGAAGTTGGGT 16

RESULT 471
AX532450
LOCUS AX532450 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1959 from Patent EP1239051.
ACCESSION AX532450
VERSION AX532450.1 GI:25256674
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1959 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1696 GTGGTGAAGTTGGGT 1711
|||||
Db 1 GTGGTGAAGTTGGGT 16

RESULT 472
AX532451
LOCUS AX532451 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1960 from Patent EP1239051.
ACCESSION AX532451
VERSION AX532451.1 GI:25256676
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1962 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1724 GATGGAGATTGGCTCC 1739
|||||
Db 2 GGTGGAGATGGGTCC 17

RESULT 473
AX532452
LOCUS AX532452 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1961 from Patent EP1239051.
ACCESSION AX532452
VERSION AX532452.1 GI:25256678
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1961 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1724 GATGGAGATTGGCTCC 1739
|||||
Db 1 GGTGGAGATGGGTCC 16

RESULT 474
AX532453
LOCUS AX532453 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1962 from Patent EP1239051.
ACCESSION AX532453
VERSION AX532453.1 GI:25256680
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1962 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1726 TGGAGATTGGCTCCA 1741
|||||
Db 2 TGGAGATGGGTCCA 17

RESULT 475
AX532454
LOCUS AX532454 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1963 from Patent EP1239051.
ACCESSION AX532454
VERSION AX532454.1 GI:25256684
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1963 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1726 TGGAGATTGGCTCCA 1741
|||||
Db 2 TGGAGATGGGTCCA 17
```

```

source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1726 TGGAGATTGGCTCCCA 1741
|||||
1 TGGAGATGGGTCCCA 16

RESULT 475
AX578661
LOCUS AX578661 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 499 from Patent WO0211674.
ACCESSION AX578661
VERSION AX578661.1 GI:27647863
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
and Grupe, A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Patent: WO 0211674-A 499 14-FEB-2002;
Thompson, James (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCTAA 1758
|||||
1 CTGCTCCTTGCTCTAA 16

RESULT 476
AX579336
LOCUS AX579336 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 1174 from Patent WO0211674.
ACCESSION AX579336
VERSION AX579336.1 GI:27648538
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
and Grupe, A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Patent: WO 0211674-A 1174 14-FEB-2002;
Thompson, James (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCTAA 1758
|||||
2 CTGCTCCTTGCTCTAA 17

RESULT 477
AX615330/c
LOCUS AX615330 17 bp DNA linear PAT 20-FEB-2003
DEFINITION Sequence 137 from Patent EP1262488.
ACCESSION AX615330
VERSION AX615330.1 GI:28446229
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Gu, Y. and Nguyen, C.T.
AUTHORS Human lcc1-domain containing protein
TITLE Patent: EP 1262488-A 137 04-DEC-2002;
JOURNAL Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1753 TCCTAAGGCCCACTG 1768
|||||
17 TCCTCATGGTCCACTG 2

RESULT 478
AX615331/c
LOCUS AX615331 17 bp DNA linear PAT 20-FEB-2003
DEFINITION Sequence 138 from Patent EP1262488.
ACCESSION AX615331
VERSION AX615331.1 GI:28446230
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Gu, Y. and Nguyen, C.T.
AUTHORS Human lcc1-domain containing protein
TITLE Patent: EP 1262488-A 138 04-DEC-2002;
JOURNAL Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1753 TCCTAAGGCCCACTG 1768
|||||
16 TCCTCATGGTCCACTG 1

RESULT 479
AX615842/c

```

```

LOCUS      AX615842                17 bp    DNA          linear      PAT 20-FEB-2003
DEFINITION Sequence 649 from Patent EP1262488.
ACCESSION  AX615842
VERSION     AX615842.1  GI:28446888
FEATURES             source
  SOURCE      Homo sapiens (human)
  ORGANISM    Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS       Gu.Y. and Nguyen,C.T.
TITLE         Human lcc1-domain containing protein
JOURNAL       Patent: EP 1262488-A 649 04-DEC-2002;
              Aeomica, Inc. (US)
FEATURES             source
  SOURCE      1..17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1696 GTGGTGAAGTTGGGT 1711
Db 17 GTGGGGGAGTTGGT 2

RESULT 480
LOCUS      AX615843                17 bp    DNA          linear      PAT 20-FEB-2003
DEFINITION Sequence 650 from Patent EP1262488.
ACCESSION  AX615843
VERSION     AX615843.1  GI:28446889
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS       Gu.Y. and Nguyen,C.T.
TITLE         Human lcc1-domain containing protein
JOURNAL       Patent: EP 1262488-A 650 04-DEC-2002;
              Aeomica, Inc. (US)
FEATURES             source
  SOURCE      1..17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1696 GTGGTGAAGTTGGGT 1711
Db 16 GTGGGGGAGTTGGT 1

RESULT 481
LOCUS      AX634562                17 bp    RNA          linear      PAT 21-FEB-2003
DEFINITION Sequence 1701 from Patent EP1260586.
ACCESSION  AX634562
VERSION     AX634562.1  GI:28470176
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE      1
AUTHORS       Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
              Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
              Mcswigen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
              Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
              Woolf,T.

```

```

Mcswigen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
Method and reagent for inhibiting the expression of disease related
genes
JOURNAL       Patent: EP 1260586-A 1701 27-NOV-2002;
              RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             source
  SOURCE      1..17
              /organism="unidentified"
              /mol_type="unassigned RNA"
              /db_xref="taxon:32644"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1704 AGTTGGGTTAGGAGTA 1719
Db 17 AGGTGGGTGAGGGTA 2

RESULT 482
LOCUS      AX634795                17 bp    RNA          linear      PAT 21-FEB-2003
DEFINITION Sequence 1934 from Patent EP1260586.
ACCESSION  AX634795
VERSION     AX634795.1  GI:28470409
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE      1
AUTHORS       Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
              Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
              Mcswigen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
              Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
              Woolf,T.
Method and reagent for inhibiting the expression of disease related
genes
JOURNAL       Patent: EP 1260586-A 1934 27-NOV-2002;
              RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             source
  SOURCE      1..17
              /organism="unidentified"
              /mol_type="unassigned RNA"
              /db_xref="taxon:32644"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1704 AGTTGGGTTAGGAGTA 1719
Db 17 AGGTGGGTGAGGGTA 2

RESULT 483
LOCUS      AX648876                17 bp    DNA          linear      PAT 22-MAR-2003
DEFINITION Sequence 716 from Patent EP1273660.
ACCESSION  AX648876
VERSION     AX648876.1  GI:29151694
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS       Gu,Y.
TITLE         Human sodium-hydrogen exchanger like protein 1
JOURNAL       Patent: EP 1273660-A 716 08-JAN-2003;
              Aeomica, Inc. (US)

```

```

FEATURES
  source
    Location/Qualifiers
      1..17
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1679 CTGGTGTCTCCCTCCAG 1694
Db 2 CTGATGTCGTCTACAG 17

RESULT 484
AX649489/c
LOCUS
  DEFINITION
    Sequence 1717 from Patent EP1273660.
  ACCESSION
    AX649489
  VERSION
    AX649489.1 GI:29152307
  KEYWORDS
    .
  SOURCE
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
  1
  AUTHORS
    Gu, Y.
  TITLE
    Human sodium-hydrogen exchanger like protein 1
  JOURNAL
    Patent: EP 1273660-A 1717 08-JAN-2003;
    Acomica, Inc. (US)
  FEATURES
    source
      1..17
        Location/Qualifiers
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"

Query Match
  Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1713 AGGAGTACGGAGATGG 1728
Db 16 AGGAGGAGGAGAGGG 1

RESULT 487
AX671672
LOCUS
  DEFINITION
    Sequence 117 from Patent WO03004526.
  ACCESSION
    AX671672
  VERSION
    AX671672.1 GI:29330020
  KEYWORDS
    .
  SOURCE
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
  1
  AUTHORS
    Telerman, A., Amson, R. and Tuijthof, M.
  TITLE
    Sequences involved in phenomena of tumour suppression, tumour
    reversion, apoptosis and/or resistance to viruses and their use as
    medicines
  JOURNAL
    Patent: WO 03004526-A 117 16-JAN-2003;
    Molecular Engines Laboratories (FR)
  FEATURES
    source
      1..17
        Location/Qualifiers
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"

Query Match
  Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCAG 1670
Db 2 ATCAACAGGCTTACAG 17

RESULT 488
AX671735/c
LOCUS
  DEFINITION
    Sequence 180 from Patent WO03004526.
  ACCESSION
    AX671735

```

VERSION AX671735.1 GI:29330083  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or resistance to viruses and their use as  
medicines  
JOURNAL Patent: WO 03004526-A 180 16-JAN-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1662 GGCTCAGCTGGGACC 1677 17 bp DNA linear PAT 27-MAR-2003  
Db 16 GTCTCAGCTTGATC 1  
RESULT 489  
AX672964  
LOCUS AX672964 17 bp DNA linear PAT 27-MAR-2003  
DEFINITION Sequence 1409 from Patent WO03004526.  
ACCESSION AX672964  
VERSION AX672964.1 GI:29331312  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or resistance to viruses and their use as  
medicines  
JOURNAL Patent: WO 03004526-A 1409 16-JAN-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1735 GCTCCCACTCTCTCCC 1750 17 bp DNA linear PAT 27-MAR-2003  
Db 1 GATCCCGAGCTTGATC 16  
RESULT 490  
AX672965  
LOCUS AX672965 17 bp DNA linear PAT 27-MAR-2003  
DEFINITION Sequence 1410 from Patent WO03004526.  
ACCESSION AX672965  
VERSION AX672965.1 GI:29331313  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1

AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or resistance to viruses and their use as  
medicines  
JOURNAL Patent: WO 03004526-A 1410 16-JAN-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1735 GCTCCCACTCTCTCCC 1750 17 bp DNA linear PAT 27-MAR-2003  
Db 1 GATCCCGAGCTTGATC 16  
RESULT 491  
AX672967  
LOCUS AX672967 17 bp DNA linear PAT 27-MAR-2003  
DEFINITION Sequence 1412 from Patent WO03004526.  
ACCESSION AX672967  
VERSION AX672967.1 GI:29331315  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or resistance to viruses and their use as  
medicines  
JOURNAL Patent: WO 03004526-A 1412 16-JAN-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1663 GCTCAGCTGGGACC 1678 17 bp DNA linear PAT 29-MAR-2003  
Db 1 GATCCCGAGCTGGGACC 16  
RESULT 492  
AX684195  
LOCUS AX684195 17 bp DNA linear PAT 29-MAR-2003  
DEFINITION Sequence 46 from Patent WO0246386.  
ACCESSION AX684195  
VERSION AX684195.1 GI:29371095  
KEYWORDS  
SOURCE Aspergillus ochraceus  
ORGANISM Aspergillus ochraceus  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
REFERENCE 1  
AUTHORS Bolton,S., Clayton,R., Easton,A., Engel,L. and Messing,D.  
TITLE Aspergillus ochraceus II alpha hydroxylase and oxidoreductase  
JOURNAL Patent: WO 0246386-A 46 13-JUN-2002;  
Pharmacia Corporation (US); Bolton, Suzanne (US); Clayton, Robert  
(US); Easton, Alan (US); Engel, Leslie (US); Messing, Dean (US)  
FEATURES  
source  
1. .17  
Location/Qualifiers

```

/organism="Aspergillus ochraceus"
/mol_type="unassigned DNA"
/db_xref="taxon:40380"
/note="Primer 45624-for1"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1722 GAGATGGAGATTGGCT 1737
||||| ||||| |||||
Db 1 GAGATCAAGATTGCCT 16

RESULT 493
AX687045/c
LOCUS AX687045 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 19 from Patent EP1281755.
ACCESSION AX687045
VERSION AX687045.1 GI:29409546
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Milos,P.M. and Webb,S.M.
TITLE Variants of the human cyp2d6 gene
JOURNAL Patent: EP 1281755-A 19 05-FEB-2003;
Pfizer Products Inc. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="probe"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAG 1670
||||| ||||| |||||
Db 17 AGCACAAAGCTCATAG 2

RESULT 494
AX687046
LOCUS AX687046 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 20 from Patent EP1281755.
ACCESSION AX687046
VERSION AX687046.1 GI:29409547
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Milos,P.M. and Webb,S.M.
TITLE Variants of the human cyp2d6 gene
JOURNAL Patent: EP 1281755-A 20 05-FEB-2003;
Pfizer Products Inc. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="probe"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAG 1670
||||| ||||| |||||
Db 17 AGCACAAAGCTCATAG 2

RESULT 495
AX687666
LOCUS AX687666 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 398 from Patent EP1281758.
ACCESSION AX687666
VERSION AX687666.1 GI:29410362
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 398 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1740 CAACTCTCTCCCTATCC 1755
||||| ||||| |||||
Db 2 CAGTTCTCTCACTATCC 17

RESULT 496
AX687742/c
LOCUS AX687742 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 474 from Patent EP1281758.
ACCESSION AX687742
VERSION AX687742.1 GI:29410438
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 474 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1687 TCCTCCAGCGTGGTGG 1702
||||| ||||| |||||
Db 17 TCCTCCACCATGCGG 2

RESULT 497
AX687743/c
LOCUS AX687743 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 475 from Patent EP1281758.
ACCESSION AX687743
VERSION AX687743.1 GI:29410439

```

KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1687 TCCTCCAGCGTGGTGG 1702  
Db 16 TCCTCCACCATGCGG 1  
RESULT 498  
AX687812/c  
LOCUS  
DEFINITION Sequence 544 from Patent EPI281758. PAT 31-MAR-2003  
ACCESSION AX687812  
VERSION AX687812.1 GI:29410508  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1687 TCCTCCAGCGTGGTGG 1702  
Db 16 TCCTCCACCATGCGG 1  
RESULT 499  
AX687813/c  
LOCUS  
DEFINITION Sequence 545 from Patent EPI281758. PAT 31-MAR-2003  
ACCESSION AX687813  
VERSION AX687813.1 GI:29410509  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1680 TGGTGTCCTCCAGC 1695  
Db 17 TGCTGTTCTCTCTGC 2  
RESULT 500  
AX687851/c  
LOCUS  
DEFINITION Sequence 583 from Patent EPI281758. PAT 31-MAR-2003  
ACCESSION AX687851  
VERSION AX687851.1 GI:29410549  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1666 CACAGCTGGAGCCCTG 1681  
Db 16 CCCAGCTGGATGCTG 1  
RESULT 501  
AX691734  
LOCUS  
DEFINITION Sequence 4466 from Patent EPI281758. PAT 31-MAR-2003  
ACCESSION AX691734  
VERSION AX691734.1 GI:29414675  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1666 CACAGCTGGAGCCCTG 1681  
Db 16 CCCAGCTGGATGCTG 1

JOURNAL Patent: EP 1281758-A 545 05-FEB-2003;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1680 TGGTGTCCTCCAGC 1695  
Db 16 TGCTGTTCTCTCTGC 1  
RESULT 500  
AX687851/c  
LOCUS  
DEFINITION Sequence 583 from Patent EPI281758. PAT 31-MAR-2003  
ACCESSION AX687851  
VERSION AX687851.1 GI:29410549  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1666 CACAGCTGGAGCCCTG 1681  
Db 16 CCCAGCTGGATGCTG 1  
RESULT 501  
AX691734  
LOCUS  
DEFINITION Sequence 4466 from Patent EPI281758. PAT 31-MAR-2003  
ACCESSION AX691734  
VERSION AX691734.1 GI:29414675  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1666 CACAGCTGGAGCCCTG 1681  
Db 16 CCCAGCTGGATGCTG 1

```
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCAGCTGGAACC 1678
Db 2 GCTCAAGCTGGGATC 17

RESULT 502
AX691735
LOCUS AX691735 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 4467 from Patent EP1281758.
ACCESSION AX691735
VERSION AX691735.1 GI:29414676
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
Patent: EP 1281758-A 4467 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCAGCTGGAACC 1678
Db 1 GCTCAAGCTGGGATC 16

RESULT 503
AX692741/c
LOCUS AX692741 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5473 from Patent EP1281758.
ACCESSION AX692741
VERSION AX692741.1 GI:29415699
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
Patent: EP 1281758-A 5473 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1716 AGTCAGGAGATCGAGA 1731
Db 17 AGTCAGGAGATCGAGA 2

RESULT 504
AX692741/c
LOCUS AX692741 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5473 from Patent EP1281758.
ACCESSION AX692741
VERSION AX692741.1 GI:29415699
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
Patent: EP 1281758-A 5473 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1716 AGTCAGGAGATCGAGA 1731
Db 17 AGTCAGGAGATCGAGA 2

RESULT 504
AX692742/c
LOCUS AX692742 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5474 from Patent EP1281758.
ACCESSION AX692742
VERSION AX692742.1 GI:29415700
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
Patent: EP 1281758-A 5474 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1716 AGTCAGGAGATCGAGA 1731
Db 16 AGTCAGGAGATCGAGA 1

RESULT 505
AX723798/c
LOCUS AX723798 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1485 from Patent WO03025176.
ACCESSION AX723798
VERSION AX723798.1 GI:30503141
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apop-osis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 1485 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1..17
Location/Qualifiers
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1697 TGCTGGAAGTTGGGAT 1712
Db 17 TGCTGGAAGTTGGGAT 2

RESULT 506
AX724082
LOCUS AX724082 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1769 from Patent WO03025176.
ACCESSION AX724082
VERSION AX724082.1 GI:30503425
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
```



JOURNAL Patent: WO 03025176-A 2961 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
1. .17  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1752 ATCTAAAGGCCACT 1767  
Db 2 ATCCCAACACCCACT 17  

RESULT 507  
AX724176/c  
LOCUS AX724176 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 1863 from Patent WO03025176.  
ACCESSION AX724176  
VERSION AX724176.1 GI:30503519  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1  
REFERENCE  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL Patent: WO 03025176-A 1863 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
1. .17  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1717 GTACGGAGATGGAGAT 1732  
Db 17 GTCCGATATGGAGAT 2  

RESULT 508  
AX725274  
LOCUS AX725274 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 2961 from Patent WO03025176.  
ACCESSION AX725274  
VERSION AX725274.1 GI:30504617  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1  
REFERENCE  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines

JOURNAL Patent: WO 03025176-A 2961 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
1. .17  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1658 ACCAGGCTCACAGCTG 1673  
Db 2 ATCAGGCCACAGCCG 17  

RESULT 509  
AX725621/c  
LOCUS AX725621 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 3308 from Patent WO03025176.  
ACCESSION AX725621  
VERSION AX725621.1 GI:30504964  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1  
REFERENCE  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL Patent: WO 03025176-A 3308 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
1. .17  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1651 GGCAAGCACAGGCTC 1666  
Db 16 GGAAGAACCAGGATC 1  

RESULT 510  
AX726666  
LOCUS AX726666 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 4353 from Patent WO03025176.  
ACCESSION AX726666  
VERSION AX726666.1 GI:30506009  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1  
REFERENCE  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL Patent: WO 03025176-A 4353 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
1. .17  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"

```
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCAGCTGGAAC 1678
Db 1 GATCAGCTGAAACC 16

RESULT 511
AX727148/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025176-A 4835 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTACAGCTGGAAC 1677
Db 16 GGTACAGCTGGATC 1

RESULT 512
AX727322/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025176-A 5009 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTACAGCTGGAAC 1677
Db 16 GGTACAGCTGGATC 1

RESULT 513
AX727322/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025175-A 3187 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1717 GTACGGAGATGGACAT 1732
Db 17 GGATGGGATGGACAT 2

RESULT 514
AX731553
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025175-A 3187 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1752 ATCCTAAAGGCCACT 1767
Db 2 ATCATAAAGACCACT 17

RESULT 515
AX731661/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025175-A 3187 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1752 ATCCTAAAGGCCACT 1767
Db 2 ATCATAAAGACCACT 17

RESULT 516
AX731661/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025175-A 3187 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1752 ATCCTAAAGGCCACT 1767
Db 2 ATCATAAAGACCACT 17
```



```
FEATURES
source
  Location/Qualifiers
  1..17
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCAG 1670
Db 2 ATCAACAGGCTTACAG 17

RESULT 520
AX736388/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
  Homo sapiens (human)
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
  TITLE
  Sequences involved in phenomena of tumour suppression, tumour
  reversion, apoptosis and/or resistance to viruses and the use
  thereof as medicaments
  JOURNAL
  Patent: WO 03025177-A 1978 27-MAR-2003;
  Molecular Engines Laboratories (FR)
FEATURES
source
  1..17
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1711 TTAGGAGTATGTGGAT 2
Db 17 TTAGGAGTATGTGGAT 2

RESULT 521
AX738496
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
  Homo sapiens (human)
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
  TITLE
  Sequences involved in phenomena of tumour suppression, tumour
  reversion, apoptosis and/or resistance to viruses and the use
  thereof as medicaments
  JOURNAL
  Patent: WO 03025177-A 4086 27-MAR-2003;
  Molecular Engines Laboratories (FR)
FEATURES
source
  1..17
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCAG 1670
Db 2 ATCAACAGGCTTACAG 17

RESULT 522
AX756774
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
  Homo sapiens (human)
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
  TITLE
  Sequences involved in tumoral suppression, tumoral reversion,
  apoptosis and/or viral resistance phenomena and their use as
  medicines
  JOURNAL
  Patent: WO 03040369-A 95 15-MAY-2003;
  Molecular Engines Laboratories (FR)
FEATURES
source
  1..17
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCACAGCTGGAACC 1678
Db 1 GATCACAGCGGGAPAC 16

RESULT 523
AX757120/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
  Homo sapiens (human)
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
  TITLE
  Sequences involved in tumoral suppression, tumoral reversion,
  apoptosis and/or viral resistance phenomena and their use as
  medicines
  JOURNAL
  Patent: WO 03040369-A 441 15-MAY-2003;
  Molecular Engines Laboratories (FR)
FEATURES
source
  1..17
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match
Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1711 TTAGGAGTATGTGGAT 2
Db 17 TTAGGAGTATGTGGAT 2
```

RESULT 524  
AX757252  
LOCUS AX757252 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 573 from Patent WO03040369.  
ACCESSION AX757252  
VERSION AX757252.1 GI:32251868  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
1  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines  
JOURNAL Patent: WO 03040369-A 573 15-MAY-2003;  
FEATURES Molecular Engines Laboratories (FR)  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1735 GCTCCCAACTCTCTCC 1750  
Db 1 GATCCCAACACCTCC 16  
RESULT 525  
AX757657  
LOCUS AX757657 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 978 from Patent WO03040369.  
ACCESSION AX757657  
VERSION AX757657.1 GI:32252273  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
1  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines  
JOURNAL Patent: WO 03040369-A 978 15-MAY-2003;  
FEATURES Molecular Engines Laboratories (FR)  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1735 GCTCCCAACTCTCTCC 1750  
Db 1 GATCCCAACACCTCC 16  
RESULT 526  
AX761860/c  
LOCUS AX761860/c 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 5181 from Patent WO03040369.  
ACCESSION AX761860  
VERSION AX761860.1 GI:32256476

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
1  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines  
JOURNAL Patent: WO 03040369-A 5181 15-MAY-2003;  
FEATURES Molecular Engines Laboratories (FR)  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1723 AGATGGAGATTGGCTC 1738  
Db 16 AATGGAAATTGGATC 1  
RESULT 527  
AX762374  
LOCUS AX762374 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 5695 from Patent WO03040369.  
ACCESSION AX762374  
VERSION AX762374.1 GI:32256990  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
1  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines  
JOURNAL Patent: WO 03040369-A 5695 15-MAY-2003;  
FEATURES Molecular Engines Laboratories (FR)  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 2.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1655 AGCACCAGGCTCAG 1670  
Db 2 ATCAACAGGCTTACAG 17  
RESULT 528  
AX762744/c  
LOCUS AX762744/c 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 6065 from Patent WO03040369.  
ACCESSION AX762744  
VERSION AX762744.1 GI:32257360  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
1  
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.

TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines

JOURNAL Patent: WO 03040369-A 6065 15-MAY-2003;

FEATURES Molecular Engines Laboratories (FR)

source Location/Qualifiers

1. .17

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 2.9e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1717 GTACGGAGATGGAGAT 1732

Db 17 GGATGGGATGGAGAT 2

RESULT 529

BD067460

LOCUS

DEFINITION BD067460 17 bp RNA linear PAT 27-AUG-2002

Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.

ACCESSION BD067460

VERSION

KEYWORDS JP 2001511003-A/300.

SOURCE unclassified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 17)

Akhtar,S., Fell,P. and Mcswiggen,J.A.

AUTHORS Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors

TITLE Patent: JP 2001511003-A/300.

JOURNAL RIBOZYME PHARMACEUTICALS INC,ASTON UNIV

COMMENT OS Unidentified

PN JP 2001511003-A/300

PD 07-AUG-2001

PF 14-JAN-1998 JP 1998532913

PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI

SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC

CL2N9/00,C07K14/71

CC Strandedness: Single;

CC Topology: Linear;

CC Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors

CC levels of epidermal growth factor receptors

FT Key Location/Qualifiers

FT source 1. .17

FEATURES

source Location/Qualifiers

1. .17

/organism="unidentified"

/mol\_type="genomic RNA"

/db\_xref="taxon:32644"

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 2.9e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1694 GCGTGTGGAGTTGG 1709

Db 17 GCACGGTAGAGTTGG 2

RESULT 531

BD091426/c

LOCUS

DEFINITION BD091426 17 bp DNA linear PAT 27-AUG-2002

Nucleic acids involved in the responder phenotype and applications thereof.

ACCESSION BD091426

VERSION BD091426.1 GI:22637037

KEYWORDS JP 2001523449-A/15.

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 17)

AUTHORS Herrmann,B., Koschorz,B. and Kispert,A.

TITLE Nucleic acids involved in the responder phenotype and applications thereof

JOURNAL Patent: JP 2001523449-A 15 27-NOV-2001;

COMMENT MAX PLANCK GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN EV

OS Artificial Sequence

PN JP 2001523449-A/15

PD 27-NOV-2001

PF 18-NOV-1998 JP 2000521181

PR 18-NOV-1997 EP 97120190,0.02-MAR-1998 EP 98103596.7 PI

BERNHARD HERMANN,BIRGIT KOSCHORZ,ANDREAS KISPERT PC

CL2N15/09,A01K67/027,A61K31/7088,A61K38/45,A61K39/395,A61K48/PC

00,A61P15/16,

PC C07K16/40,CL2N1/15,CL2N1/19,CL2N1/21,CL2N5/10,CL2N9/12 PC

C12Q1/68//A61K35/12,

PC C12P21/08,C.2N15/00,A61K37/52,CL2N5/00

CC Description of Artificial Sequence: synthetic no-natural

CC to levels of epidermal growth factor receptors.

FT Key Location/Qualifiers

FT source 1. .17

VERSION BD067531.1 GI:22613134

KEYWORDS JP 2001511003-A/371.

SOURCE unclassified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 17)

Akhtar,S., Fell,P. and Mcswiggen,J.A.

AUTHORS Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors

TITLE Patent: JP 2001511003-A 371 07-AUG-2001;

JOURNAL RIBOZYME PHARMACEUTICALS INC,ASTON UNIV

COMMENT OS Unidentified

PN JP 2001511003-A/371

PD 07-AUG-2001

PF 14-JAN-1998 JP 1998532913

PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI

SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC

CL2N9/00,C07K14/71

CC Strandedness: Single;

CC Topology: Linear;

CC Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors

CC levels of epidermal growth factor receptors

FT Key Location/Qualifiers

FT source 1. .17

FEATURES

source Location/Qualifiers

1. .17

/organism="unidentified"

/mol\_type="genomic RNA"

/db\_xref="taxon:32644"

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 2.9e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1694 GCGTGTGGAGTTGG 1709

Db 17 GCACGGTAGAGTTGG 2

RESULT 531

BD091426/c

LOCUS

DEFINITION BD091426 17 bp DNA linear PAT 27-AUG-2002

Nucleic acids involved in the responder phenotype and applications thereof.

ACCESSION BD091426

VERSION BD091426.1 GI:22637037

KEYWORDS JP 2001523449-A/15.

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 17)

AUTHORS Herrmann,B., Koschorz,B. and Kispert,A.

TITLE Nucleic acids involved in the responder phenotype and applications thereof

JOURNAL Patent: JP 2001523449-A 15 27-NOV-2001;

COMMENT MAX PLANCK GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN EV

OS Artificial Sequence

PN JP 2001523449-A/15

PD 27-NOV-2001

PF 18-NOV-1998 JP 2000521181

PR 18-NOV-1997 EP 97120190,0.02-MAR-1998 EP 98103596.7 PI

BERNHARD HERMANN,BIRGIT KOSCHORZ,ANDREAS KISPERT PC

CL2N15/09,A01K67/027,A61K31/7088,A61K38/45,A61K39/395,A61K48/PC

00,A61P15/16,

PC C07K16/40,CL2N1/15,CL2N1/19,CL2N1/21,CL2N5/10,CL2N9/12 PC

C12Q1/68//A61K35/12,

PC C12P21/08,C.2N15/00,A61K37/52,CL2N5/00

CC Description of Artificial Sequence: synthetic no-natural

CC to levels of epidermal growth factor receptors.

FT Key Location/Qualifiers

FT source 1. .17

```

AUTHORS      Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
              Nishida,M.
TITLE        Kit and method for determining HLA type
JOURNAL      Patent: WO 0192572-A 1161 06-DEC-2001;
              NISSHINBO INDUSTRIES INC.SYSTEM RESEARCH INC.HIDETOSHI INOKO, TAEKO
              KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
              NISHIDA
COMMENT      OS Artificial Sequence
              PN WO 0192572-A/1161
              PD 06-DEC-2001
              PF 01-JUN-2001 WO 2001JP004662
              PR 01-JUN-2000 JP 00P 164798
              PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
              MATSUMURA,
              PC SHOGO MORIYA,MICHIO NISHIDA
              PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
              CC Description of Artificial Sequence:capture
              FH Key Location/Qualifiers
              FT source 1..17
              FT /organism='Artificial Sequence'.
FEATURES
  source
    Location/Qualifiers
      1..17
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1690 TCCAGCGTGGTGGAG 1705
Db 16 TCCAGCGAGGGGGAAG 1
      ||||| |||||
      ||||| |||||

RESULT 532
LOCUS      BD104174
DEFINITION Kit and method for determining HLA type.
ACCESSION  BD104174
VERSION    BD104174.1 GI:22649748
KEYWORDS   WO 0192572-A/278.
SOURCE     synthetic construct
           artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
           Nishida,M.
TITLE     Kit and method for determining HLA type
JOURNAL   Patent: WO 0192572-A 278 06-DEC-2001;
           NISSHINBO INDUSTRIES INC.SYSTEM RESEARCH INC.HIDETOSHI INOKO, TAEKO
           KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
           NISHIDA
COMMENT   OS Artificial Sequence
           PN WO 0192572-A/278
           PD 06-DEC-2001
           PF 01-JUN-2001 WO 2001JP004662
           PR 01-JUN-2000 JP 00P 164798
           PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
           MATSUMURA,
           PC SHOGO MORIYA,MICHIO NISHIDA
           PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
           CC Description of Artificial Sequence:capture
           FH key Location/Qualifiers
           FT source 1..17
           FT /organism='Artificial Sequence'.
FEATURES
  source
    Location/Qualifiers
      1..17
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1716 AGTACGGAGTGGAGA 1731
Db 2 ACTACGGAGTGGTGA 17
      ||||| |||||
      ||||| |||||

RESULT 533
LOCUS      BD105057/c
DEFINITION Kit and method for determining HLA type.
ACCESSION  BD105057
VERSION    BD105057.1 GI:22650631
KEYWORDS   WO 0192572-A/1161.
SOURCE     synthetic construct
           artificial sequences.
REFERENCE  1 (bases 1 to 17)

```

```

AUTHORS      Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
              Nishida,M.
TITLE        Kit and method for determining HLA type
JOURNAL      Patent: WO 0192572-A 1161 06-DEC-2001;
              NISSHINBO INDUSTRIES INC.SYSTEM RESEARCH INC.HIDETOSHI INOKO, TAEKO
              KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
              NISHIDA
COMMENT      OS Artificial Sequence
              PN WO 0192572-A/1161
              PD 06-DEC-2001
              PF 01-JUN-2001 WO 2001JP004662
              PR 01-JUN-2000 JP 00P 164798
              PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
              MATSUMURA,
              PC SHOGO MORIYA,MICHIO NISHIDA
              PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
              CC Description of Artificial Sequence:capture
              FH Key Location/Qualifiers
              FT source 1..17
              FT /organism='Artificial Sequence'.
FEATURES
  source
    Location/Qualifiers
      1..17
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1734 GGCTCCCACTCTCTCC 1749
Db 17 GGCTCTCCACTGCTCC 2
      ||||| |||||
      ||||| |||||

RESULT 534
LOCUS      BD137018
DEFINITION GFR alpha 3 and its uses.
ACCESSION  BD137018
VERSION    BD137018.1 GI:23231963
KEYWORDS   JP 2002507421-A/15.
SOURCE     synthetic construct
           artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Sauvage,F.J.D., Klein,R.D., Phillips,H.S. and Rosenthal,A.
TITLE     GFR alpha 3 and its uses
JOURNAL   Patent: JP 2002507421-A 15 12-MAR-2002;
           GENENTECH INC
COMMENT   OS Artificial Sequence
           PN JP 2002507421-A/15
           PD 12-MAR-2002
           PF 19-MAR-1999 JP 2000538000
           PR 23-MAR-1998 US 60/079124,13-APR-1998 US 60/081569 PI
           FREDERIC J DE SAUVAGE, ROBERT D KLEIN, HEIDI S PHILLIPS, ARNON PI
           ROSENTHAL
           PC C12N15/09,A61K39/395,A61K45/00,A61P1/02,A61P1/10,A61P11/06, PC
           A61P17/02,
           PC A61P25/02,A61P25/06,A61P27/02,C07K14/71,C07K16/28,C07K19/00,
           PC C12N1/19,
           PC C12N1/21,C12N5/10,C12Q1/42,G01N33/68,C12N15/00,C12N5/00 CC
           /note=synthetic
           FH Key Location/Qualifiers
           FT source 1..17
           FT /organism='Artificial Sequence'.
FEATURES
  source
    Location/Qualifiers
      1..17
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
Query Match      8.1%; Score 11.2; DB 1; Length 17;

```

```

Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1739 CCAACTCTCCCTATC 1754
Db 2 CCCAGTCTCCCTACC 17

RESULT 535
BD198908
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
PAT 17-JUL-2003
RIBOZYME PHARMACEUTICALS INC
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
method participating in vasculogenic response
Patent: JP 2002509721-A 1934 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/1934
PD 02-APR-2002
PR 24-MAR-1999 JP 2000541291
PF 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PC JAMES A MCSWIGGEN
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
FEATURES
source
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1685 TCTCTCCAGCGTGGT 1700
Db 16 TCTCATTAAGCGTGGT 1

RESULT 537
BD200826/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
PAT 17-JUL-2003
RIBOZYME PHARMACEUTICALS INC
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
method participating in vasculogenic response
Patent: JP 2002509721-A 3852 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/3852
PD 02-APR-2002
PR 24-MAR-1999 JP 2000541291
PF 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PC JAMES A MCSWIGGEN
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
FEATURES
source
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1665 TCACGCTGGAACCT 1680
Db 1 TCACGCTGGAACCT 16

RESULT 536
BD199121/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
PAT 17-JUL-2003
RIBOZYME PHARMACEUTICALS INC
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
method participating in vasculogenic response
Patent: JP 2002509721-A 2147 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/2147
PD 02-APR-2002
PR 24-MAR-1999 JP 2000541291
PF 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PC JAMES A MCSWIGGEN
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
FEATURES
source
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1739 CCAACTCTCCCTATC 1754
Db 2 CCCAGTCTCCCTACC 17

RESULT 535
BD198908
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
PAT 17-JUL-2003
RIBOZYME PHARMACEUTICALS INC
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
method participating in vasculogenic response
Patent: JP 2002509721-A 1934 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/1934
PD 02-APR-2002
PR 24-MAR-1999 JP 2000541291
PF 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PC JAMES A MCSWIGGEN
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
FEATURES
source
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1685 TCTCTCCAGCGTGGT 1700
Db 16 TCTCATTAAGCGTGGT 1

RESULT 537
BD200826/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
PAT 17-JUL-2003
RIBOZYME PHARMACEUTICALS INC
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
method participating in vasculogenic response
Patent: JP 2002509721-A 3852 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/3852
PD 02-APR-2002
PR 24-MAR-1999 JP 2000541291
PF 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PC JAMES A MCSWIGGEN
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
FEATURES
source
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1665 TCACGCTGGAACCT 1680
Db 1 TCACGCTGGAACCT 16

RESULT 536
BD199121/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
PAT 17-JUL-2003
RIBOZYME PHARMACEUTICALS INC
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
method participating in vasculogenic response
Patent: JP 2002509721-A 2147 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/2147
PD 02-APR-2002
PR 24-MAR-1999 JP 2000541291
PF 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PC JAMES A MCSWIGGEN
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
FEATURES
source

```



```
FEATURES
  source
    Location/Qualifiers
      1..17
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 81.1%; Score 11.2; DB 1; Length 17;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1704 AGTTGGGTAGGAGTA 1719
  ||| ||||| |||||
Db 17 AGCGGGTACGAGTA 2

RESULT 538
BD223385 17 bp DNA linear PAT 17-JUL-2003
LOCUS BD223385 Nucleic acid encoding rat agouti related protein.
ACCESSION BD223385
VERSION BD223385.1 GI:33033155
KEYWORDS JP 2002512786-A/5.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Der, L.H.T.V., Guan, X., Yu, H. and Trivedi, P.G.
TITLE Nucleic acid encoding rat agouti related protein
JOURNAL Patent: JP 2002512786-A 5 08-MAY-2002;
MERCK AND CO INC
COMMENT OS Unidentified
PN JP 2002512786-A/5
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545978
PR 29-APR-1998 US 60/083549
PI LEONARDUS H T VAN DER PLOEG, XIAOMING GUAN, HONG YU, PRASHANT G
PT TRIVEDI
PC C12Q1/68, C07K5/00, C07K14/47, C12N1/15, C12N1/19, C12N1/21, C12N5/
PC 10, C12N15/09,
PC C12P21/02
CC PCR primer
FH Key
FT source
  Location/Qualifiers
    1..17
      /organism="Unidentified".

FEATURES
  source
    Location/Qualifiers
      1..17
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

Query Match
  Best Local Similarity 8.1%; Score 11.2; DB 1; Length 17;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1656 GCACATGGGTACAGC 1671
  ||||| ||||| |||||
Db 1 GCACATGGGTACAGC 16

RESULT 539
AR106914/c 18 bp DNA linear PAT 14-FEB-2001
LOCUS AR106914 Sequence 75 from patent US 6107092.
ACCESSION AR106914
VERSION AR106914.1 GI:12821444
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cowsett, L.M., Bennett, C.Frank, and O'Malley, B.W.
TITLE Antisense modulation of SRA expression
JOURNAL Patent: US 6107092-A 75 22-AUG-2000;

FEATURES
  source
    Location/Qualifiers
      1..18
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 81.2%; Score 11.2; DB 1; Length 18;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1658 ACCAGGCTCACAGCTG 1673
  ||||| ||||| |||||
Db 16 ACCAGGCTTCCAGCAG 1

RESULT 540
AR381288/c 20 bp DNA linear PAT 18-DEC-2003
LOCUS AR381288 Sequence 19 from patent US 6607915.
ACCESSION AR381288
VERSION AR381288.1 GI:40089107
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia, B.P. and Wanciewicz, E.
TITLE Antisense inhibition of E2A-Pbx1 expression
JOURNAL Patent: US 6607915-A 19 19-AUG-2003;
JOURNAL Location/Qualifiers
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match
  Best Local Similarity 81.2%; Score 11.2; DB 1; Length 20;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1668 CAGCTGGAACTCTGGT 1693
  ||||| ||||| |||||
Db 16 CAGCTGTCAGCTGGT 1

RESULT 541
AX623106 11 bp DNA linear PAT 21-FEB-2003
LOCUS AX623106 Sequence 147 from Patent WO02053774.
ACCESSION AX623106
VERSION AX623106.1 GI:28451047
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn, D., Conradt, M. and Hofmann, K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 147 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    Location/Qualifiers
      1..11
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 7.9%; Score 11; DB 1; Length 11;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1681 GGTGTCTCTC 1691
  ||||| |||||
Db 1 GGTGTCTCTC 11
```

```

RESULT 542
AX630527
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7568 from Patent WO02053774.
ACCESSION  AX630527
VERSION     AX630527.1 GI:28458565
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7568 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      7.9%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1681  GGTGTCCTCTC 1691
Db      1  GGTGTCCTCTC 11

RESULT 543
AL5061/c
LOCUS      15 bp      DNA      linear      PAT 07-FEB-1994
DEFINITION  oligonucleotide.
ACCESSION  AL5061
VERSION    AL5061.1 GI:492828
KEYWORDS   unidentified
SOURCE      unidentified
ORGANISM    unclassified.
            1 (bases 1 to 15)
REFERENCE   Roskam,W. and Ferrara,P.
AUTHORS     Non-amidated derivatives of somatotroline and process for the
TITLE       preparation by genetic engineering
JOURNAL     Patent: EP 0206863-A 2 30-DEC-1986;
            SANOFI S.A.
FEATURES
source      1..15
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
Query Match      7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1666  CACAGCTGGAA 1676
Db      13  CACAGCTGGAA 3

RESULT 544
BD251646/c
LOCUS      15 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION  Selection of animal based on character imprinted by parent.
ACCESSION  BD251646
VERSION    BD251646.1 GI:33061416
KEYWORDS   JP 2002535963-A/166.
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

```

```

REFERENCE
1 (bases 1 to 15)
Andersson,L., Georges,M., Spincemaille,G. and Nezer,C.D.A.
Selection of animal based on character imprinted by parent
Patent: JP 2002535963-A 166 29-OCT-2002;
UNIVERSITY OF L'EGE,MELICA HB,SEGHERS GENTEC NV
COMMENT
OS      Sus scrofa (pig)
PN      JP 2002535963-A/166
PD      29-OCT-2002
PF      16-DEC-1999 JP 2000589390
PI      16-DEC-1998 EP 98204291.3
PR      LEIF ANDERSSON,MICHEL GEORGES,GEERT SPINCEMAILLE, PI
CARINE
DANIELLE ANDREE NEZER
PC      C12N15/09,A01K67/027,C12N5/06,C12Q1/68,C12N15/00,C12N5/00 CC
/Note='Polymorphism Insulin-IGF2'
FH      Key      Location/Qualifiers
FT      source      1..15
            /organism='Sus scrofa (pig)'
            Location/Qualifiers
            1..15
            /organism="Sus scrofa"
            /mol_type="genomic DNA"
            /db_xref="taxon:9823"
Query Match      7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1631  GGATGGGCTT 1641
Db      12  GGATGGGCTT 2

RESULT 545
AR180150
LOCUS      15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION  Sequence 218 from patent US 6333152.
ACCESSION  AR180150
VERSION    AR180150.1 GI:20222183
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
            1 (bases 1 to 15)
REFERENCE   Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
AUTHORS     Gene expression profiles in normal and cancer cells
TITLE       Patent: US 6333152-A 218 25-DEC-2001;
JOURNAL
FEATURES
source      1..15
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1672  TGGAACTCTGG 1682
Db      3  TGGAACTCTGG 13

RESULT 546
AR180787
LOCUS      15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION  Sequence 855 from patent US 6333152.
ACCESSION  AR180787
VERSION    AR180787.1 GI:20222820
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
            1 (bases 1 to 15)
REFERENCE   Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
AUTHORS     Gene expression profiles in normal and cancer cells
TITLE

```

```
JOURNAL Patent: US 633152-A 855 25-DEC-2001;
FEATURES Location/Qualifiers
  source
    1..15
      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match 7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1672 TGAACCTGG 1682
Db 3 TGAACCTGG 13

RESULT 547
AX028347/C
LOCUS AX028347 15 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 166 from Patent WO0036143.
ACCESSION AX028347
VERSION AX028347.1 GI:10189560
KEYWORDS
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1
AUTHORS Georges,M., Spincemalle,G. and Andersson,L.
TITLE Selecting animals for parentally imprinted traits
JOURNAL Patent: WO 0036143-A 166 22-JUN-2000;
  SEGHERSGENTEC N V (BE) ; GEORGES MICHEL (BE) ; UNIV LIEGE (BE) ;
  SPINCEMAILLE GERET (BE) ; MELICA HB (SE) ; ANDERSSON LEIF (SE)
FEATURES Location/Qualifiers
  source
    1..15
      /organism="Sus scrofa"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9823"
      /note="Polymorphism Insulin-IGF2"
Query Match 7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1631 GGATGGGCTT 1641
Db 12 GGATGGGCTT 2

RESULT 548
AR008042
LOCUS AR008042 16 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 2 from patent US 5753431.
ACCESSION AR008042
VERSION AR008042.1 GI:3967151
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Chiang,J.,Young,Ling.
TITLE Cholesterol 7.alpha.-hydroxylase gene regulatory elements and
  transcription factors
JOURNAL Patent: US 5753431-A 2 19-MAY-1998;
FEATURES Location/Qualifiers
  source
    1..16
      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match 7.9%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1740 CAACTCCTCCC 1750
Db 1740 CAACTCCTCCC 1750

JOURNAL Patent: US 633152-A 855 25-DEC-2001;
FEATURES Location/Qualifiers
  source
    1..15
      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match 7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1672 TGAACCTGG 1682
Db 3 TGAACCTGG 13

RESULT 547
AX028347/C
LOCUS AX028347 15 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 166 from Patent WO0036143.
ACCESSION AX028347
VERSION AX028347.1 GI:10189560
KEYWORDS
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1
AUTHORS Georges,M., Spincemalle,G. and Andersson,L.
TITLE Selecting animals for parentally imprinted traits
JOURNAL Patent: WO 0036143-A 166 22-JUN-2000;
  SEGHERSGENTEC N V (BE) ; GEORGES MICHEL (BE) ; UNIV LIEGE (BE) ;
  SPINCEMAILLE GERET (BE) ; MELICA HB (SE) ; ANDERSSON LEIF (SE)
FEATURES Location/Qualifiers
  source
    1..15
      /organism="Sus scrofa"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9823"
      /note="Polymorphism Insulin-IGF2"
Query Match 7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1631 GGATGGGCTT 1641
Db 12 GGATGGGCTT 2

RESULT 548
AR008042
LOCUS AR008042 16 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 2 from patent US 5753431.
ACCESSION AR008042
VERSION AR008042.1 GI:3967151
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Chiang,J.,Young,Ling.
TITLE Cholesterol 7.alpha.-hydroxylase gene regulatory elements and
  transcription factors
JOURNAL Patent: US 5753431-A 2 19-MAY-1998;
FEATURES Location/Qualifiers
  source
    1..16
      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match 7.9%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1740 CAACTCCTCCC 1750
Db 1740 CAACTCCTCCC 1750

JOURNAL Patent: US 633152-A 855 25-DEC-2001;
FEATURES Location/Qualifiers
  source
    1..15
      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match 7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1672 TGAACCTGG 1682
Db 3 TGAACCTGG 13

RESULT 547
AX028347/C
LOCUS AR028494 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5859334.
ACCESSION AR028494
VERSION AR028494.1 GI:5941467
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Brugliera,F. and Holton,T.Albert.
TITLE Generic sequences encoding glycosyltransferase enzymes and uses
  therefor
JOURNAL Patent: US 5859334-A 6 12-JAN-1999;
FEATURES Location/Qualifiers
  source
    1..16
      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match 7.9%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1683 TGTCTCCTCCA 1693
Db 2 TGTCTCCTCCA 12

RESULT 550
AR110507
LOCUS AR110507 16 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 16 from patent US 6114598.
ACCESSION AR110507
VERSION AR110507.1 GI:12826783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kucherlapati,R., Jakobovits,A., Kalpholz,S., Brenner,D.G. and
  Capon,D.J.
TITLE Generation of xenogeneic antibodies
JOURNAL Patent: US 6114598-A 16 05-SEP-2000;
FEATURES Location/Qualifiers
  source
    1..16
      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match 7.9%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1669 AGCTGGAACCC 1679
Db 1 AGCTGGAACCC 11

RESULT 551
AR137060
LOCUS AR137060 16 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 16 from patent US 6162963.
ACCESSION AR137060
VERSION AR137060.1 GI:14478310
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 16)
```

AUTHORS Kucherlapati,R., Jakobovits,A., Klapholz,S., Brenner,D.G. and Capon,D.J.  
TITLE Generation of Xenogenetic antibodies  
JOURNAL Patent: US 6162963-A 16 19-DEC-2000;  
FEATURES Location/Qualifiers  
source  
1. .16  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 7.9%; Score 11; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1669 AGCTGGAACCC 1679  
Db 1 AGCTGGAACCC 11  
RESULT 552  
LOCUS 126587  
DEFINITION Sequence 2 from patent US 5558999.  
ACCESSION 126587  
VERSION 126587.1 GI:1606457  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Chiang,J.Y.L.  
TITLE Cholesterol 7.alpha.-hydroxylase gene regulatory elements and methods for using them  
JOURNAL Patent: US 5558999-A 2 24-SEP-1996;  
FEATURES Location/Qualifiers  
source  
1. .16  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 7.9%; Score 11; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1740 CAACCTCTCCC 1750  
Db 1 CAACCTCTCCC 11  
RESULT 553  
AX349231/c  
LOCUS AX349231  
DEFINITION Sequence 15 from Patent WO0202810.  
ACCESSION AX349231  
VERSION AX349231.1 GI:18615263  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Bickel,R., Ehrlich,R., Ellinger,T., Ermantraut,E., Kaiser,T., Schulz,T. and Wagner,G.  
TITLE Method for qualitative and/or quantitative detecting of molecular interactions on probe arrays  
JOURNAL Patent: WO 0202810-A 15 10-JAN-2002;  
FEATURES Clondlag Chip Technologies GmbH (DE)  
Location/Qualifiers  
source  
1. .16  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonukleotidsonde"  
Query Match 7.9%; Score 11; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1753 TCCTAAGGCC 1763  
Db 13 TCCTAAGGCC 3  
RESULT 554  
A64216  
LOCUS A64216  
DEFINITION Sequence 4 from Patent WO9727332.  
ACCESSION A64216  
VERSION A64216.1 GI:377647  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Stuyver,L., Louwagie,J. and Rosau,R.  
TITLE METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE TRANSCRIPTASE GENE  
JOURNAL Patent: WO 9727332-A 4 31-JUL-1997;  
COMMENT INNOGENETICS NV (BE)  
FEATURES Other publication AU 1444397 19970820.  
Location/Qualifiers  
source  
1. .14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 7.8%; Score 10.8; DB 1; Length 14;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1718 TACGAGATGGAGA 1731  
Db 1 TACAGAGATGGA 14  
RESULT 555  
A88858/c  
LOCUS A88858  
DEFINITION Sequence 1006 from Patent WO9833904.  
ACCESSION A88858  
VERSION A88858.1 GI:6737428  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Brysch,W. and Schlingensiepen,K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 1006 06-AUG-1998;  
FEATURES BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)  
Location/Qualifiers  
source  
1. .14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 7.8%; Score 10.8; DB 1; Length 14;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1726 TGGAGATTGGCTCC 1739  
Db 14 TGGAGATAGACTCC 1  
RESULT 556  
AR029990  
LOCUS AR029990  
DEFINITION Sequence 179 from patent US 5861244.  
Location/Qualifiers  
source  
14 bp DNA  
linear PAT 29-SEP-1999



Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1726 TGGAGATTGGCTCC 1739  
Db 14 TGGAGATAGACTCC 1

RESULT 561  
A42347  
LOCUS A42347 15 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 7 from Patent WO9501363.  
ACCESSION A42347  
VERSION A42347.1 GI:2297823  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Uhlmann,E. and Meier,C.  
TITLE METHYLPHOSPHONIC ACID ESTER, PROCESS FOR PREPARING THE SAME AND ITS  
JOURNAL US  
COMMENT Patent: WO 9501363-A 7 12-JAN-1995;  
HOECHST AG (DE)  
Other publication FI 956341 960219  
Other publication CA 2165971 950112  
Other publication NO 955352 960214  
Other publication AU 7073594 950124  
Other publication DE 4321946 950112.  
Other publication Location/Qualifiers  
FEATURES  
source 1. .15  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
1. .15  
/note="C-HA-RAS"

Query Match 7.8%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAAACCCCTG 1681  
Db 1 CAGCTGCAACCCAG 14

RESULT 562  
A44378  
LOCUS A44378 15 bp DNA linear PAT 07-MAR-1997  
DEFINITION Sequence 8 from Patent EP0653439.  
ACCESSION A44378  
VERSION A44378.1 GI:2299207  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE Peyman,A.D., Uhlmann,E.D., Mag,M., Kretzschmar,G.D., Helsing,M.D.  
JOURNAL and Winkler,I.D.  
COMMENT Stabilized oligonucleotids and the use thereof  
Patent: EP 0653439-A 8 17-MAY-1995;  
HOECHST AG (DE)  
Other publication JP 7194385 950801  
Other publication CA 2135591 950513  
Other publication AU 7779994 950518  
Other publication DE 4338704 950518.  
Other publication Location/Qualifiers  
FEATURES  
source 1. .15  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
1. .15

/note="C-HA-RAS"

Query Match 7.8%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAAACCCCTG 1681  
Db 1 CAGCTGCAACCCAG 14

RESULT 563  
A47165  
LOCUS A47165 15 bp DNA linear PAT 07-MAR-1997  
DEFINITION Sequence 8 from Patent EP0680969.  
ACCESSION A47165  
VERSION A47165.1 GI:2301207  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE Seela,F.P. and Lampe,S.D.  
JOURNAL Modified oligonucleotides, their preparation and their use  
COMMENT Patent: EP 0680969-A 8 08-NOV-1995;  
HOECHST AG (DE)  
Other publication JP 8003186 960109  
Other publication AU 1778295 951109  
Other publication DE 4415370 951109.  
Other publication Location/Qualifiers  
FEATURES  
source 1. .15  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
1. .15  
/note="C-HA-RAS"

Query Match 7.8%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAAACCCCTG 1681  
Db 1 CAGCTGCAACCCAG 14

RESULT 564  
A56641  
LOCUS A56641 15 bp DNA linear PAT 03-MAR-1998  
DEFINITION Sequence 8 from Patent EP0739898.  
ACCESSION A56641  
VERSION A56641.1 GI:3712686  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE unclassified.  
AUTHORS Peyman,A.D., Uhlmann,E.D., Breipohl,G.D. and Wallmeier,H.D.  
TITLE Phosphonomonoester nucleic acids, methods for their preparation and  
JOURNAL their use  
COMMENT Patent: EP 0739898-A 8 30-OCT-1996;  
HOECHST AG (DE)  
Other publication CZ 9600743 961016  
Other publication CN 1138588 961225  
Other publication PL 313207 960916  
Other publication JP 8259579 961008  
Other publication NO 961006 960916  
Other publication CA 2171589 960914  
Other publication AU 4802896 960926  
Other publication DE 19508923 960919.  
Other publication Location/Qualifiers  
FEATURES  
source 1. .15

```

/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1668 CAGCTGGAACCTG 1691
      ||||| |||||
Db 1 CAGCTGCAACCCAG 14

RESULT 565
LOCUS      A80362      15 bp      DNA      linear      PAT 20-OCT-1999
DEFINITION Sequence 8 from Patent EP0726274.
ACCESSION  A80362
VERSION    A80362.1 GI:6093089
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1 (bases 1 to 15)
AUTHORS    Peyman, A.D. and Uhlmann, E.D.
TITLE      G-CAP STABILIZED OLIGONUCLEOTIDES
JOURNAL    HOECHST AG (DE)
FEATURES   Location/Qualifiers
            source
              1..15
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"
            exon

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1668 CAGCTGGAACCTG 1681
      ||||| |||||
Db 1 CAGCTGCAACCCAG 14

RESULT 566
LOCUS      A88333      15 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 481 from Patent WO9833904.
ACCESSION  A88333
VERSION    A88333.1 GI:6736903
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1 (bases 1 to 15)
AUTHORS    Brysch, W. and Schlingensiepen, K.
TITLE      AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL    Patent: WO 9833904-A 481 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES   Location/Qualifiers
            source
              1..15
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCGTGG 1699
      ||||| |||||
Db 14 CTCCTCCAGCATGG 1

RESULT 569
LOCUS      AR041808      15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 598 from patent US 5811300.
ACCESSION  AR041808
VERSION    AR041808.1 GI:5962304
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1 (bases 1 to 15)
AUTHORS    Sullivan, S., Draper, K., Kisich, K., Stinchcomb, D.T. and McSwiggen, J.

```

```

RESULT 567
LOCUS      A89423      15 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 1571 from Patent WO9833904.
ACCESSION  A89423
VERSION    A89423.1 GI:6737993
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1 (bases 1 to 15)
AUTHORS    Brysch, W. and Schlingensiepen, K.
TITLE      AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL    Patent: WO 9833904-A 1571 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES   Location/Qualifiers
            source
              1..15
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1753 TCCTAAAGGCCAC 1766
      ||||| |||||
Db 14 TCCGAAAGGTCCAC 1

RESULT 568
LOCUS      A90300      15 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 481 from Patent EP0856579.
ACCESSION  A90300
VERSION    A90300.1 GI:6738814
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1 (bases 1 to 15)
AUTHORS    Brysch, W.D. and Schlingensiepen, K.D.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: EP 0856579-A 481 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES   Location/Qualifiers
            source
              1..15
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCGTGG 1699
      ||||| |||||
Db 14 CTCCTCCAGCATGG 1

RESULT 569
LOCUS      AR041808      15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 598 from patent US 5811300.
ACCESSION  AR041808
VERSION    AR041808.1 GI:5962304
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1 (bases 1 to 15)
AUTHORS    Sullivan, S., Draper, K., Kisich, K., Stinchcomb, D.T. and McSwiggen, J.

```

```
TITLE      TNF- $\alpha$  ribozymes
JOURNAL    Patent: US 5811300-A 598 22-SEP-1998;
FEATURES   Location/Qualifiers
           source
           1..15
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1708 GGGTTAGGAGTACG 1721
      |||||
Db 15 GGGTGAGGAGCAG 2

RESULT 570
AR041809/c
LOCUS      AR041809      15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 599 from patent US 5811300.
ACCESSION AR041809
VERSION    AR041809.1 GI:5962305
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.
TITLE     TNF- $\alpha$  ribozymes
JOURNAL    Patent: US 5811300-A 599 22-SEP-1998;
FEATURES   Location/Qualifiers
           source
           1..15
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1708 GGGTTAGGAGTACG 1721
      |||||
Db 15 GGGTGAGGAGCAG 2

RESULT 571
AR073553
LOCUS      AR073553      15 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION Sequence 18 from patent US 5952011.
ACCESSION AR073553
VERSION    AR073553.1 GI:10000317
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   O'Hara,P.J., Grant,F.J. and Sheppard,P.O.
TITLE     Human transglutaminases
JOURNAL    Patent: US 5952011-A 18 14-SEP-1999;
FEATURES   Location/Qualifiers
           source
           1..15
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1663 GCTCAGCTGGAA 1676
      |||||
Db 1 GCGCTCAGCTGGAA 14

RESULT 572
AR111765
LOCUS      AR111765      15 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 8 from patent US 6127346.
ACCESSION AR111765
VERSION    AR111765.1 GI:12828613
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Peyman,A., Uhlmann,E., Breipohl,G. and Wallmeier,H.
TITLE     Phosphonomonoester nucleic acids process for their preparation and
           their use
JOURNAL    Patent: US 6127346-A 8 03-OCT-2000;
FEATURES   Location/Qualifiers
           source
           1..15
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCTCG 1681
      |||||
Db 1 CAGCTGCAACCCAG 14

RESULT 573
AR133622
LOCUS      AR133622      15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 2047 from patent US 6194150.
ACCESSION AR133622
VERSION    AR133622.1 GI:14122527
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE     Nucleic acid based inhibition of CD40
JOURNAL    Patent: US 6194150-A 2047 27-FEB-2001;
FEATURES   Location/Qualifiers
           source
           1..15
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 CCTGGTGTCCTCTC 1691
      |||||
Db 2 CCTGGTCTCACCTC 15

RESULT 574
I20495
LOCUS      I20495      15 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 18 from patent US 5514579.
ACCESSION I20495
VERSION    I20495.1 GI:16C0850
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   O'Hara,P.J., Grant,F.J. and Sheppard,P.O.
TITLE     Human transglutaminases
JOURNAL    Patent: US 5514579-A 18 07-MAY-1996;
FEATURES   Location/Qualifiers
           source
           1..15
           /organism="unknown"
```



```
/mol_type="unassigned DNA"

Query Match          7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1663 GCTCAGCTGGAA 1676
||| |||||
Db 1 GCGCTCAGCTGGAA 14

RESULT 575
LOCUS I33987 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5594121.
ACCESSION I33987
VERSION I33987.1 GI:1824778
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Froehler,B. and Matteucci,M.
TITLE Enhanced triple-helix and double-helix formation with oligomers
JOURNAL Patent: US 5594121-A 1 14-JAN-1997;
FEATURES Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"

Query Match          7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1743 CTCCTCCCTATCCT 1756
||| |||||
Db 14 CTCCTCCCTTCCT 1

RESULT 576
LOCUS I33988 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 2 from patent US 5594121.
ACCESSION I33988
VERSION I33988.1 GI:1824779
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Froehler,B. and Matteucci,M.
TITLE Enhanced triple-helix and double-helix formation with oligomers
JOURNAL Patent: US 5594121-A 2 14-JAN-1997;
FEATURES Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"

Query Match          7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1743 CTCCTCCCTATCCT 1756
||| |||||
Db 2 CTCCTCCCTTCCT 15

RESULT 577
LOCUS I84720 15 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 8 from patent US 5696248.

ACCESSION I84720 GI:3022240
VERSION I84720.1
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Peyman,A., Uhlmann,E. and Carolus,C.
TITLE 3'-modified oligonucleotide derivatives
JOURNAL Patent: US 5696248-A 8 09-DEC-1997;
FEATURES Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"

Query Match          7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1668 CAGCTGGAACCTG 1681
||| |||||
Db 1 CAGCTGCAACCCAG 14

RESULT 578
LOCUS AR179805 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 8 from patent US 6326487.
ACCESSION AR179805
VERSION AR179805.1 GI:20221360
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Peyman,A., Uhlmann,E. and Carolus,C.
TITLE 3 modified oligonucleotide derivatives
JOURNAL Patent: US 6326487-A 8 04-DEC-2001;
FEATURES Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"

Query Match          7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1668 CAGCTGGAACCTG 1681
||| |||||
Db 1 CAGCTGCAACCCAG 14

RESULT 579
LOCUS AR193504 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 8 from patent US 6348312.
ACCESSION AR193504
VERSION AR193504.1 GI:20240096
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Peyman,A., Uhlmann,E., Mag,M., Kretschmar,G., Helsberg,M. and Winkler,I.
TITLE Stabilized oligonucleotides and their use
JOURNAL Patent: US 6348312-A 8 19-FEB-2002;
FEATURES Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"

Query Match          7.8%; Score 10.8; DB 1; Length 15;
```

Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCCCTG 1681  
||||| |||||  
Db 1 CAGCTGCAACCCAG 14

RESULT 580  
AX283167  
LOCUS AX254155 AR254155 15 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 7 from patent US 6479651.  
ACCESSION AR254155  
VERSION AR254155.1 GI:27302892  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Seela, F. and Thomas, H.  
TITLE Modified oligonucleotides, their preparation and their use  
JOURNAL Patent: US 6479651-A 7 12-NOV-2002;  
FEATURES Location/Qualifiers  
source  
1..15  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 7.8%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCCCTG 1681  
||||| |||||  
Db 1 CAGCTGCAACCCAG 14

RESULT 581  
AX081337  
LOCUS AX081337 15 bp DNA linear PAT 27-FEB-2001  
DEFINITION Sequence 16 from Patent WO0108707.  
ACCESSION AX081337  
VERSION AX081337.1 GI:13170179  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Uhlmann, E., Greiner, B., Unger, E., Gothe, G. and Schwerdel, M.  
TITLE Conjugates and methods for the production thereof, and their use  
JOURNAL for transporting molecules via biological membranes  
Patent: WO 0108707-A 16 08-FEB-2001;  
Aventis Pharma Deutschland GmbH (DE)  
FEATURES Location/Qualifiers  
source  
1..15  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"

Query Match 7.8%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCCCTG 1681  
||||| |||||  
Db 1 CAGCTGCAACCCAG 14

RESULT 582  
AX283167  
LOCUS AX283167 15 bp DNA linear PAT 20-NOV-2001  
DEFINITION Sequence 5 from Patent WO0179216.  
ACCESSION AX283167

VERSION AX283167.1 GI:17044048  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Uhlmann, E., Breipohl, G. and Will, D.W.  
TITLE Polyamide nucleic acid derivatives, agents and methods for  
producing them  
JOURNAL Patent: WO 0179216-A 5 25-OCT-2001;  
Aventis Pharma Deutschland GmbH (DE)  
FEATURES Location/Qualifiers  
source  
1..15  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Beschreibung der kuenstlichen  
Sequenz:Oligonukleotide"

Query Match 7.8%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCCCTG 1681  
||||| |||||  
Db 1 CAGCTGCAACCCAG 14

RESULT 583  
AX283281  
LOCUS AX283281 15 bp DNA linear PAT 20-NOV-2001  
DEFINITION Sequence 45 from Patent WO0179249.  
ACCESSION AX283281  
VERSION AX283281.1 GI:17044162  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Uhlmann, E., Breipohl, G. and Will, D.W.  
TITLE Polyamide nucleic acid derivatives, agents and methods for  
producing the same  
JOURNAL Patent: WO 0179249-A 45 25-OCT-2001;  
Aventis Pharma Deutschland GmbH (DE)  
FEATURES Location/Qualifiers  
source  
1..15  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Beschreibung der kuenstlichen Sequenz:  
Oligonukleotide"

Query Match 7.8%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCCCTG 1681  
||||| |||||  
Db 1 CAGCTGCAACCCAG 14

RESULT 584  
AX637264/c  
LOCUS AX637264/c 15 bp RNA linear PAT 21-FEB-2003  
DEFINITION Sequence 4403 from Patent EP1260586.  
ACCESSION AX637264  
VERSION AX637264.1 GI:28472878  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified.  
REFERENCE 1  
AUTHORS Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Direnzo, A.,

Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,G.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.  
**TITLE** Method and reagent for inhibiting the expression of disease related genes  
**JOURNAL** Patent: EP 1260586-A 4403 27-NOV-2002;  
**FEATURES** RIBOZYME PHARMACEUTICALS, INC. (US)  
 source location/Qualifiers  
 1. .15  
 /organism="unidentified"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32644"

**Query Match** 7.8%; Score 10.8; DB 1; Length 15;  
**Best Local Similarity** 85.7%; Pred. No. 2.9e+02;  
**Matches** 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY** 1708 GGGTTAGGATGACG 1721  
 ||||| ||||| |||||  
**Db** 15 GGGTGAGGAGCAG 2

**RESULT 585**  
**AX637266/c**  
**LOCUS** AX637266 15 bp RNA linear PAT 21-FEB-2003  
**DEFINITION** Sequence 4405 from Patent EP1260586.  
**ACCESSION** AX637266  
**VERSION** AX637266.1 GI:28472880  
**KEYWORDS** unidentified  
**SOURCE** unclassified.  
**ORGANISM** unclassified.  
**REFERENCE** 1  
**AUTHORS** Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,G.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.  
**TITLE** Method and reagent for inhibiting the expression of disease related genes  
**JOURNAL** Patent: EP 1260586-A 4405 27-NOV-2002;  
**FEATURES** RIBOZYME PHARMACEUTICALS, INC. (US)  
 source location/Qualifiers  
 1. .15  
 /organism="unidentified"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32644"

**Query Match** 7.8%; Score 10.8; DB 1; Length 15;  
**Best Local Similarity** 85.7%; Pred. No. 2.9e+02;  
**Matches** 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY** 1708 GGGTTAGGATGACG 1721  
 ||||| ||||| |||||  
**Db** 15 GGGTGAGGAGCAG 2

**RESULT 586**  
**AX742553/c**  
**LOCUS** AX742553 15 bp DNA linear PAT 12-MAY-2003  
**DEFINITION** Sequence 356 from Patent EP1302550.  
**ACCESSION** AX742553  
**VERSION** AX742553.1 GI:30576521  
**KEYWORDS** synthetic construct  
**SOURCE** synthetic construct  
**ORGANISM** artificial sequences.  
**REFERENCE** 1  
**AUTHORS** Lin,C.Y., Lin,R.W., You,C.M., Huang,H.H., Lee,B.H., Lee,H.H., Lin,Y.J., Fan,C.C., Hsu,H.C., Shih,C.W., Yeh,C.H., Kao,Y.F., Pan,C.L. and Chan,P.  
**TITLE** Method and detector for identifying subtypes of human papilloma

viruses  
**JOURNAL** Patent: EP 1302550-A 356 16-APR-2003;  
**FEATURES** King Car Food Industrial Co., Ltd. (TW)  
 source location/Qualifiers  
 1. .15  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="Oligonucleotide for Identifying HPV 61"

**Query Match** 7.8%; Score 10.8; DB 1; Length 15;  
**Best Local Similarity** 85.7%; Pred. No. 2.9e+02;  
**Matches** 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY** 1635 GGGGTTGTAGCAG 1648  
 ||||| ||||| |||||  
**Db** 14 GGGGATGTAGCAG 1

**RESULT 597**  
**BD065846/c**  
**LOCUS** BD065846 15 bp DNA linear PAT 27-AUG-2002  
**DEFINITION** An antisense oligonucleotide preparation method.  
**ACCESSION** BD065846  
**VERSION** BD065846.1 GI:22611449  
**KEYWORDS** JP 2001511000-A/481.  
**SOURCE** unidentified  
**ORGANISM** unclassified.  
**REFERENCE** 1 (bases 1 to 15)  
**AUTHORS** Schlingensiepen,K.H. and Brysch,W.  
**TITLE** An antisense oligonucleotide preparation method  
**JOURNAL** Patent: JP 2001511000-A 481 07-AUG-2001;  
**COMMENT** BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
 OS Unknown  
 PN JP 2001511000-A/481  
 PD 07-AUG-2001  
 PF 30-JAN-1998 JP 1998532533  
 PI 31-JAN-1997 EP 97101531.8  
 PR KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
 PC C12N15/11.C07H21/04.A61K31/70  
 CC An antisense oligonucleotide preparation method FH Key  
 Location/Qualifiers  
 FT source 1. .15  
 /organism='Unknown'.  
**FEATURES** location/Qualifiers  
 source 1. .15  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

**Query Match** 7.8%; Score 10.8; DB 1; Length 15;  
**Best Local Similarity** 85.7%; Pred. No. 2.9e+02;  
**Matches** 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY** 1686 CTCCTCCAGCGTGG 1699  
 ||||| ||||| |||||  
**Db** 14 CTTCTCCAGCATGG 1

**RESULT 598**  
**BD066936/c**  
**LOCUS** BD066936 15 bp DNA linear PAT 27-AUG-2002  
**DEFINITION** An antisense oligonucleotide preparation method.  
**ACCESSION** BD066936  
**VERSION** BD066936.1 GI:22612539  
**KEYWORDS** JP 2001511000-A/1571.  
**SOURCE** unidentified  
**ORGANISM** unclassified.  
**REFERENCE** 1 (bases 1 to 15)  
**AUTHORS** Schlingensiepen,K.H. and Brysch,W.  
**TITLE** An antisense oligonucleotide preparation method

QY	1635	GCGGCTTGAGCAG	1648
Db		 14 GGGGATGTAGCAG	1
RESULT 590			
AR057424			
LOCUS	AR057424	16 bp	DNA
DEFINITION	Sequence 1628 from patent US 5837542.		
ACCESSION	AR057424		
VERSION	AR057424.1	GI:5983001	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 16)		
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.		
TITLE	Intracellular adhesion molecule-1 (ICAM-1) ribozymes		
JOURNAL	Patent: US 5837542-A 1628 17-NOV-1998;		
FEATURES	Location/Qualifiers		
source	1..16		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	7.8%;	Score 10.8; DB 1;	Length 16;
Best Local Similarity	85.7%;	Pred. No. 3.2e+02;	
Matches	12; Conservative	0; Mismatches	2; Indels 0; Gaps 0;
QY	1689	CTCCAGCGTGGTC	1702
Db		 1 CTACAGCCTGGTGC	14
RESULT 591			
AR115182			
LOCUS	AR115182	16 bp	DNA
DEFINITION	Sequence 1628 from patent US 6132967.		
ACCESSION	AR115182		
VERSION	AR115182.1	GI:14095504	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 16)		
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.		
TITLE	Ribozyme treatment of diseases or conditions related to levels of intracellular adhesion molecule-1 (ICAM-1)		
JOURNAL	Patent: US 6132567-A 1628 17-OCT-2000;		
FEATURES	Location/Qualifiers		
source	1..16		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	7.8%;	Score 10.8; DB 1;	Length 16;
Best Local Similarity	85.7%;	Pred. No. 3.2e+02;	
Matches	12; Conservative	0; Mismatches	2; Indels 0; Gaps 0;
QY	1689	CTCCAGCGTGGTC	1702
Db		 1 CTACAGCCTGGTGC	14
RESULT 592			
BD233053			
LOCUS	BD233053	16 bp	DNA
DEFINITION	Method of detecting mutation selected by drug in HIV protease gene.		
ACCESSION	BD233053		
VERSION	BD233053.1	GI:53042823	
KEYWORDS	JP 2002518065-A/149.		
ORGANISM	Aids-associated retrovirus		
SOURCE	Aids-associated retrovirus		

Viruses; Retroviral viruses; Retroviridae.  
1 (bases 1 to 16)  
Stuyver, L.  
Method of detecting mutation selected by drug in HIV protease gene  
Patent: JP 2002518065-A 149 25-JUN-2002;  
INNOGENETICS NV  
OS Aids-associated retrovirus  
PN JP 2002518065-A/149  
PD 25-JUN-2002  
PR 22-JUN-1999 JP 2000556068  
PF 24-JUN-1998 EP 98870143.9  
PI LIEVEN STUYVER  
PC C12N15/09, C12Q1/68, C12Q1/70, C12N15/00  
CC Method of detecting mutation selected by drug in HIV protease  
gene  
FH Key Location/Qualifiers  
FT source 1..16  
FT Location/Qualifiers  
FEATURES  
source  
1..16  
/organism="Aids-associated retrovirus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:11966"  
Query Match 7.8%; Score 10.8; DB 1; Length 16;  
Best Local Similarity 85.7%; Pred. No. 3.2e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1721 GGAGATGGAGATTG 1734  
|||||  
Db 3 GGAGTTGGAGGTTG 16  
RESULT 593  
E39140  
LOCUS E39140 16 bp DNA linear PAT 18-JUN-2001  
DEFINITION Improved PCR method for primer elongation pre-amplification.  
ACCESSION E39140  
VERSION E39140.1 GI:13017702  
KEYWORDS JP 1999318498-A/6.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Urufuganku, D. and Joseph, R.  
TITLE Improved PCR method for primer elongation pre-amplification  
JOURNAL Patent: JP 1999318498-A 6 24-NOV-1999;  
COMMENT OS Artificial Sequence  
PN JP 1999318498-A/6  
PD 24-NOV-1999  
PF 26-MAR-1999 JP 1999084967  
PR 26-MAR-1998 DE 19813317:0  
PI URUFUGANKU DIETOMATYA JOSEPH RUSSHOFU  
PC C12Q1/68, C12N15/09, C12N15/00  
CC  
FH Key Location/Qualifiers  
FT source 1..16  
FT Location/Qualifiers  
FEATURES  
source  
1..16  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
Query Match 7.8%; Score 10.8; DB 1; Length 16;  
Best Local Similarity 85.7%; Pred. No. 3.2e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1713 AGGAGTACGAGAT 1726  
|||||  
Db 2 AGCAGTAAGGAGAT 15

RESULT 594  
I50741/c  
LOCUS I50741 16 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 23 from patent US 5643724.  
ACCESSION I50741  
VERSION I50741.1 GI:2472444  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Fildes, N. Jane. and Reynolds, R. Lynne.  
TITLE Methods and reagents for Glycophorin A typing  
JOURNAL Patent: US 5643724-A 23 01-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 7.8%; Score 10.8; DB 1; Length 16;  
Best Local Similarity 85.7%; Pred. No. 3.2e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1672 TGGAAACCTTGTTG 1685  
|||||  
Db 15 TGGAAAGCTTGTTG 2  
RESULT 595  
AR203385  
LOCUS AR203385 16 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 6 from patent US 6365375.  
ACCESSION AR203385  
VERSION AR203385.1 GI:21499760  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Dietmaier, W. and Ruschoff, J.  
TITLE Method of primer-extension preamplification PCR  
JOURNAL Patent: US 6365375-A 6 02-APR-2002;  
FEATURES Location/Qualifiers  
source 1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 7.8%; Score 10.8; DB 1; Length 16;  
Best Local Similarity 85.7%; Pred. No. 3.2e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1713 AGGAGTACGAGAT 1726  
|||||  
Db 2 AGCAGTAAGGAGAT 15  
RESULT 596  
AR328401  
LOCUS AR328401 16 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 5803 from patent US 6566127.  
ACCESSION AR328401  
VERSION AR328401.1 GI:33714209  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Pavco, P., McSwiggen, J. A., Stinchcomb, D. T. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 5803 20-MAY-2003;  
FEATURES Location/Qualifiers

```
source 1..16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 7.8%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1746 CTCCTTATCCTAA 1759
|||||
Db 1 CTCCTTATCGAAA 14

RESULT 597
AR328478
LOCUS AR328478 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5880 from patent US 6566127.
ACCESSION AR328478
VERSION AR328478.1 GI:33714286
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5880 20-MAY-2003;
FEATURES
source 1..16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 7.8%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1738 CCCACTCTCTCCT 1751
|||||
Db 1 CTCCACTCTGCT 14

RESULT 598
AR328510/c
LOCUS AR328510 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5912 from patent US 6566127.
ACCESSION AR328510
VERSION AR328510.1 GI:33714318
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5912 20-MAY-2003;
FEATURES
source 1..16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 7.8%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1692 CAGCGTGGTGAG 1705
|||||
Db 14 CAGCGTGGTGAG 1

RESULT 599
AX007607
LOCUS AX007607 16 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 149 from Patent WO9967428.
ACCESSION AX007607
VERSION AX007607.1 GI:9995304
KEYWORDS Aids-associated retrovirus
SOURCE Aids-associated retrovirus
ORGANISM Viruses; Retrovirdae; Retroviridae.
REFERENCE
AUTHORS Stuyver,L.
TITLE Method for detection of drug-selected mutations in the hiv protease
gene
JOURNAL Patent: WO 9967428-A 149 29-DEC-1999;
INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
FEATURES
source 1..16
/organism="Aids-associated retrovirus"
/mol_type="unassigned DNA"
/db_xref="taxon:11966"

Query Match
Best Local Similarity 7.8%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTC 1734
|||||
Db 3 GGAGTGGAGGTTG 16

RESULT 600
AX011283
LOCUS AX011283 16 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 6 from Patent EP0957177.
ACCESSION AX011283
VERSION AX011283.1 GI:9997834
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Dietmaier,W.D. and Rueschoff,J.P.
TITLE Improved method for primer extension preamplification-pcr
JOURNAL Patent: EP 0957177-A 6 17-NOV-1999;
ROCHE DIAGNOSTICS GMBH (DE)
FEATURES
source 1..16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 7.8%; Score 10.8; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1713 AGGAGTACGAGAT 1726
|||||
Db 2 AGCAGTAGGAGAT 15

RESULT 601
AX384636
LOCUS AX384636 16 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 8 from Patent EP1182206.
ACCESSION AX384636
VERSION AX384636.1 GI:19577831
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Peymann,A., Uhlmann,E., Mag,M., Kretschmar,G., Helsenberg,M. and
Winkler,I.
```

```

TITLE      Stabilized oligonucleotides and the use thereof
JOURNAL    Patent: EP 1182206-A 8 27-FEB-2002;
           HOECHST AKTIENGESELLSCHAFT (DE)
FEATURES   source
           1..16
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="Antisense Oligonukleotid"

Query Match      7.8%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCTG 1681
Db 1 CAGCTGCACCCAG 14

RESULT 602
LOCUS      AX419931/c
DEFINITION Sequence 268 from Patent WO0198537.
ACCESSION  AX419931
VERSION     AX419931.1 GI:21524298
KEYWORDS   synthetic construct
SOURCE     artificial sequences.
REFERENCE  1
AUTHORS    Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.
TITLE      Nucleic acid accessible hybridization sites
JOURNAL    Patent: WO 0198537-A 268 27-DEC-2001;
           THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES   source
           1..16
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"

Query Match      7.8%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1685 TCTCTCCAGCGTG 1698
Db 16 TCTCTCCATCATG 3

RESULT 603
LOCUS      AX521635/c
DEFINITION Sequence 15 from Patent WO0227031.
ACCESSION  AX521635
VERSION     AX521635.1 GI:23572675
KEYWORDS   synthetic construct
SOURCE     synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Busa,W.B.
TITLE      Methods and reagents for live-cell gene expression quantification
JOURNAL    Patent: WO 0227031-A 15 04-APR-2002;
           Celloomics, Inc. (US)
FEATURES   source
           1..16
           /organism="synthetic construct"
           /mol_type="unassigned RNA"
           /db_xref="taxon:32630"
           /note="synthetic oligonucleotide"

Query Match      7.8%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;

QY 1661 AGGCTCAGCTGG 1674
Db 16 AGGCTCAGATCTGG 3

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 604
LOCUS      AX634479
DEFINITION Sequence 1618 from Patent EPI260586.
ACCESSION  AX634479
VERSION     AX634479.1 GI:28470093
KEYWORDS   unidentified
SOURCE     unidentified
           unclassified.
REFERENCE  1
AUTHORS    Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
           Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
           McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
           Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
           Woolf,T.
TITLE      Method and reagent for inhibiting the expression of disease related
           genes
JOURNAL    Patent: EP 1260586-A 1618 27-NOV-2002;
           RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES   source
           1..16
           /organism="unidentified"
           /mol_type="unassigned RNA"
           /db_xref="taxon:32644"

Query Match      7.8%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1689 CTCACAGCTGGTG 1702
Db 1 CTACAGCTGGTGG 14

RESULT 605
LOCUS      AR106948/c
DEFINITION Sequence 109 from patent US 6107092.
ACCESSION  AR106948
VERSION     AR106948.1 GI:12821478
KEYWORDS   Unknown.
SOURCE     Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Cowsert,L.M., Bennett,C.Frank. and O'Malley,B.W.
TITLE      Antisense modulation of SRA expression
JOURNAL    Patent: US 6107092-A 109 22-AUG-2000;
           location/Qualifiers
           1..18
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      7.8%; Score 10.8; DB 1; Length 18;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1658 ACCAGGCTCAGC 1671
Db 15 ACCAGGCTCCAGC 2

RESULT 606
LOCUS      AX532451/c
FEATURES   source
           1..16
           /organism="synthetic construct"
           /mol_type="unassigned RNA"
           /db_xref="taxon:32630"
           /note="synthetic oligonucleotide"

Query Match      7.8%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
```

DEFINITION Sequence 1960 from Patent EP1239051.  
ACCESSION AX532451  
VERSION AX532451.1 GI:25256676  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Shannon,M.  
TITLE Human posh-like protein 1  
JOURNAL Patent: EP 1239051-A 1960 11-SEP-2002;  
Aeomica, Inc. (US)  
FEATURES  
source  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 7.6%; Score 10.6; DB 1; Length 17;  
Best Local Similarity 76.5%; Pred. No. 3.8e+02;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1733 TGGCTCCCACTCTCC 1749  
Db 17 TGGACCCCATCTCCAC 1  
RESULT 607  
AX532452/C  
LOCUS  
DEFINITION Sequence 1961 from Patent EP1239051.  
ACCESSION AX532452  
VERSION AX532452.1 GI:25256678  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Shannon,M.  
TITLE Human posh-like protein 1  
JOURNAL Patent: EP 1239051-A 1961 11-SEP-2002;  
Aeomica, Inc. (US)  
FEATURES  
source  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 7.6%; Score 10.6; DB 1; Length 17;  
Best Local Similarity 76.5%; Pred. No. 3.8e+02;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1732 TTGGTCCCACTCTCC 1748  
Db 17 TTGGACCCCATCTCCAC 1  
RESULT 608  
AR382702  
LOCUS  
DEFINITION Sequence 56 from patent US 6610533.  
ACCESSION AR382702  
VERSION AR382702.1 GI:40091489  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Inouye,M., Wang,N. and Yamanaka,K.  
TITLE Cold-shock regulatory elements, constructs thereof, and methods of use

JOURNAL Patent: US 6610533-A 56 26-AUG-2003;  
FEATURES  
source  
1..13  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 7.5%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 2.7e+02;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1754 CCTAAGGCCCA 1765  
Db 2 CCGAAGGCCCA 13  
RESULT 609  
A09968/c  
LOCUS  
DEFINITION Probe 33.6.  
ACCESSION A09968  
VERSION A09968.1 GI:485097  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Vijg,J. and Uitterlinden,A.G.  
TITLE A method for the simultaneous determination of DNA sequence variations at a large number of sites, and a kit therefor  
JOURNAL Patent: EP 0349024-A 3 03-JAN-1990;  
NEDERLANDSE ORGANISATIE VOOR TOEGEPAST-NATUURWETENSCHAPPELIJK ONDERZOEK TWO  
FEATURES  
source  
1..14  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
Query Match 7.5%; Score 10.4; DB 1; Length 14;  
Best Local Similarity 91.7%; Pred. No. 3.1e+02;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1686 CTCCTCCAGCGT 1697  
Db 14 CTCCTCCAGCCT 3  
RESULT 610  
A40553/c  
LOCUS  
DEFINITION Sequence 90 from Patent WO9425578.  
ACCESSION A40553  
VERSION A40553.1 GI:2296588  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS  
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))  
JOURNAL Patent: WO 9425578-A 90 10-NOV-1994;  
BIOGNOSTIK GES (DE)  
FEATURES  
source  
1..14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 7.5%; Score 10.4; DB 1; Length 14;  
Best Local Similarity 91.7%; Pred. No. 3.1e+02;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



```
QY 1644 AGCAGAGGCCAA 1655
Db 14 AGCAGAGGCCGA 3

RESULT 611
A89078/c
LOCUS 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1226 from Patent WO9833904.
ACCESSION A89078
VERSION A89078.1 GI:6737648
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1226 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
    source
        Location/Qualifiers
            1..14
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match 7.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAGGCCAA 1655
Db 14 AGCAGAGGCCGA 3

RESULT 612
A89078/c
LOCUS 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 90 from patent US 6455689.
ACCESSION AR232833
VERSION AR232833.1 GI:27275171
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 90 24-SEP-2002;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
    source
        Location/Qualifiers
            1..14
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 7.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAGGCCAA 1655
Db 14 AGCAGAGGCCGA 3

RESULT 613
AR403509/c
LOCUS 14 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1849 from patent US 6623962.
ACCESSION AR403509
VERSION AR403509.1 GI:40150959
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases of conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: US 6623962-A 1849 23-SEP-2003;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
    source
        Location/Qualifiers
            1..14
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 7.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1639 CTTGTAGCAGAA 1650
Db 13 CTTGAGCAGAA 2

RESULT 614
AX030128/c
LOCUS 14 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 90 from Patent EP1008649.
ACCESSION AX030128
VERSION AX030128.1 GI:10190345
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 90 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
    source
        Location/Qualifiers
            1..14
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match 7.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AGCAGAGGCCAA 1655
Db 14 AGCAGAGGCCGA 3

RESULT 615
AX316449/c
LOCUS 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 90 from Patent EP1160319.
ACCESSION AX316449
VERSION AX316449.1 GI:17899622
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 90 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
    source
        Location/Qualifiers
            1..14
```



```
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1667 ACAGCTGGAC 1678
Db 3 ACAGCTGGAC 14

RESULT 619
A07567/c
LOCUS A07567 15 bp DNA linear PAT 28-JUN-1993
DEFINITION p11196 DNA sequence, J-region.
ACCESSION A07567
VERSION A07567.1 GI:413080
KEYWORDS
ORGANISM synthetic construct
SOURCE synthetic construct
REFERENCE 1 (bases 1 to 15)
AUTHORS Kaluza,B. and Lenz,H.
TITLE Diagnostic method using chimeric antibodies
JOURNAL Patent: EP 0378175-A 18 JUL-1990;
BOEHRINGER MANNHEIM GMBH
FEATURES
Source
1..15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
CDS
1..15
/codon_start=1
/transl_table=11
/product="K gene, J-region rearranged"
/protein_id="CAA00680.1"
/db_xref="GI:4526619"
/db_xref="RENTREMBL:CAA00680"
/translation="GTKLE"

Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1689 CTCACGCTGGT 1700
Db 15 CTCACGCTGGT 4

RESULT 620
A07569
LOCUS A07569 15 bp DNA linear PAT 28-JUN-1993
DEFINITION p11196 DNA sequence, J-region, Reverse complement.
ACCESSION A07569
VERSION A07569.1 GI:411488
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 15)
AUTHORS Kaluza,B. and Lenz,H.
TITLE Diagnostic method using chimeric antibodies
JOURNAL Patent: EP 0378175-A 20 JUL-1990;
BOEHRINGER MANNHEIM GMBH
FEATURES
Source
1..15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1689 CTCACGCTGGT 1700
Db 1 CTCACGCTGGT 12
```

```
RESULT 621
AR033573/c
LOCUS AR033573 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 339 from patent US 5869253.
ACCESSION AR033573
VERSION AR033573.1 GI:5949178
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 339 09-FEB-1999;
FEATURES
Source
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1695 CGTGGTGGAGT 1706
Db 15 CGTAGTGGAGT 4

RESULT 622
AR113395/c
LOCUS AR113395 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 339 from patent US 6132966.
ACCESSION AR113395
VERSION AR113395.1 GI:14093717
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 6132966-A 339 17-OCT-2000;
FEATURES
Source
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1695 CGTGGTGGAGT 1706
Db 15 CGTAGTGGAGT 4

RESULT 623
AR132845
LOCUS AR132845 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1270 from patent US 6194150.
ACCESSION AR132845
VERSION AR132845.1 GI:14121750
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 1270 27-FEB-2001;
FEATURES
Location/Qualifiers
```

```
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 7.5%; Score 10.4; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1636 GGGCTGTAGCA 1647
|||||
Db 3 GGGCTGTATCA 14

RESULT 624
LOCUS AR143397/c 15 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 42 from patent US 6204252.
ACCESSION AR143397
VERSION AR143397.1 GI:15104683
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Murphy, C., Storey, J., Beltz, G.A. and Coughlin, R.T.
TITLE Characterization of granulocytic ehrlichia and methods of use.
JOURNAL Patent: US 6204252-A 42 20-MAR-2001;
FEATURES
Location/Qualifiers
1..15
source
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 7.5%; Score 10.4; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 GTAGCAGAGGC 1653
|||||
Db 15 GTAGAGAGGC 4

RESULT 625
E05479
LOCUS PCR primer. 15 bp DNA linear PAT 29-SEP-1997
DEFINITION
ACCESSION E05479
VERSION E05479.1 GI:2173668
KEYWORDS
SOURCE JP 1993244982-A/7.
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 15)
AUTHORS Nakatani, T., Gomi, H., Jiyon, W. and Noguchi, H.
TITLE ANTHROPOMORPHISM B-B10
JOURNAL Patent: JP 1993244982-A 7 24-SEP-1993;
SUMITOMO CHEM CO LTD, SUMITOMO PHARMACEUT CO LTD, BIOTEST AG,
INOTERAPII LAB
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1993244982-A/7
PD 24-SEP-1993
PF 06-DEC-1991 JP 1991323319
PI NAKATANI TOMOSUKE, GOMI HIROYUKI, JIYON WAIDENESU, PI
NOGUCHI HIROSHI
PC C12P21/08, A61K39/395//C12N5/10, C12N15/13, G01N33/577; CC
strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.
Location/Qualifiers
1..15
source
/organism="synthetic construct"
/mol_type="genomic DNA"

source /db_xref="taxon:32630"

Query Match
Best Local Similarity 7.5%; Score 10.4; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1689 CTCGAGCTGGT 1700
|||||
Db 1 CTCGAGCTGGT 12

RESULT 626
LOCUS I15197/c 15 bp DNA linear PAT 02-APR-1996
DEFINITION Sequence 14 from patent US 5460949.
ACCESSION I15197
VERSION I15197.1 GI:1250105
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Saunders, C.A., Wolf, F.R. and Mukharji, I.
TITLE Method and composition for increasing the accumulation of squalene
and specific sterols in yeast
JOURNAL Patent: US 5460949-A 14 24-OCT-1995;
FEATURES
Location/Qualifiers
1..15
source
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 7.5%; Score 10.4; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAAC 1677
|||||
Db 12 CACAGCTGGATC 1

RESULT 627
LOCUS I57802/c 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 339 from patent US 5610054.
ACCESSION I57802
VERSION I57802.1 GI:2482866
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Draper, K.G.
TITLE Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL Patent: US 5610054-A 339 11-MAR-1997;
FEATURES
Location/Qualifiers
1..15
source
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 7.5%; Score 10.4; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1695 CGTGGTGGAGT 1706
|||||
Db 15 CGTAGTGGAGT 4

RESULT 628
LOCUS I61657/c 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 211 from patent US 5658780.
ACCESSION I61657
```



```

AX636078/c
LOCUS AX636078 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 3217 from Patent EP1260586.
ACCESSION AX636078
VERSION AX636078.1 GI:28471692
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpelisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 3217 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
1..15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1639 CTTGTAGCGGAA 1650
DB 12 CTTGTAGCGGAA 1

RESULT 634
LOCUS BD207306/c
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD207306
VERSION BD207306.1 GI:33017076
KEYWORDS JP 2002512791-A/896.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 896 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/896
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO.
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
PH Key Location/Qualifiers
FT source 1..15
FT /organism='Hepatitis virus (hepatitis C FT
virus)',
Location/Qualifiers
1..15
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1688 CTTCCAGCGTGG 1699
DB 1 CTTCCAGCGTGG 12

RESULT 636
LOCUS S45933/c
DEFINITION COL2A1-procollagen II [human, Genomic Mutant, 15 nt].
ACCESSION S45933
VERSION S45933.1 GI:1679995
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

/mol_type="genomic RNA"
/db_xref="taxon:32644"
Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1695 CGTGGTGGAGT 706
DB 15 CGTAGTGGAGT 4

RESULT 635
LOCUS BD208694
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD208694
VERSION BD208694.1 GI:33018464
KEYWORDS JP 2002512791-A/2284.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 2284 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2284
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO.
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
PH Key Location/Qualifiers
FT source 1..15
FT /organism='Hepatitis virus (hepatitis C FT
virus)',
Location/Qualifiers
1..15
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
Query Match 7.5%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1688 CTTCCAGCGTGG 1699
DB 1 CTTCCAGCGTGG 12

RESULT 636
LOCUS S45933/c
DEFINITION COL2A1-procollagen II [human, Genomic Mutant, 15 nt].
ACCESSION S45933
VERSION S45933.1 GI:1679995
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 15)  
 AUTHORS Ahmad,N.N., Ala-Kokko,L., Knowlton,R.G., Jimenez,S.A., Weaver,E.J.,  
 Maguire,J.I., Tasman,W. and Prockop,D.J.  
 TITLE Stop codon in the procollagen II gene (COL2A1) in a family with the  
 Stickler syndrome (arthro-ophthalmopathy)  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (15), 6624-6627 (1991)  
 MEDLINE 91319736  
 PUBMED 1677770  
 REMARK GenBank staff at the National Library of Medicine created this  
 entry [NCBI gisseq 45933] from the original journal article.  
 This sequence comes from fig 3.  
 COMMENT On Nov 21, 1996 this sequence version replaced gi:1619744.  
 FEATURES  
 source  
 1..15  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 gene 1..15 "COL2A1"  
 /gene="COL2A1"  
 /note="procollagen II"

Query Match 7.5%; Score 10.4; DB 1; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 3.4e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1684 GTCTCTCCAGC 1695  
 |||||  
 Db 15 GTCTCTCAAGC 4

RESULT 637  
 128863/c  
 LOCUS 128863 Sequence 8 from patent US 5574142.  
 DEFINITION 128863  
 ACCESSION 128863.1 GI:1819650  
 VERSION 128863.1  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Meyer,R.B., Jx., Gall,A.A. and Reed,M.W.  
 TITLE Peptide linkers for improved oligonucleotide delivery  
 JOURNAL Patent: US 5574142-A 8 12-NOV-1996;  
 FEATURES  
 source  
 1..16  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 7.5%; Score 10.4; DB 1; Length 16;  
 Best Local Similarity 91.7%; Pred. No. 3.8e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1719 ACGAGATGGAG 1730  
 |||||  
 Db 12 ACGAAGTGGAG 1

RESULT 638  
 AR328508  
 LOCUS AR328508 Sequence 5910 from patent US 6566127.  
 DEFINITION AR328508  
 ACCESSION AR328508  
 VERSION AR328508.1 GI:33714316  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
 TITLE Method and reagent for the treatment of diseases or conditions  
 related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6566127-A 5910 20-MAY-2003;  
 FEATURES  
 source  
 1..16  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

Query Match 7.5%; Score 10.4; DB 1; Length 16;  
 Best Local Similarity 91.7%; Pred. No. 3.8e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1648 GAAGGCAAGCAC 1659  
 |||||  
 Db 1 GAAGGCAAGCGC 12

RESULT 639  
 AR329723/c  
 LOCUS AR329723 Sequence 7125 from patent US 6566127.  
 DEFINITION AR329723  
 ACCESSION AR329723  
 VERSION AR329723.1 GI:33715531  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 16)  
 AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
 TITLE Method and reagent for the treatment of diseases or conditions  
 related to levels of vascular endothelial growth factor receptor  
 JOURNAL Patent: US 6566127-A 7125 20-MAY-2003;  
 FEATURES  
 source  
 1..16  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

Query Match 7.5%; Score 10.4; DB 1; Length 16;  
 Best Local Similarity 91.7%; Pred. No. 3.8e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1650 AGGCAAGCACCA 1661  
 |||||  
 Db 14 AGGCAAGAACCA 3

RESULT 640  
 AX349227  
 LOCUS AX349227 Sequence 11 from Patent WO0202810.  
 DEFINITION AX349227  
 ACCESSION AX349227  
 VERSION AX349227.1 GI:18615259  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1  
 AUTHORS Bickel,R., Ehrlich,R., Ellinger,T., Ermantraut,E., Kaiser,T.,  
 Schulz,I. and Wagner,G.  
 TITLE Method for qualitative and/or quantitative detecting of molecular  
 interactions on probe arrays  
 JOURNAL Patent: WO 0202810-A 11 10-JAN-2002;  
 FEATURES  
 source  
 1..16  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Oligonukleotidsende"

Query Match 7.5%; Score 10.4; DB 1; Length 16;  
 Best Local Similarity 91.7%; Pred. No. 3.8e+02;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1636 GGGCTTGTAGCA 1647

Db 2 GGGCTTTAGCA 13  
||||| |||||  
RESULT 641  
AX103735/c  
LOCUS AX103735 18 bp DNA linear PAT 30-APR-2001  
DEFINITION Sequence 52 from Patent WO0125458.  
ACCESSION AX103735  
VERSION AX103735.1 GI:13919945  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Olivier,J., Deslandes,L. and Marco,Y.  
TITLE Novel class of proteins and uses thereof for plant resistance to  
JOURNAL various pathogenic agents  
PATENT: WO 0125458-A 52 12-APR-2001;  
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (I.N.R.A.) (FR) ;  
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)  
FEATURES  
source  
1..18  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 7.5%; Score 10.4; DB 1; Length 18;  
Best Local Similarity 91.7%; Pred. No. 4.5e+02;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1719 ACGGACATGCGAG 1730  
Db 17 ACGGACATGCGAG 6  
||||| |||||  
RESULT 642  
A70767  
LOCUS A70767 20 bp DNA linear PAT 07-MAY-1999  
DEFINITION Sequence 88 from Patent WO9813490.  
ACCESSION A70767  
VERSION A70767.1 GI:4774770  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Ophoff,R.A., Terwindt,G.M., Ferrari,M.D. and Frants,R.R.  
TITLE A gene related to migraine in man  
JOURNAL Patent: WO 9813490-A 88 02-APR-1998;  
OPHOFF ROEL ANDRE (NL)  
FEATURES  
source  
1..20  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 7.5%; Score 10.4; DB 1; Length 20;  
Best Local Similarity 70.0%; Pred. No. 5.1e+02;  
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1665 TCACAGCTGGACCCCTGGTG 1684  
Db 1 TGACTTCGCCACCCCTGGTG 20  
||||| |||||  
RESULT 643  
A79251  
LOCUS A79251 20 bp DNA linear PAT 20-OCT-1999  
DEFINITION Sequence 88 from Patent EP0834561.  
ACCESSION A79251  
VERSION A79251.1 GI:6092296

KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 20)  
AUTHORS  
TITLE A GENE RELATED TO MIGRAINE IN MAN  
JOURNAL Patent: EP 0834561-A 88 08-APR-1998;  
UNIV LEIDEN (NL)  
FEATURES  
Location/Qualifiers  
1..20  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 7.5%; Score 10.4; DB 1; Length 20;  
Best Local Similarity 70.0%; Pred. No. 5.1e+02;  
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1665 TCACAGCTGGACCCCTGGTG 1684  
Db 1 TGACTTCGCCACCCCTGGTG 20  
||||| |||||  
RESULT 644  
BD003481  
LOCUS BD003481 20 bp DNA linear PAT 31-JAN-2002  
DEFINITION A gene related to migraine in man.  
ACCESSION BD003481  
VERSION BD003481.1 GI:18631442  
KEYWORDS JP 2001500743-A/50.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Frantz,R.R.I.B., Ferrari,M.D., Teruvinato,H.M. and Opuhofu,R.A.  
TITLE A gene related to migraine in man  
JOURNAL Patent: JP 2001500743-A 50 23-JAN-2001;  
RYUKUS UNIVERSITY TO RAIDEN  
COMMENT OS Homo sapiens (human)  
PN JP 2001500743-A/50  
PD 23-JAN-2001  
PF 26-SEP-1997 JP 1998515527  
PR 27-SEP-1996 EP 96202707.4  
PI RENE ROBERT ISAAK ERIK FRANTZ,MICHEL DOMINIQUE FERRARI, PI  
HISERA MARRY TERUVINTO,RURU ANDRE OPUHOFU  
PC C12N15/09,F01K67/027,C07K14/435,C07K16/18,C12N1/15,C12N1/19,  
PC C12N1/21,  
PC C12N5/10,C12Q1/02,C12Q1/68,C12N15/00,C12N5/00 CC  
FH Key Location/Qualifiers  
FT primer bind. (1)..(20).  
FEATURES  
source  
1..20  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
Query Match 7.5%; Score 10.4; DB 1; Length 20;  
Best Local Similarity 70.0%; Pred. No. 5.1e+02;  
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1665 TCACAGCTGGACCCCTGGTG 1684  
Db 1 TGACTTCGCCACCCCTGGTG 20  
||||| |||||  
RESULT 645  
A20991/c  
LOCUS A20991 15 bp DNA linear PAT 29-SEP-1994  
DEFINITION N-terminal coding sequence.  
ACCESSION A20991  
VERSION A20991.1 GI:641297



```
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 15)
AUTHORS
TITLE       SYNTHESIS OF MATURE HUMAN PARATHYROID HORMONE
JOURNAL     Patent: WO 9105050-A 6 18-APR-1991;
FEATURES
            Location/Qualifiers
                1..15
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1715 GACTACGAGATGGA 1729
Db 15 GATTTCGAGACGGA 1

RESULT 646
A64273/c
LOCUS      A64273      15 bp      DNA      linear      PAT 29-MAR-1999
DEFINITION Sequence 61 from Patent WO9727332.
ACCESSION  A64273
VERSION     A64273.1 GI:3717704
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1
AUTHORS    Stuyver,L., Louwagie,J. and Rossau,R.
TITLE      METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE
JOURNAL    TRANSCRIPTASE GENE
COMMENT    Patent: WO 9727332-A 61 31-JUL-1997;
            INNOGENETICS NV (BE)
            Other publication AU 1444397 19970820.
FEATURES
            Location/Qualifiers
                1..15
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1691 CCACGCTGCTGAAG 1705
Db 15 CCATCCTGTGGAAG 1

RESULT 647
A78578/c
LOCUS      A78578      15 bp      DNA      linear      PAT 19-OCT-1999
DEFINITION Sequence 4 from Patent EP0576842.
ACCESSION  A78578
VERSION     A78578.1 GI:6090239
KEYWORDS   Listeria monocytogenes
SOURCE     Listeria monocytogenes
            Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Goebel,W.P. and Bubert,A.
TITLE      METHOD AND MEANS FOR DETECTING LISTERIA
JOURNAL    MERCK PATENT GMBH (DE)
FEATURES
            Location/Qualifiers
                1..15
                /organism="Listeria monocytogenes"

KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 15)
AUTHORS
TITLE       SYNTHESIS OF MATURE HUMAN PARATHYROID HORMONE
JOURNAL     Patent: WO 9105050-A 6 18-APR-1991;
FEATURES
            Location/Qualifiers
                1..15
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:1639"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1704 AGTTGGGTTAGGAGT 1718
Db 15 AGCTGTGTAGCAGT 1

RESULT 648
AR026479/c
LOCUS      AR026479      15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5856096.
ACCESSION  AR026479
VERSION     AR026479.1 GI:5937319
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Windle,B.E., Qiu,M., Chen,S.-P., Fletcher,T.M. and Maine,I.
TITLE      Rapid and sensitive assays for detecting and distinguishing between
            processive and non-processive telomerase activities
JOURNAL    Patent: US 5856096-A 4 05-JAN-1999;
            Location/Qualifiers
                1..15
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1708 GGGTTAGGAGTACGG 1722
Db 15 GGGTTAGGTTAGGG 1

RESULT 649
AR041292/c
LOCUS      AR041292      15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 82 from patent US 5811300.
ACCESSION  AR041292
VERSION     AR041292.1 GI:5961788
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.
TITLE      TNF- $\alpha$  ribozymes
JOURNAL    Patent: US 5811300-A 82 22-SEP-1998;
            Location/Qualifiers
                1..15
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1639 CTTGTAGCAGAGGC 1653
Db 15 CTGTAGGAGACGGC 1

RESULT 650
AR041361
LOCUS      AR041361      15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 151 from patent US 5811300.
```

ACCESSION AR041361  
VERSION AR041361.1 GI:5961857  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.  
TITLE TNF- alpha. ribozymes  
JOURNAL Patent: US 5811300-A 151 22-SEP-1998;  
FEATURES Location/Qualifiers  
source  
1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 7.3%; Score 10.2; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1664 CTCACAGCTGGGAACC 1678  
Db 1 CTGACATCTGGATC 15  
RESULT 651  
LOCUS AR041957  
DEFINITION Sequence 747 from patent US 5811300.  
ACCESSION AR041957  
VERSION AR041957.1 GI:5962453  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.  
TITLE TNF- alpha. ribozymes  
JOURNAL Patent: US 5811300-A 747 22-SEP-1998;  
FEATURES Location/Qualifiers  
source  
1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 7.3%; Score 10.2; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1676 ACCTGGTGTCTCCT 1690  
Db 1 ACCTGTGTGCTCCT 15  
RESULT 652  
LOCUS AR056148  
DEFINITION Sequence 352 from patent US 5837542.  
ACCESSION AR056148  
VERSION AR056148.1 GI:5981725  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 352 17-NOV-1998;  
FEATURES Location/Qualifiers  
source  
1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 7.3%; Score 10.2; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1731 ATGGCTCCCACTC 1745  
Db 1 ATAGGCTCACACAC 15  
RESULT 653  
LOCUS AR056220/c  
DEFINITION Sequence 424 from patent US 5837542.  
ACCESSION AR056220  
VERSION AR056220.1 GI:5981797  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 424 17-NOV-1998;  
FEATURES Location/Qualifiers  
source  
1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 7.3%; Score 10.2; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1650 AGGCAAGCACCAGGC 1664  
Db 15 AGGCAAGAAACAGGC 1  
RESULT 654  
LOCUS AR056325/c  
DEFINITION Sequence 529 from patent US 5837542.  
ACCESSION AR056325  
VERSION AR056325.1 GI:5981902  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 529 17-NOV-1998;  
FEATURES Location/Qualifiers  
source  
1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 7.3%; Score 10.2; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1650 AGGCAAGCACCAGGC 1664  
Db 15 AGGCAAGAAACAGGC 1  
RESULT 655  
LOCUS AR102572/c  
DEFINITION Sequence 61 from patent US 6087093.  
ACCESSION AR102572  
VERSION AR102572.1 GI:12814160  
KEYWORDS

```

SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Lieven,S., Joost,L. and Rudi.R.
TITLE
Method for detection of drug-induced mutations in the reverse
transcriptase gene
JOURNAL
Patent: US 6087093-A 61 11-JUL-2000;
FEATURES
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1691 CCAGCGTGTGGAG 1705
Db 15 CCATCCTTGTGGAG 1
RESULT 656
AR113906
LOCUS
AR113906 15 bp DNA linear PAT 16-MAY-2001
DEFINITION
Sequence 352 from patent US 6132967.
ACCESSION
AR113906
VERSION
AR113906.1 GI:14094228
KEYWORDS
.
SOURCE
Unknown.
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE
Ribozyme treatment of diseases or conditions related to levels of
intercellular adhesion molecule-1 (ICAM-1)
JOURNAL
Patent: US 6132967-A 352 17-OCT-2000;
FEATURES
Location/Qualifiers
1..15
/mol_type="unassigned DNA"
Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1731 ATTGGCTCCCACTC 1745
Db 1 ATAGGCTCAACAC 15
RESULT 657
AR113978/c
LOCUS
AR113978 15 bp DNA linear PAT 16-MAY-2001
DEFINITION
Sequence 424 from patent US 6132967.
ACCESSION
AR113978
VERSION
AR113978.1 GI:14094300
KEYWORDS
.
SOURCE
Unknown.
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE
Ribozyme treatment of diseases or conditions related to levels of
intercellular adhesion molecule-1 (ICAM-1)
JOURNAL
Patent: US 6132967-A 424 17-OCT-2000;
FEATURES
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"
SOURCE
source
Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1731 ATTGGCTCCCACTC 1745
Db 1 ATAGGCTCAACAC 15
RESULT 657
AR113978/c
LOCUS
AR113978 15 bp DNA linear PAT 16-MAY-2001
DEFINITION
Sequence 263 from patent US 6194150.
ACCESSION
AR131838
VERSION
AR131838.1 GI:14120741
KEYWORDS
.
SOURCE
Unknown.
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE
Nucleic acid based inhibition of CD40
JOURNAL
Patent: US 6194150-A 263 27-FEB-2001;
FEATURES
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"
SOURCE
source
Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1715 GAGTACGGAGATGGA 1729
Db 15 GAGAAAGGAGAGGGA 1
RESULT 660
AR132776/c
LOCUS
AR132776 15 bp DNA linear PAT 16-MAY-2001
DEFINITION
Sequence 1201 from patent US 6194150.
ACCESSION
AR132776
VERSION
AR132776.1 GI:14121681
```

```

KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Unclassified.
TITLE       Stinchcomb,D.T., Jarvis,T. and McSwiggan,J.
JOURNAL     Nucleic acid based inhibition of CD40
FEATURES    Location/Qualifiers
            source
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 7.3%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AGCAGAGGCAAGCA 1658
Db 15 AGCAGCAGAGCA 1

RESULT 661
LOCUS      BD233013/C
DEFINITION Method of detecting mutation selected by drug in HIV protease gene.
ACCESSION BD233013
VERSION    BD233013.1 GI:33042783
KEYWORDS   JP 2002518065-A/109.
SOURCE     Aids-associated retrovirus
ORGANISM   Viruses; Retroid viruses; Retroviridae.
REFERENCE  1 (bases 1 to 15)
AUTHORS     Stuyver,L.
TITLE       Method of detecting mutation selected by drug in HIV protease gene
JOURNAL     Patent: JP 2002518065-A 109 25-JUN-2002;
COMMENT     INNOGENETICS NV
            OS Aids-associated retrovirus
            PN JP 2002518065-A/109
            PD 25-JUN-2002
            PP 22-JUN-1999 JP 2000556068
            PR 24-JUN-1998 EP 98870143.9
            PI LIEVEN STUYVER
            PC C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
            CC Method of detecting mutation selected by drug in HIV protease
            CC Key gene Location/Qualifiers
            FH source 1..15
            FT Location/Qualifiers
            FT 1..15
            /organism='Aids-associated retrovirus'.

FEATURES
source
1..15
/organism="Aids-associated retrovirus"
/mol_type="genomic DNA"
/db_xref="taxon:11966"

Query Match
Best Local Similarity 7.3%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGG 1735
Db 1 GGAGTTGGAGTTTG 15

RESULT 663
LOCUS      BD233297
DEFINITION Method of detecting mutation selected by drug in HIV protease gene.
ACCESSION BD233297
VERSION    BD233297.1 GI:33043067
KEYWORDS   JP 2002518065-A/393.
SOURCE     Aids-associated retrovirus
ORGANISM   Viruses; Retroid viruses; Retroviridae.
REFERENCE  1 (bases 1 to 15)
AUTHORS     Stuyver,L.
TITLE       Method of detecting mutation selected by drug in HIV protease gene
JOURNAL     Patent: JP 2002518065-A 393 25-JUN-2002;
COMMENT     INNOGENETICS NV
            OS Aids-associated retrovirus
            PN JP 2002518065-A/393
            PD 25-JUN-2002
            PP 22-JUN-1999 JP 2000556068
            PR 24-JUN-1998 EP 98870143.9
            PI LIEVEN STUYVER
            PC C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
            CC Method of detecting mutation selected by drug in HIV protease
            CC Key gene Location/Qualifiers
            FH source 1..15
            FT Location/Qualifiers
            FT 1..15
            /organism='Aids-associated retrovirus'.

FEATURES
source
1..15
/organism="Aids-associated retrovirus"
/mol_type="genomic DNA"
/db_xref="taxon:11966"

Query Match
Best Local Similarity 7.3%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1742 ACTCTCCCTATCCT 1756
Db 15 AATCCCCCTATCAT 1

RESULT 662
LOCUS      BD233078
DEFINITION Method of detecting mutation selected by drug in HIV protease gene.
ACCESSION BD233078
VERSION    BD233078.1 GI:33042848
KEYWORDS   JP 2002518065-A/174.
SOURCE     Aids-associated retrovirus
ORGANISM   Aids-associated retrovirus

Viruses; Retroid viruses; Retroviridae.
Stuyver,L.
Method of detecting mutation selected by drug in HIV protease gene
Patent: JP 2002518065-A 174 25-JUN-2002;
INNOGENETICS NV
Aids-associated retrovirus
JP 2002518065-A/174
25-JUN-2002
22-JUN-1999 JP 2000556068
24-JUN-1998 EP 98870143.9
LIEVEN STUYVER
C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
Method of detecting mutation selected by drug in HIV protease
Key gene Location/Qualifiers
source 1..15
Location/Qualifiers
1..15
/organism="Aids-associated retrovirus"
/mol_type="genomic DNA"
/db_xref="taxon:11966"

Query Match
Best Local Similarity 7.3%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1742 ACTCTCCCTATCCT 1756
Db 15 AATCCCCCTATCAT 1

RESULT 662
LOCUS      BD233078
DEFINITION Method of detecting mutation selected by drug in HIV protease gene.
ACCESSION BD233078
VERSION    BD233078.1 GI:33042848
KEYWORDS   JP 2002518065-A/174.
SOURCE     Aids-associated retrovirus
ORGANISM   Aids-associated retrovirus

Viruses; Retroid viruses; Retroviridae.
Stuyver,L.
Method of detecting mutation selected by drug in HIV protease gene
Patent: JP 2002518065-A 174 25-JUN-2002;
INNOGENETICS NV
Aids-associated retrovirus
JP 2002518065-A/174
25-JUN-2002
22-JUN-1999 JP 2000556068
24-JUN-1998 EP 98870143.9
LIEVEN STUYVER
C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
Method of detecting mutation selected by drug in HIV protease
Key gene Location/Qualifiers
source 1..15
Location/Qualifiers
1..15
/organism="Aids-associated retrovirus"
/mol_type="genomic DNA"
/db_xref="taxon:11966"

Query Match
Best Local Similarity 7.3%; Score 10.2; DB 1; Length 15;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGTGTCTC 1688
Db 1 GAACCTGTGTCTC 15

```

```
RESULT 664
BD233300      15 bp      DNA      linear      PAT 17-JUL-2003
LOCUS          Method of detecting mutation selected by drug in HIV protease gene.
DEFINITION
ACCESSION      BD233300
VERSION        BD233300.1 GI:33043070
KEYWORDS       JP 2002518065-A/396.
SOURCE         Aids-associated retrovirus
ORGANISM       Viruses; Retrovirdae.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Stuyver,L.
TITLE         Method of detecting mutation selected by drug in HIV protease gene
JOURNAL       Patent: JP 2002518065-A 396 25-JUN-2002;
INNOGENETICS NV
COMMENT       OS Aids-associated retrovirus
PN JP 2002518065-A/396
PD 25-JUN-2002
PF 22-JUN-1999 JP 2000556068
PI 24-JUN-1998 EP 98870143.9
PT LIEVEN STUYVER
PC C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
CC Method of detecting mutation selected by drug in HIV protease
CC gene
CC Key Location/Qualifiers
CC FT source 1. .15
CC FT /organism='Aids-associated retrovirus'.
CC FT Location/Qualifiers
CC FT 1. .15
CC FT /organism='Aids-associated retrovirus'
CC FT /mol_type='genomic DNA'
CC FT /db_xref='taxon:11966'

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGGTGCTC 1688
Db 1 GAACCTGTTGACTC 15

FEATURES
source
Location/Qualifiers
1. .15
/organism='Aids-associated retrovirus'
/mol_type='genomic DNA'
/db_xref='taxon:11966'

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGGTGCTC 1688
Db 1 GAACCTGTTGACTC 15

RESULT 665
BD233419/c
LOCUS          Method of detecting mutation selected by drug in HIV protease gene.
DEFINITION
ACCESSION      BD233419
VERSION        BD233419.1 GI:33043189
KEYWORDS       JP 2002518065-A/515.
SOURCE         Aids-associated retrovirus
ORGANISM       Viruses; Retrovirdae.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Stuyver,L.
TITLE         Method of detecting mutation selected by drug in HIV protease gene
JOURNAL       Patent: JP 2002518065-A 515 25-JUN-2002;
INNOGENETICS NV
COMMENT       OS Aids-associated retrovirus
PN JP 2002518065-A/515
PD 25-JUN-2002
PF 22-JUN-1999 JP 2000556068
PI 24-JUN-1998 EP 98870143.9
PT LIEVEN STUYVER
PC C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
CC Method of detecting mutation selected by drug in HIV protease
CC gene
CC Key Location/Qualifiers
CC FT source 1. .15
CC FT /organism='Aids-associated retrovirus'.
CC FT Location/Qualifiers
CC FT 1. .15
CC FT /organism='Aids-associated retrovirus'
CC FT /mol_type='genomic DNA'
CC FT /db_xref='taxon:11966'

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGGTGCTC 1688
Db 1 GAACCTGTTGACTC 15

RESULT 666
BD233419/c
LOCUS          Method of detecting mutation selected by drug in HIV protease gene.
DEFINITION
ACCESSION      BD233419
VERSION        BD233419.1 GI:33043189
KEYWORDS       JP 2002518065-A/515.
SOURCE         Aids-associated retrovirus
ORGANISM       Viruses; Retrovirdae.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Stuyver,L.
TITLE         Method of detecting mutation selected by drug in HIV protease gene
JOURNAL       Patent: JP 2002518065-A 515 25-JUN-2002;
INNOGENETICS NV
COMMENT       OS Aids-associated retrovirus
PN JP 2002518065-A/515
PD 25-JUN-2002
PF 22-JUN-1999 JP 2000556068
PI 24-JUN-1998 EP 98870143.9
PT LIEVEN STUYVER
PC C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
CC Method of detecting mutation selected by drug in HIV protease
CC gene
CC Key Location/Qualifiers
CC FT source 1. .15
CC FT /organism='Aids-associated retrovirus'.
CC FT Location/Qualifiers
CC FT 1. .15
CC FT /organism='Aids-associated retrovirus'
CC FT /mol_type='genomic DNA'
CC FT /db_xref='taxon:11966'

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGGTGCTC 1688
Db 1 GAACCTGTTGACTC 15
```

```
/organism='Aids-associated retrovirus'
/mol_type='genomic DNA'
/db_xref='taxon:11966'

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1674 GAACCTGGTGCTC 1688
Db 15 GAACCTGTTGACTC 1

RESULT 666
105468/c
LOCUS          Sequence 3 from Patent EP 0266190.
DEFINITION
ACCESSION      I05468
VERSION        I05468
KEYWORDS       I05468.1 GI:591022
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Foster,D.C., Murray,M.J. and Berkner,K.L.
TITLE         Expression of protein C
JOURNAL       Patent: EP 0266190-A2 3 04-MAY-1988;
FEATURES       Location/Qualifiers
source 1. .15
/organism='unknown'
/mol_type='unassigned DNA'

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1735 GCTCCCACTCCTCC 1749
Db 15 GCTCAGAATCCTCC 1

RESULT 667
I30549/c
LOCUS          Sequence 12 from patent US 5580969.
DEFINITION
ACCESSION      I30549
VERSION        I30549.1 GI:1821340
KEYWORDS       Unknown.
SOURCE         Unclassified.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Hoke,G.D., Bradley,M.O., Williams,T.J. and Lee,C.-H.
TITLE         Antisense oligonucleotides directed against human ICAM-1 RNA
JOURNAL       Patent: US 5580969-A 12 03-DEC-1996;
FEATURES       Location/Qualifiers
source 1. .15
/organism='unknown'
/mol_type='unassigned DNA'

Query Match      7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGAACC 1678
Db 15 CTCACAGTTCGAACC 1

RESULT 668
I39340/c
LOCUS          Sequence 378 from patent US 5616488.
DEFINITION
```



REFERENCE 1 (bases 1 to 15)  
AUTHORS Lieven,S., Joost,L. and Rudi,R.  
TITLE Method for detection of drug-induced mutations in the reverse transcriptase gene  
JOURNAL Patent: US 6311389-A 61 18-DEC-2001;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 7.3%; Score 10.2; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1691 CCAGCGTGTGGAAG 1705  
Db 15 CCATCCTTGTGGAAG 1

RESULT 674  
AX0079380/c  
LOCUS AR279380 15 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 24 from patent US 6514699.  
ACCESSION AR279380  
VERSION AR279380.1 GI:29714132  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS O'Neill,R.A.; Chen,J.-K.; Chiesa,C. and Fry,G.  
TITLE Multiplex polynucleotide capture methods and compositions  
JOURNAL Patent: US 6514699-A 24 04-FEB-2003;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 7.3%; Score 10.2; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1636 GGGCTTGTAGCAGAA 1650  
Db 15 GCGATAGTAGCAGAA 1

RESULT 675  
AX007567/c  
LOCUS AX007567 15 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 109 from Patent WO9967428.  
ACCESSION AX007567  
VERSION AX007567.1 GI:9995264  
KEYWORDS  
SOURCE Aids-associated retrovirus  
ORGANISM Aids-associated retrovirus  
Viruses; Retroid viruses; Retroviridae.  
REFERENCE 1  
AUTHORS Stuyver,L.  
TITLE Method for detection of drug-selected mutations in the hiv protease gene  
JOURNAL Patent: WO 9967428-A 109 29-DEC-1999;  
INNOGENETICS NV (BE); STUYVER LIEVEN (BE)  
FEATURES Location/Qualifiers  
source 1..15  
/organism="Aids-associated retrovirus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:11966"

Query Match 7.3%; Score 10.2; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1674 GAACCTCGTGTCTC 1688  
Db 1 GAACCTCTGTGACTC 15

RESULT 678  
AX007854  
LOCUS AX007854 15 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 396 from Patent WO9967428.  
ACCESSION AX007854  
VERSION AX007854.1 GI:9995551

Qy 1742 ACTCTCCCTATCTCT 1756  
Db 15 AATCCCCCTATCAT 1

RESULT 676  
AX007632  
LOCUS AX007632 15 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 174 from Patent WO9967428.  
ACCESSION AX007632  
VERSION AX007632.1 GI:9995329  
KEYWORDS  
SOURCE Aids-associated retrovirus  
ORGANISM Aids-associated retrovirus  
Viruses; Retroid viruses; Retroviridae.  
REFERENCE 1  
AUTHORS Stuyver,L.  
TITLE Method for detection of drug-selected mutations in the hiv protease gene  
JOURNAL Patent: WO 9967428-A 174 29-DEC-1999;  
INNOGENETICS NV (BE); STUYVER LIEVEN (BE)  
FEATURES Location/Qualifiers  
source 1..15  
/organism="Aids-associated retrovirus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:11966"

Query Match 7.3%; Score 10.2; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1721 GGAGTGGAGATTGG 1735  
Db 1 GGAGTTGGAGGTTTG 15

RESULT 677  
AX007851  
LOCUS AX007851 15 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 393 from Patent WO9967428.  
ACCESSION AX007851  
VERSION AX007851.1 GI:9995548  
KEYWORDS  
SOURCE Aids-associated retrovirus  
ORGANISM Aids-associated retrovirus  
Viruses; Retroid viruses; Retroviridae.  
REFERENCE 1  
AUTHORS Stuyver,L.  
TITLE Method for detection of drug-selected mutations in the hiv protease gene  
JOURNAL Patent: WO 9967428-A 393 29-DEC-1999;  
INNOGENETICS NV (BE); STUYVER LIEVEN (BE)  
FEATURES Location/Qualifiers  
source 1..15  
/organism="Aids-associated retrovirus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:11966"

Query Match 7.3%; Score 10.2; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1674 GAACCTCGTGTCTC 1688  
Db 1 GAACCTCTGTGACTC 15

RESULT 678  
AX007854  
LOCUS AX007854 15 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 396 from Patent WO9967428.  
ACCESSION AX007854  
VERSION AX007854.1 GI:9995551





```

QY 1690 TCCAGCGTGTGGAA 1704
|||||
Db 15 TCCATCCTGTGGAA 1

RESULT 683
AX587077/c
LOCUS AX587077 15 bp DNA linear PAT 10-JAN-2003
DEFINITION Sequence 99 from Patent WO02072883.
ACCESSION AX587077
VERSION AX587077.1 GI:27655952
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE Nucleotide carrier for diagnosing and treating oral diseases
JOURNAL
FEATURES
source
1. 15
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Bacteria"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1653 CAAGCACCAGGCTCA 1667
|||||
Db 15 CGAGAACCAAGCTCA 1

RESULT 684
AX633179
LOCUS AX633179 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 318 from Patent EP1260586.
ACCESSION AX633179
VERSION AX633179.1 GI:28468793
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL
PATENT: EP 1260586-A 318 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
Location/Qualifiers
source
1. 15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1731 ATGGCTCCCAACTC 1745
|||||
Db 1 ATAGGCTCAACAC 15

RESULT 685
AX633279/c
LOCUS AX633279 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 418 from Patent EP1260586.
ACCESSION AX633279
VERSION AX633279.1 GI:28468893
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL
PATENT: EP 1260586-A 418 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
Location/Qualifiers
source
1. 15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1650 AGGCAAGCACCAGGC 1664
|||||
Db 15 AGGCAGGAACAGGC 1

RESULT 686
AX633526/c
LOCUS AX633526 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 665 from Patent EP1260586.
ACCESSION AX633526
VERSION AX633526.1 GI:28469140
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL
PATENT: EP 1260586-A 665 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
Location/Qualifiers
source
1. 15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1650 AGGCAAGCACCAGGC 1664
|||||
Db 15 AGGCAGGAACAGGC 1

RESULT 687
AX635641/c
LOCUS AX635641 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 2780 from Patent EP1260586.

```

[illegible]

```

1
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
Karpelsky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Wolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 4507 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source 1..15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1676 ACCCTGGTGTCTCTCT 1690
|||||
Db 1 ACCTTGTGTCCTCTCT 15

RESULT 692
LOCUS BD007196 15 bp DNA linear PAT 31-JAN-2002
DEFINITION Method and composition for capturing multiple polynucleotide.
ACCESSION BD007196
VERSION BD007196.1 GI:18635567
KEYWORDS JP 2001503973-A/24.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS O'Neill,R.A., Chen,J.C., Chiesa,C. and Fry,G.
TITLE Method and composition for capturing multiple polynucleotide
JOURNAL Patent: JP 2001503973-A 24 27-MAR-2001;
THE PERKIN ELMAR CORP
COMMENT OS Unidentified
PN JP 2001503973-A/24
PD 27-MAR-2001
PF 02-OCT-1997 JP 1998516839
PR 04-OCT-1996 US 60/027832,12-JUN-1997 US 08/873437 PI
ROGER A O'NEILL,JAR CAIN CHEN,CLAUDIA CHIESA,GEORGE FRY PC
C1201/68,C12N15/09,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..15
FT FT /organism='Unidentified'.
FEATURES
source 1..15
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 7.3%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1636 GGCCTTGTAGCAGAA 1650
|||||
Db 15 GCGATAGTAGCAGAA 1

RESULT 693
LOCUS AX687848 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 580 from Patent EP1281758.
ACCESSION AX687848
VERSION AX687848.1 GI:29410544
KEYWORDS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
SOURCE Shannon,M., Gu,Y. and Nguyen,C.T.
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 583 05-FEB-2003;

```

```

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 580 05-FEB-2003;
Aecomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 7.3%; Score 10.2; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1659 CCAGGCTCACAGCTG 1673
|||||
Db 3 CCAGGCATCCAGCTG 17

RESULT 694
LOCUS AX532453/c 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1962 from Patent EP1239051.
ACCESSION AX532453
VERSION AX532453.1 GI:25256680
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1962 11-SEP-2002;
Aecomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 7.3%; Score 10.2; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1732 TTGGCTCCCACTCC 1746
|||||
Db 16 TTGGACCCCATCTCC 2

RESULT 695
LOCUS AX687851 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 583 from Patent EP1281758.
ACCESSION AX687851
VERSION AX687851.1 GI:29410549
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 583 05-FEB-2003;

```

Qy

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 1 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/1
PD 02-JUL-2002
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
Location/Qualifiers
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 7.2%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1654 AAGCACCAGG 1663
|||||
Db 10 AAGCACCAGG 1
|||||

RESULT 701
BD161279/c
LOCUS BD161279 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161279
VERSION BD161279.1 GI:27867037
KEYWORDS JP 2002186482-A/101.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 101 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/101
PD 02-JUL-2002
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
Location/Qualifiers
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 7.2%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1654 AAGCACCAGG 1663
|||||
Db 10 AAGCACCAGG 1
|||||

RESULT 702
BD161279/c
LOCUS BD161279 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161279
VERSION BD161279.1 GI:27867037
KEYWORDS JP 2002186482-A/101.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 101 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/101
PD 02-JUL-2002
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
Location/Qualifiers
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 7.2%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1654 AAGCACCAGG 1663
|||||
Db 10 AAGCACCAGG 1
|||||

RESULT 703
BD161279/c
LOCUS BD161279 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161279
VERSION BD161279.1 GI:27867037
KEYWORDS JP 2002186482-A/101.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 101 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/101
PD 02-JUL-2002
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
Location/Qualifiers
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 7.2%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1654 AAGCACCAGG 1663
|||||
Db 10 AAGCACCAGG 1
|||||

```

```

AX471317/c
LOCUS AX471317 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 894 from Patent WO02053773.
ACCESSION AX471317
VERSION AX471317.1 GI:22206442
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 894 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
FT source 1..11
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'
Query Match 7.2%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1671 CTGGAACCCCT 1680
|||||
Db 11 CTGGAACCCCT 2
|||||

RESULT 703
AX471659
LOCUS AX471659 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1236 from Patent WO02053773.
ACCESSION AX471659
VERSION AX471659.1 GI:22206784
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1236 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
FT source 1..11
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'
Query Match 7.2%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1647 AGAGGCAAG 1656
|||||
Db 2 AGAGGCAAG 11
|||||

RESULT 704
AX471723/c
LOCUS AX471723 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1300 from Patent WO02053773.
ACCESSION AX471723
VERSION AX471723.1 GI:22206848
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1

```

```

AUTHORS      Hofmann,K., Conradt,M. and Petersohn,D.
TITLE        Method for determining skin stress or skin ageing in vitro
JOURNAL      HENKEL KGAA (DE)
FEATURES
  source      Location/Qualifiers
              1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      7.2%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1693 AGCGTGGTGG 1702
Db      10 AGCGTGGTGG 1

RESULT 705
AX622975/c
LOCUS      AX622975      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 16 from Patent WO02053774.
ACCESSION  AX622975
VERSION     AX622975.1 GI:28450916
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 16 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source      Location/Qualifiers
              1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      7.2%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1693 AGCGTGGTGG 1702
Db      10 AGCGTGGTGG 1

RESULT 706
AX624360/c
LOCUS      AX624360      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 1401 from Patent WO02053774.
ACCESSION  AX624360
VERSION     AX624360.1 GI:28452301
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 1401 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source      Location/Qualifiers
              1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      7.2%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1693 AGCGTGGTGG 1702
Db      10 AGCGTGGTGG 1

RESULT 707
AX625117
LOCUS      AX625117      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2158 from Patent WO02053774.
ACCESSION  AX625117
VERSION     AX625117.1 GI:28453058
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 2158 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source      Location/Qualifiers
              1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      7.2%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1648 GAAGGCAAGC 1657
Db      2 GAAGGCAAGC 11

RESULT 708
AX625409
LOCUS      AX625409      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2450 from Patent WO02053774.
ACCESSION  AX625409
VERSION     AX625409.1 GI:28453350
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 2450 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source      Location/Qualifiers
              1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      7.2%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1647 AGAAGGCAAG 1656
Db      2 AGAAGGCAAG 11

RESULT 709
AX625899
LOCUS      AX625899      11 bp      DNA      linear      PAT 21-FEB-2003

```

DEFINITION Sequence 2940 from Patent WO02053774.  
 ACCESSION AX625899  
 VERSION AX625899.1 GI:28453937  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.  
 TITLE Method for determining homeostasis of the skin  
 JOURNAL Patent: WO 02053774-A 2940 11-JUL-2002;  
 Henkel Kommanditgesellschaft auf Aktien (DE)  
 FEATURES  
 source  
 1. 11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 7.2%; Score 10; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1721 GGAGATGGAG 1730  
 Db 2 GGAGATGGAG 11  
 RESULT 710  
 AX626201/c  
 LOCUS AX626201 11 bp DNA linear PAT 21-FEB-2003  
 DEFINITION Sequence 3242 from Patent WO02053774.  
 ACCESSION AX626201  
 VERSION AX626201.1 GI:28454239  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.  
 TITLE Method for determining homeostasis of the skin  
 JOURNAL Patent: WO 02053774-A 3242 11-JUL-2002;  
 Henkel Kommanditgesellschaft auf Aktien (DE)  
 FEATURES  
 source  
 1. 11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 7.2%; Score 10; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1671 CTGGAACCT 1680  
 Db 11 CTGGAACCT 2  
 RESULT 711  
 AX626758  
 LOCUS AX626758 11 bp DNA linear PAT 21-FEB-2003  
 DEFINITION Sequence 3799 from Patent WO02053774.  
 ACCESSION AX626758  
 VERSION AX626758.1 GI:28454796  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.  
 TITLE Method for determining homeostasis of the skin

JOURNAL Patent: WO 02053774-A 3799 11-JUL-2002;  
 Henkel Kommanditgesellschaft auf Aktien (DE)  
 FEATURES  
 source  
 1. 11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 7.2%; Score 10; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1744 TCCTCCCTAT 1753  
 Db 2 TCCTCCCTAT 11  
 RESULT 712  
 AX627300  
 LOCUS AX627300 11 bp DNA linear PAT 21-FEB-2003  
 DEFINITION Sequence 4341 from Patent WO02053774.  
 ACCESSION AX627300  
 VERSION AX627300.1 GI:28455338  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.  
 TITLE Method for determining homeostasis of the skin  
 JOURNAL Patent: WO 02053774-A 4341 11-JUL-2002;  
 Henkel Kommanditgesellschaft auf Aktien (DE)  
 FEATURES  
 source  
 1. 11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 7.2%; Score 10; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1741 AACTCTCCC 1750  
 Db 2 AACTCTCCC 11  
 RESULT 713  
 AX627599/c  
 LOCUS AX627599 11 bp DNA linear PAT 21-FEB-2003  
 DEFINITION Sequence 4640 from Patent WO02053774.  
 ACCESSION AX627599  
 VERSION AX627599.1 GI:28455637  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Petersohn,D., Conrad,M. and Hofmann,K.  
 TITLE Method for determining homeostasis of the skin  
 JOURNAL Patent: WO 02053774-A 4640 11-JUL-2002;  
 Henkel Kommanditgesellschaft auf Aktien (DE)  
 FEATURES  
 source  
 1. 11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 Query Match 7.2%; Score 10; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTA 1752  
Db 11 CTCCTCCCTA 2

RESULT 714  
AX628274  
LOCUS AX628274 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 5315 from Patent WO02053774.  
ACCESSION AX628274  
VERSION AX628274.1 GI:28456312  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 5315 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 7.2%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1678 CCTGGTGCTC 1687  
Db 2 CCTGGTGCTC 11

RESULT 715  
AX629280  
LOCUS AX629280 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 6321 from Patent WO02053774.  
ACCESSION AX629280  
VERSION AX629280.1 GI:28457318  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 6321 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 7.2%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1667 ACAGCTGGAA 1676  
Db 2 ACAGCTGGAA 11

RESULT 716  
AX630396/c  
LOCUS AX630396 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 7437 from Patent WO02053774.  
ACCESSION AX630396

VERSION AX630396.1 GI:28458434  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 7437 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 7.2%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1693 AGCGTGTGG 1702  
Db 10 AGCGTGTGG 1

RESULT 717  
AX631781/c  
LOCUS AX631781 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 8823 from Patent WO02053774.  
ACCESSION AX631781  
VERSION AX631781.1 GI:28459888  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 8823 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source  
1. .11  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 7.2%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1669 AGCTGGAAC 1678  
Db 11 AGCTGGAAC 2

RESULT 718  
AX632538  
LOCUS AX632538 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 9580 from Patent WO02053774.  
ACCESSION AX632538  
VERSION AX632538.1 GI:28468153  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 9580 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)



```
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 GAAGGCAAGC 1657
|||||
Db 2 GAAGGCAAGC 11

RESULT 719
BD187463/c
LOCUS BD187463 11 bp RNA linear PAT 17-JUL-2003
DEFINITION A nucleic acid involving generation of presenilin-2 gene lacking
exon 5 type-aberrant splicing.
ACCESSION BD187463
VERSION BD187463.1 GI:32997202
KEYWORDS JP 2003018991-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 11)
Toyama,M., Imaizumi,K., Ikeda,Y., Katayama,T. and Manabe,T.
A nucleic acid involving generation of presenilin-2 gene lacking
exon 5 type-aberrant splicing
TITLE A nucleic acid involving generation of presenilin-2 gene lacking
JOURNAL Patent: JP 2003018991-A 2 21-JAN-2003;
Japan Science and Technology Corporation, Taisho Pharmaceutical Co
Ltd
COMMENT OS Artificial Sequence
PN JP 2003018991-A/2
PD 21-JAN-2003
PF 27-JUN-2001 JP 2001195472
PI masaya toyama,kazunori imaizumi,yoko ikeda,taichi katayama pi
takayuki manabe
CC Description of Artificial Sequence: a sequence for binding CC
region.
FH Key Location/Qualifiers.
FEATURES
source
1. .11
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1639 CTTGTAGCAG 1648
|||||
Db 11 CTTGTAGCAG 2

RESULT 720
BD189593/c
LOCUS BD189593 11 bp RNA linear PAT 17-JUL-2003
DEFINITION A nucleic acid involving generation of presenilin-2 gene lacking
exon 5 type-aberrant splicing.
ACCESSION BD189593
VERSION BD189593.1 GI:32999332
KEYWORDS WO 03002742-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 11)
Toyama,M., Katayama,T., Manabe,T., Kazunori, Imaizumi and Ikeda,Y.
A nucleic acid involving generation of presenilin-2 gene lacking
exon 5 type-aberrant splicing
TITLE A nucleic acid involving generation of presenilin-2 gene lacking
JOURNAL Patent: WO 03002742-A 2 09-JAN-2003;
Japan Science and Technology Corp, Taisho Pharmaceutical Co Ltd,
MASAYA TOYAMA,TAIICHI KATAYAMA,TAKAYUKI MANABE,KAZUNORI
IMAIZUMI,YOKO IKEDA
COMMENT OS Artificial Sequence
PN WO 03002146-A/2
PD 09-JAN-2003
PF 27-JUN-2002 WO 2002JP006461
PI MASAYA TOYAMA,TAIICHI KATAYAMA,TAKAYUKI MANABE,KAZUNORI PI
IMAIZUMI,YOKO IKEDA
PC A61K45/00,A61K48/00,A61P25/00,A61P25/16,A61P25/28,A61P43/00 CC
Description of Artificial Sequence: a sequence of binding CC
region
FH Key Location/Qualifiers
FT source 1. .11
/organism='Artificial Sequence'.
FEATURES
source
1. .11
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1639 CTTGTAGCAG 1648
|||||
```

```
JAPAN SCIENCE AND TECHNOLOGY CORP,TAISHO PHARMACEUTICAL CO LTD,
MASAYA TOYAMA,TAIICHI KATAYAMA,TAKAYUKI MANABE,KAZUNORI
IMAIZUMI,YOKO IKEDA
COMMENT OS Artificial Sequence
PN WO 03002742-A/2
PD 09-JAN-2003
PF 27-JUN-2002 WO 2002JP006462
PI MASAYA TOYAMA,TAIICHI KATAYAMA,TAKAYUKI MANABE,KAZUNORI PI
IMAIZUMI,YOKO IKEDA
PC C12N15/12,C12Q1/68,G01N33/50
CC Description of Artificial Sequence: a sequence of binding CC
region
FH Key Location/Qualifiers
FT source 1. .11
/organism='Artificial Sequence'.
FEATURES
source
1. .11
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1639 CTTGTAGCAG 1648
|||||
Db 11 CTTGTAGCAG 2

RESULT 721
BD190136/c
LOCUS BD190136 11 bp RNA linear PAT 17-JUL-2003
DEFINITION Pharmaceutical composition.
ACCESSION BD190136
VERSION BD190136.1 GI:32999875
KEYWORDS WO 03002146-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 11)
Toyama,M., Katayama,T., Manabe,T., Kazunori, Imaizumi and Ikeda,Y.
Pharmaceutical composition
TITLE Patent: WO 03002146-A 2 09-JAN-2003;
JAPAN SCIENCE AND TECHNOLOGY CORP,TAISHO PHARMACEUTICAL CO LTD,
MASAYA TOYAMA,TAIICHI KATAYAMA,TAKAYUKI MANABE,KAZUNORI
IMAIZUMI,YOKO IKEDA
COMMENT OS Artificial Sequence
PN WO 03002146-A/2
PD 09-JAN-2003
PF 27-JUN-2002 WO 2002JP006461
PI MASAYA TOYAMA,TAIICHI KATAYAMA,TAKAYUKI MANABE,KAZUNORI PI
IMAIZUMI,YOKO IKEDA
PC A61K45/00,A61K48/00,A61P25/00,A61P25/16,A61P25/28,A61P43/00 CC
Description of Artificial Sequence: a sequence of binding CC
region
FH Key Location/Qualifiers
FT source 1. .11
/organism='Artificial Sequence'.
FEATURES
source
1. .11
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1639 CTTGTAGCAG 1648
|||||
Db 11 CTTGTAGCAG 2
```

```

Db      11 CTTGTAGCAG 2

RESULT 722
AR030066
LOCUS      AR030066      12 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 255 from patent US 5861244.
ACCESSION AR030066
VERSION   AR030066.1 GI:5943280
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS   Wang, C.-G. and Hepburn, A.G.
TITLE     Genetic sequence assay using DNA triple strand formation
JOURNAL   Patent: US 5861244-A 255 19-JAN-1999;
FEATURES  Location/Qualifiers
            source
              1..12
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      7.2%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1747 TCCTATCCT 1756
        |||||
        1 TCCTATCCT 10

Db

RESULT 723
AR0303946/c
LOCUS      AR0303946      12 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 11 from patent US 6544755.
ACCESSION AR0303946
VERSION   AR0303946.1 GI:31692817
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS   Thompson, J.D. and Draper, K.G.
TITLE     Method and reagent for treatment of diseases by expression of the
JOURNAL   c-Myc gene
FEATURES  Patent: US 6544755-A 11 08-APR-2003;
            Location/Qualifiers
              source
                1..12
                  /organism="unknown"
                  /mol_type="genomic DNA"

Query Match      7.2%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1683 TGTCTCCTCC 1692
        |||||
        11 TGTCTCCTCC 2

Db

RESULT 724
A08720/c
LOCUS      A08720      14 bp      DNA      linear      PAT 09-AUG-1993
DEFINITION Nucleotide sequence 7 from patent number WO9010713.
ACCESSION A08720
VERSION   A08720.1 GI:411729
KEYWORDS
SOURCE    unidentified
ORGANISM  unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS
TITLE     METHOD FOR STABILIZING THE HYBRIDIZATION OF COMPLEMENTARY

POLYNUCLEOTIDE SEQUENCES
JOURNAL   Patent: WO 9010713-A 7 20-SEP-1990;
FEATURES  Location/Qualifiers
            source
              1..14
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match      7.2%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1634 TGGGGCTTGT 1643
        |||||
        13 TGGGGCTTGT 4

Db

RESULT 725
A08721
LOCUS      A08721      14 bp      DNA      linear      PAT 09-AUG-1993
DEFINITION reverse complement.
ACCESSION A08721
VERSION   A08721.1 GI:411730
KEYWORDS
SOURCE    unidentified
ORGANISM  unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS
TITLE     METHOD FOR STABILIZING THE HYBRIDIZATION OF COMPLEMENTARY
JOURNAL   POLYNUCLEOTIDE SEQUENCES
FEATURES  Patent: WO 9010713-A 8 20-SEP-1990;
            Location/Qualifiers
              source
                1..14
                  /organism="unidentified"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:32644"

Query Match      7.2%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1634 TGGGGCTTGT 1643
        |||||
        2 TGGGGCTTGT 11

Db

RESULT 726
E03997
LOCUS      E03997      14 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Allele-specific probe for the apolipoprotein E gene.
ACCESSION E03997
VERSION   E03997.1 GI:2172208
KEYWORDS  JP 1992320700-A/8.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS   Toyosato, M., Kosaka, T. and Mizuno, K.
TITLE     METHOD FOR TESTING APOLIPOPROTEIN E GENOTYPE AND PRIMER AND PROBE
JOURNAL   Patent: JP 1992320700-A 8 11-NOV-1992;
            NIPPON SHOJI KK
COMMENT   OS Artificial gene
            OC Artificial sequence; Genes.
            PN JP 1992320700-A/8
            PD 11-NOV-1992
            PF 17-APR-1991 JP 1991112435
            PI TOYOSATO MITSUYOSHI, KOSAKA TETSUYA, MIZUNO KOJI PC
            CI 201/68, C07H21/04, C12N15/10, C12N15/11, G01N33/50; CC
            CC strandedness: Single;
            CC topology: Linear;
            FH Key
            Location/Qualifiers

```

```

FH      allele      replace(6,'t')
FT      /note='epsilon 7 allele'.
FT      Location/Qualifiers
FEATURES
    source
        1..14
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match      7.2%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGC 1695
      |||||
Db 4 CTCCTCCAGC 13

RESULT 727
E04001/c
LOCUS      14 bp DNA linear PAT 29-SEP-1997
DEFINITION Allele-specific probe for the apolipoprotein E gene.
ACCESSION E04001
VERSION E04001.1 GI:2172212
KEYWORDS JP 1992320700-A/12.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 14)
AUTHORS      Toyosato,M., Kosaka T. and Mizuno,K.
TITLE      METHOD FOR TESTING APOLIPOPROTEIN E GENOTYPE AND PRIMER AND PROBE
JOURNAL      SUITABLE FOR ITS TESTING
PATENT      JP 1992320700-A 12 11-NOV-1992;
            NIPPON SHOJI KK
COMMENT      OS Artificial gene
            OC Artificial sequence; Genes.
            PN JP 1992320700-A/12
            PD 11-NOV-1992
            PF 17-APR-1991 JP 1991112435
            PI TOYOSATO MITSUYOSHI, KOSAKA TETSUYA, MIZUNO KOJI PC
            C1201/68.C07H21/04.C12N15/10.C12N15/11.G01N33/50; CC
            strandedness: Single;
            CC topology: Linear;
            FH Key
            FT Location/Qualifiers
FEATURES
    source
        1..14
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match      7.2%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGC 1695
      |||||
Db 11 CTCCTCCAGC 2

RESULT 728
I39737/c
LOCUS      14 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 10 from patent US 5616490.
ACCESSION I39737
VERSION I39737.1 GI:2084217
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 14)

AUTHORS      Sullivan,S.M. and Draper,K.G.
TITLE      Ribozymes targeted to TNF-.alpha. RNA
JOURNAL      Patent: US 5616490-A 10 01-APR-1997;
FEATURES      Location/Qualifiers
    source
        1..14
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match      7.2%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1693 AGCGTGGTGG 1702
      |||||
Db 10 AGCGTGGTGG 1

RESULT 729
AR055901/c
LOCUS      15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 105 from patent US 5837542.
ACCESSION AR055901
VERSION AR055901.1 GI:5981478
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
TITLE      Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL      Patent: US 5837542-A 105 17-NOV-1998;
FEATURES      Location/Qualifiers
    source
        1..15
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match      7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1670 GCTGGAACCC 1679
      |||||
Db 13 GCTGGAACCC 4

RESULT 730
AR055902/c
LOCUS      15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 106 from patent US 5837542.
ACCESSION AR055902
VERSION AR055902.1 GI:5981479
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
TITLE      Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL      Patent: US 5837542-A 106 17-NOV-1998;
FEATURES      Location/Qualifiers
    source
        1..15
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match      7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1670 GCTGGAACCC 1679
      |||||
Db 12 GCTGGAACCC 3

```

```

RESULT 731
AR113659/c
LOCUS AR113659 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 105 from patent US 6132967.
ACCESSION AR113659
VERSION AR113659.1 GI:14093981
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 105 17-OCT-2000;
FEATURES
source
    1. .15
    /organism="unknown"
    /mol_type="unassigned DNA"
Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1670 GCTGGAACCC 1679
Db 13 GCTGGAACCC 4

RESULT 732
AR113660/c
LOCUS AR113660 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 106 from patent US 6132967.
ACCESSION AR113660
VERSION AR113660.1 GI:14093982
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 106 17-OCT-2000;
FEATURES
source
    1. .15
    /organism="unknown"
    /mol_type="unassigned DNA"
Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1670 GCTGGAACCC 1679
Db 13 GCTGGAACCC 4

RESULT 733
AR116338
LOCUS AR116338 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 26 from patent US 6133031.
ACCESSION AR116338
VERSION AR116338.1 GI:14096660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)

```

```

AUTHORS Monia,B.P. and Jaarde,W.A.
TITLE Antisense inhibition of focal adhesion kinase expression
JOURNAL Patent: US 6133031-A 26 17-OCT-2000;
FEATURES
source
    1. .15
    /organism="unknown"
    /mol_type="unassigned DNA"
Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1645 GCAGAGGCCA 1634
Db 5 GCAGAGGCCA 14

RESULT 734
AX084987/c
LOCUS AX084987 15 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 164 from Patent WO0113117.
ACCESSION AX084987
VERSION AX084987.1 GI:13275135
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Herath,H.M.
TITLE Proteins, genes and their use for diagnosis and treatment of breast cancer
JOURNAL Patent: WO 0113:17-A 164 22-FEB-2001;
FEATURES
source
    1. .15
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Probe"
Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1659 CCAGGCTCAC 1668
Db 10 CCAGGCTCAC 1

RESULT 735
AX374605/c
LOCUS AX374605 15 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 26 from Patent WO0210454.
ACCESSION AX374605
VERSION AX374605.1 GI:19169502
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Choi,J.Y., Koshiy,B., Kliem,S. and Stephens,J.C.
TITLE Haplotypes of the alas2 gene
JOURNAL Patent: WO 0210454-A 26 07-FEB-2002;
FEATURES
source
    1. .15
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;

```

```
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1757 AAAGGCCACTG 1768
Db 14 RAAGGCCACTG 3
|||||
|||||

RESULT 736
AX632978/c
LOCUS AX632978 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 117 from Patent EP1260586.
ACCESSION AX632978
VERSION AX632978.1 GI:28468592
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Wolf,T.
Method and reagent for inhibiting the expression of disease related
Genes
Patent: EP 1260586-A 117 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
1. .15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1670 GCTGGAACCC 1679
Db 13 GCTGGAACCC 4
|||||
|||||

RESULT 737
AX632980/c
LOCUS AX632980 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 119 from Patent EP1260586.
ACCESSION AX632980
VERSION AX632980.1 GI:28468594
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Wolf,T.
Method and reagent for inhibiting the expression of disease related
Genes
Patent: EP 1260586-A 119 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
1. .15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1670 GCTGGAACCC 1679
```

```
Db 12 GCTGGAACCC 3
|||||
|||||

RESULT 738
AX763334/c
LOCUS AX763334 15 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 27 from Patent WO03039703.
ACCESSION AX763334
VERSION AX763334.1 GI:32257902
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Weizenegger,M.
Method in the form of a dry rapid test for detecting nucleic acids
Patent: WO 03039703-A 27 15-MAY-2003;
Hain Lifeschience GmbH (DE)
Location/Qualifiers
1. .15
/organism="Treponema denticola"
/mol_type="unassigned DNA"
/db_xref="taxon:158"

Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1749 CCTATCCTTAAG 1760
Db 12 CCTATCCTTAAG 1
|||||
|||||

RESULT 739
AX763665/c
LOCUS AX763665 15 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 26 from Patent WO03040388.
ACCESSION AX763665
VERSION AX763665.1 GI:32258032
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Treponema denticola
Treponema denticola
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
Weizenegger,M.
Method for detecting bacteria associated with parodontitis and
tooth decay
Patent: WO 03040388-A 26 15-MAY-2003;
Hain Lifeschience GmbH (DE)
Location/Qualifiers
1. .15
/organism="Treponema denticola"
/mol_type="unassigned DNA"
/db_xref="taxon:158"

Query Match 7.2%; Score 10; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1749 CCTATCCTTAAG 1760
Db 12 CCTATCCTTAAG 1
|||||
|||||

Search completed: August 30, 2004, 09:17:59
Job time : 3 secs
```



GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 09:20:29 ; Search time 1 Seconds

(without alignments)

5.663 Million cell updates/sec

Title: US-09-925-139-3

Perfect score: 139

Sequence: 1 ggatggggctgttagcagaa.....ctatcctaaggccactgg 139

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 0.5

Searched: 1315 seqs, 20372 residues

Total number of hits satisfying chosen parameters: 2630

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1332 summaries

Database : rng3.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	24.5	50	1	ABZ01904
C 2	21	15.1	21	1	AAI66686
C 3	20	14.4	20	1	ABT13031
C 4	20	14.4	20	1	ABX12200
C 5	20	14.4	20	1	ABX12198
C 6	20	14.4	20	1	ABX12217
C 7	20	14.4	20	1	ABX12175
C 8	20	14.4	20	1	ABX12219
C 9	20	14.4	20	1	ABX12220
C 10	20	14.4	20	1	ABX12199
C 11	20	14.4	20	1	ABX12218
C 12	18	12.9	18	1	AAI56642
C 13	17.2	12.4	22	1	AAI37644
C 14	17	12.2	17	1	AAI22550
C 15	16.8	12.1	21	1	AAI19829
C 16	16.4	11.8	20	1	ADH66783
C 17	16.2	11.7	22	1	AAV52705
C 18	15.6	11.2	24	1	ABZ57102
C 19	15.2	10.9	20	1	AAI24930
C 20	15.2	10.9	23	1	AAI30209
C 21	15	10.8	15	1	AAI49837
C 22	15	10.8	15	1	AAI49841
C 23	15	10.8	15	1	AAI49823
C 24	15	10.8	15	1	AAI49825
C 25	15	10.8	15	1	AAI49811
C 26	15	10.8	15	1	AAI49809
C 27	15	10.8	15	1	AAI49827
C 28	15	10.8	15	1	AAI49829
C 29	15	10.8	15	1	AAI49815
C 30	15	10.8	15	1	AAI49821
C 31	15	10.8	15	1	AAI49831
C 32	15	10.8	15	1	AAI49819
C 33	15	10.8	15	1	AAI49817

Human CETP HH ribo	1	10.8	15	1	AAI49833
Human CETP HH ribo	15	10.8	15	1	AAI49839
Human CETP HH ribo	15	10.8	15	1	AAI49813
Human CETP HH ribo	15	10.8	15	1	AAI49835
Human genotyping P	20	10.6	20	1	ABZ05987
Human oligonucleot	20	10.6	20	1	ABZ85226
Human dysterlin PC	21	10.5	21	1	AAI1514
Human dysterlin ex	21	10.5	21	1	AAI36969
Cyp-C probe genera	18	10.4	18	1	ABZ8444
S. albulus plasmid	20	10.4	20	1	ABV73609
Candida albicans G	20	10.4	20	1	ABZ31506
Capure oligonucle	20	10.4	20	1	ABZ31783
Human DISC1/DISC2	21	10.4	21	1	ABZ33591
Europium (III) tex	20	10.2	20	1	AAQ08079
Europium (III) tex	20	10.2	20	1	AAQ08080
Dysprosium (III) t	20	10.2	20	1	AAQ91455
Hepatitis B virus	20	10.2	20	1	AAQ81567
pi42, PCR primer u	20	10.2	20	1	AAQ81567
Oligonucleotide #4	20	10.2	20	1	AAV07290
Texaphyrin oligonu	20	10.2	20	1	AAV07037
Antisense primer f	20	10.2	20	1	AAV99212
Exemplary texaphyr	20	10.2	20	1	AAZ88439
Human diacylglycer	20	10.2	20	1	AAZ05958
Human RECQ2 antis	20	10.2	20	1	AAZ41746
Stabilising reagen	20	10.2	20	1	ADT23628
STB1877 amplifica	20	10.2	20	1	ACD13735
Antisense oligonu	20	10.2	20	1	ADB89990
Antisense oligo (S	20	10.2	20	1	ADB81543
Cosmid amplificati	20	10.2	20	1	ADB83449
Human VH PCR prime	21	10.2	21	1	ADD13897
Oct-4 transcript R	20	10.1	20	1	AAZ58421
Human C-raf target	17	9.9	17	1	AAV91006
Human C-raf target	17	9.9	17	1	AAV91005
HBV hammerhead rib	17	9.9	17	1	ACD50855
HBV amberzyme subs	17	9.9	17	1	ACD55655
HBV hammerhead rib	17	9.9	17	1	ACD50854
HBV G-cleaver subs	17	9.9	17	1	ACD53478
PCR primer for hum	18	9.9	18	1	AAZ28045
Tricyclic dextroca	19	9.9	19	1	ADE15603
PCR primer "A gamm	20	9.9	20	1	AAV26436
Human uteroglobin	20	9.9	20	1	AAZ65593
Probe for mechan	20	9.9	20	1	AAI78641
Human delta-6-des	20	9.9	20	1	AAI19416
CD34 cell marker D	20	9.9	20	1	AAZ22845
Human bifunctional	20	9.9	20	1	ABZ78257
Human oligonucleot	20	9.9	20	1	ABZ92121
Coryneform bacteri	20	9.9	20	1	ABX10128
Probe #1 used to i	20	9.9	20	1	AAZ5794
Human collapsin re	20	9.9	20	1	ADC66381
Human testosterone	21	9.9	21	1	AAA94234
Reverse PCR primer	21	9.9	21	1	AAZ57821
TRPM-2 antisense o	21	9.9	21	1	ACF36406
Sequence of PCR pr	20	9.8	20	1	AAQ46059
Primer derived fro	20	9.8	20	1	AAI42248
Plasminogen activa	20	9.8	20	1	AAI66085
L monocytogenes hl	20	9.8	20	1	AAV62008
PCR primer 82689,	20	9.8	20	1	AAZ22801
PCR primer used to	20	9.8	20	1	AAZ04070
Rat GAPDH primer 3	20	9.8	20	1	AAZ78426
GAPDH reverse prim	20	9.8	20	1	AAZ25929
Primer used to amp	20	9.8	20	1	AAZ97388
Primer used to amp	20	9.8	20	1	AAZ97331
Human biallelic ma	20	9.8	20	1	AAZ76046
SNP specific lower	20	9.8	20	1	AAH38150
Human telomeric re	20	9.8	20	1	AAH20719
Oligonucleotide hy	20	9.8	20	1	AAH80623
Glycerolaldehyde-3-p	20	9.8	20	1	ABN83384
Human oligonucleot	20	9.8	20	1	ABZ93876
Human PDB4C oligon	20	9.8	20	1	ABZ99199
Glycerolaldehyde-3-p	20	9.8	20	1	ABZ55740
HBV PRT antisense	20	9.8	20	1	ADD81514
HBV zinzyme substr	17	9.6	17	1	ACD53920
Murine oligonucleo	17	9.6	17	1	ACC64154

107	13.4	9.6	18	1	AA050940	T-cell antigen rec	180	12.8	9.2	18	1	AAA92609	Antisense oligonuc
108	13.4	9.6	18	1	ABL88809	HIV-1 related bind	c 181	12.8	9.2	19	1	AAV01272	Chromatypsinogen p
109	13.4	9.6	18	1	ACC83346	T7 forward PCR pri	c 182	12.8	9.2	19	1	BRCA1 exon 21 reve	BRCA1 exon 21 reve
110	13.4	9.6	18	1	ACF05396	Bacteriophage T7 f	183	12.8	9.2	19	1	AAV4507	Raf-1 PCR primer,
111	13.4	9.6	19	1	AA082923	cdk4 ribozyme bind	184	12.8	9.2	19	1	AAA07015	cdk3 ribozyme bind
112	13.4	9.6	19	1	AA051763	Primer to amplify	185	12.8	9.2	19	1	AA082742	Cell-cycle depende
113	13.4	9.6	19	1	AA058085	Cell-cycle depende	186	12.6	9.1	13	1	AA057904	Oligonucleotide SE
114	13.4	9.6	19	1	AA058085	Human chromosome 1	c 187	12.6	9.1	13	1	ABF35838	Oligonucleotide SE
115	13.4	9.6	19	1	ABL43426	Human chromosome 1	188	12.6	9.1	19	1	ABF35839	Spinoscerebellar at
116	13.4	9.6	19	1	ABL43434	Human chromosome 1	c 189	12.6	9.1	19	1	AA084806	Pathogenic filamen
117	13.4	9.6	20	1	AA060107	Human ATM gene exo	189	12.6	9.1	19	1	AA085482	Primer/probe #4 fo
118	13.4	9.6	20	1	AA060107	Human cytohesin-2	190	12.6	9.1	19	1	AA085482	Wheat microsatelli
119	13.4	9.6	20	1	AA060107	Human IFNGR2 antis	191	12.6	9.1	19	1	AA077561	Cyclin D1 ribozyme
120	13.4	9.6	20	1	AA060107	Collagen gene prom	192	12.6	9.1	19	1	AA085488	Cyclin D1 ribozyme
121	13.2	9.5	18	1	AA060107	Human leukocyte an	c 193	12.6	9.1	19	1	AA084289	Human biallelic ma
122	13.2	9.5	18	1	AA060107	Smad2 antisense ol	194	12.6	9.1	19	1	AA073322	Cyclin A1 ribozyme
123	13.2	9.5	18	1	AA060107	Collagen promoter	195	12.6	9.1	19	1	AA060650	Cyclin D1 ribozyme
124	13.2	9.5	18	1	AA060107	Antisense oligonuc	196	12.6	9.1	19	1	AA059451	Oligo 9, a PCR pri
125	13.2	9.5	18	1	AA060107	Antisense oligo, I	197	12.4	8.9	15	1	AA034483	PCR primer for amp
126	13.2	9.5	18	1	AA060107	Mouse WP-1 antisen	198	12.4	8.9	15	1	AA056245	B allele probe VP5
127	13.2	9.5	18	1	AA060107	Human chromosome 1	c 199	12.4	8.9	16	1	AA029808	Haemoglobin G gamm
128	13.2	9.5	18	1	AA060107	Human SRC-1 antise	c 200	12.4	8.9	16	1	AA070569	Alzheimer's diseas
129	13.2	9.5	19	1	AA060107	Dysprosium (III) t	201	12.4	8.9	16	1	AA067540	Human mitochondria
130	13.2	9.5	19	1	AA060107	Metallotexaphyrin-	202	12.4	8.9	16	1	ADD43463	B allele probe VP0
131	13.2	9.5	19	1	AA060107	Human tankyrase II	c 203	12.4	8.9	17	1	AA029806	Histocyte-secrete
132	13.2	9.5	19	1	AA060107	Human connexin 45	204	12.4	8.9	17	1	AA014821	Hammerhead ribozym
133	13.2	9.5	19	1	AA060107	Mitogen activated	c 205	12.4	8.9	17	1	AA029229	Hammerhead ribozym
134	13.2	9.5	19	1	AA060107	Mitogen activated	c 206	12.4	8.9	17	1	AA029230	APOE mutation corr
135	13.2	9.5	20	1	AA060107	A allele probe VP6	c 207	12.4	8.9	17	1	ABA80624	APOE mutation corr
136	13.2	9.5	20	1	AA060107	Primer amplifies p	c 208	12.4	8.9	17	1	ABA80625	HBV hammerhead rib
137	13.2	9.5	20	1	AA060107	Primer #4 for ente	c 209	12.4	8.9	17	1	ACD51040	Murine oligonucleo
138	13.2	9.5	20	1	AA060107	Calcium ion channe	c 210	12.4	8.9	17	1	ACC68047	Tumour suppression
139	13.2	9.5	20	1	AA060107	PCR primer used to	211	12.4	8.9	17	1	AD840159	Human AMLPia scann
140	13.2	9.5	20	1	AA060107	PI3K antisense inh	212	12.4	8.9	17	1	AD037715	Human AMLPia scann
141	13.2	9.5	20	1	AA060107	Mouse GAPDH PCR pr	c 213	12.4	8.9	17	1	AD037716	A allele probe VP6
142	13.2	9.5	20	1	AA060107	Primer JNF14 to is	c 214	12.4	8.9	18	1	AA029798	Collagen gene prom
143	13.2	9.5	20	1	AA060107	16S/23S rRNA spacer	c 215	12.4	8.9	18	1	AA060160	Collagen gene prom
144	13.2	9.5	20	1	AA060107	Human hepsin antis	c 216	12.4	8.9	18	1	AA060158	Collagen gene prom
145	13.2	9.5	20	1	AA060107	Human hepsin antis	c 217	12.4	8.9	18	1	AA070230	Human fit1 VEGF re
146	13.2	9.5	20	1	AA060107	Mouse C/EBP beta p	c 218	12.4	8.9	18	1	AA029823	Forward PCR primer
147	13.2	9.5	20	1	AA060107	Human oligonucleot	c 219	12.4	8.9	18	1	AA029823	Collagen promoter
148	13.2	9.5	20	1	AA060107	Kappa light chain	c 220	12.4	8.9	18	1	AA029823	Collagen promoter
149	13.2	9.5	20	1	AA060107	Human connective t	c 221	12.4	8.9	18	1	AA0298706	Collagen promoter
150	13.2	9.5	20	1	AA060107	Oligonucleotide SE	c 222	12.4	8.9	18	1	AA0298706	Collagen promoter
151	13.2	9.5	20	1	AA060107	Oligonucleotide SE	c 223	12.4	8.9	18	1	AA0298706	Collagen promoter
152	13.2	9.5	20	1	AA060107	Oligonucleotide SE	c 224	12.4	8.9	18	1	AA0298706	Collagen promoter
153	13.2	9.5	20	1	AA060107	Oligonucleotide SE	c 225	12.4	8.9	18	1	AA0298706	Collagen promoter
154	13.2	9.5	20	1	AA060107	Rabbit CERP HH rib	c 226	12.4	8.9	18	1	AA0298706	Collagen promoter
155	13.2	9.5	20	1	AA060107	HBV amebzyme subs	c 227	12.4	8.9	18	1	AA0298706	Collagen promoter
156	13.2	9.5	20	1	AA060107	Leptin gene-specif	c 228	12.4	8.9	18	1	AA0298706	Collagen promoter
157	13.2	9.5	20	1	AA060107	Human Oct-4 specif	c 229	12.4	8.9	18	1	AA0298706	Collagen promoter
158	13.2	9.5	20	1	AA060107	Human superoxide d	c 230	12.4	8.9	18	1	AA0298706	Collagen promoter
159	13.2	9.5	20	1	AA060107	Dysprosium (III) t	c 231	12.4	8.9	18	1	AA0298706	Collagen promoter
160	12.8	9.2	17	1	AA060107	Mouse flt-1 VEGF r	c 232	12.4	8.9	18	1	AA0298706	Collagen promoter
161	12.8	9.2	17	1	AA060107	Metallotexaphyrin-	c 233	12.4	8.9	18	1	AA0298706	Collagen promoter
162	12.8	9.2	17	1	AA060107	Human C-raf target	c 234	12.2	8.8	17	1	AA0298706	Collagen promoter
163	12.8	9.2	17	1	AA060107	Human B-raf subutr	c 235	12.2	8.8	17	1	AA0298706	Collagen promoter
164	12.8	9.2	17	1	AA060107	Human B-raf subutr	c 236	12.2	8.8	17	1	AA0298706	Collagen promoter
165	12.8	9.2	17	1	AA060107	Hspatitits B virus	c 237	12.2	8.8	17	1	AA0298706	Collagen promoter
166	12.8	9.2	17	1	AA060107	Human urokinase ge	c 238	12.2	8.8	17	1	AA0298706	Collagen promoter
167	12.8	9.2	17	1	AA060107	Human ERG G-cleave	c 239	12.2	8.8	17	1	AA0298706	Collagen promoter
168	12.8	9.2	17	1	AA060107	Human ERG hammerhe	c 240	12.2	8.8	17	1	AA0298706	Collagen promoter
169	12.8	9.2	17	1	AA060107	Human HLA genotypi	c 241	12.2	8.8	17	1	AA0298706	Collagen promoter
170	12.8	9.2	17	1	AA060107	Human tumour suppr	c 242	12.2	8.8	17	1	AA0298706	Collagen promoter
171	12.8	9.2	17	1	AA060107	HBV inozyme subutr	c 243	12.2	8.8	17	1	AA0298706	Collagen promoter
172	12.8	9.2	17	1	AA060107	HBV G-cleave subs	c 244	12.2	8.8	17	1	AA0298706	Collagen promoter
173	12.8	9.2	17	1	AA060107	Murine oligonucleo	c 245	12.2	8.8	17	1	AA0298706	Collagen promoter
174	12.8	9.2	17	1	AA060107	Human AMLPia scann	c 246	12.2	8.8	17	1	AA0298706	Collagen promoter
175	12.8	9.2	17	1	AA060107	Human AMLPia scann	c 247	12.2	8.8	17	1	AA0298706	Collagen promoter
176	12.8	9.2	17	1	AA060107	Oreochromis niloti	c 248	12.2	8.8	17	1	AA0298706	Collagen promoter
177	12.8	9.2	17	1	AA060107	Dysprosium (III) t	c 249	12.2	8.8	17	1	AA0298706	Collagen promoter
178	12.8	9.2	18	1	AA060107	Metallotexaphyrin-	c 250	12.2	8.8	17	1	AA0298706	Collagen promoter
179	12.8	9.2	18	1	AA060107	Antisense oligonuc	c 251	12.2	8.8	17	1	AA0298706	Collagen promoter
							c 252	12.2	8.8	17	1	AA0298706	Collagen promoter



C 253	12.2	8.8	17	1	ABT34389	Tumour suppression	C 326	11.8	8.5	15	1	AAV07304	Metallotexaphyrin-Primer KC155 used
C 254	12.2	8.8	17	1	ABT40165	Tumour suppression	C 327	11.8	8.5	15	1	AAV54266	Soluble sc-TCR fus
C 255	12.2	8.8	17	1	ACA07738	NFKB sub-unit modu	C 328	11.8	8.5	15	1	AAV55348	Human leukocyte an
C 256	12.2	8.8	17	1	ACA09103	NFKB sub-unit modu	C 329	11.8	8.5	15	1	AAV66971	IGFBP3 oligonucleo
C 257	12.2	8.8	17	1	ACA09103	NFKB sub-unit modu	C 330	11.8	8.5	15	1	AAV47176	IGFBP3 oligonucleo
C 258	12.2	8.8	17	1	ADA99593	Human MD23 scannin	C 331	11.8	8.5	15	1	AAV52890	IGFBP3 oligonucleo
C 259	12.2	8.8	17	1	ADA99410	Human MD23 scannin	C 332	11.8	8.5	15	1	AAV47174	IGFBP3 oligonucleo
C 260	12.2	8.8	17	1	AB265014	Human HER2 DNzyme	C 333	11.8	8.5	15	1	AAV52891	IGFBP3 oligonucleo
C 261	12.2	8.8	17	1	AD55654	HBV amberyze subs	C 334	11.8	8.5	15	1	AAV52891	IGFBP3 oligonucleo
C 262	12.2	8.8	17	1	AC671113	Murine oligonucleo	C 335	11.8	8.5	15	1	AAV52891	IGFBP3 oligonucleo
C 263	12.2	8.8	17	1	AD55651	Tumour suppression	C 336	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 264	12.2	8.8	17	1	AD55651	Tumour suppression	C 337	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 265	12.2	8.8	17	1	ADA30685	Cholesterol homeos	C 338	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 266	12.2	8.8	17	1	ADA92642	Antisense oligonuc	C 339	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 267	12.2	8.8	17	1	AAV61371	Amidophosphoribos	C 340	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 268	12.2	8.8	17	1	AAV35472	Immunoglobulin hea	C 341	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 269	12.2	8.8	17	1	AAV16095	PCR primer used in	C 342	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 270	12.2	8.8	17	1	AAV08683	Primer ATP/20RT fo	C 343	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 271	12.2	8.8	17	1	AAV24515	Human SR-BI gene e	C 344	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 272	12.2	8.8	17	1	AAV24607	Human SR-BI gene e	C 345	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 273	12.2	8.8	17	1	AAV38311	Human ATL regulato	C 346	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 274	12.2	8.8	17	1	AAV61311	Human ACE, AGT and	C 347	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 275	12.2	8.8	17	1	AAV61109	PCR primer SQ ID	C 348	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 276	12.2	8.8	17	1	AAV58358	Human PRO2145 reve	C 349	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 277	12.2	8.8	17	1	AAV75254	Human inducible NO	C 350	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 278	12.2	8.8	17	1	AAV14080	Forward PCR primer	C 351	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 279	12.2	8.8	17	1	AAV25354	Antisense oligonuc	C 352	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 280	12.2	8.8	17	1	AAV59542	Otoferlin exon PCR	C 353	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 281	12.2	8.8	17	1	AAV79532	Caspase-4 protease	C 354	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 282	12.2	8.8	17	1	ABZ80661	Magnaporthe grisea	C 355	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 283	12.2	8.8	17	1	ABZ8053	Human multidrug re	C 356	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 284	12.2	8.8	17	1	ABX10592	PCR primer, ZC22,1	C 357	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 285	12.2	8.8	17	1	ACD44968	Human SR-BI gene P	C 358	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 286	12.2	8.8	17	1	ABC24242	Human NOV1b revers	C 359	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 287	12.2	8.8	17	1	AD58350	ACLP06 polymorphis	C 360	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 288	12.2	8.8	17	1	AD578579	Endogenous caroten	C 361	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 289	12.2	8.8	17	1	AAI66686	Human CETP DNA rel	C 362	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 290	12.2	8.8	17	1	ABH93471	Oligonucleotide pr	C 363	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 291	12.2	8.8	17	1	ABH80452	Oligonucleotide pr	C 364	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 292	12.2	8.8	17	1	ABH12177	Oligonucleotide pr	C 365	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 293	12.2	8.8	17	1	ABC63273	Oligonucleotide SE	C 366	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 294	12.2	8.8	17	1	ABF24345	Oligonucleotide SE	C 367	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 295	12.2	8.8	17	1	ABH00388	Oligonucleotide SE	C 368	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 296	12.2	8.8	17	1	ABH00389	Oligonucleotide SE	C 369	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 297	12.2	8.8	17	1	ABH47625	Oligonucleotide SE	C 370	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 298	12.2	8.8	17	1	ABF95704	Oligonucleotide SE	C 371	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 299	12.2	8.8	17	1	ABC84321	Oligonucleotide SE	C 372	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 300	12.2	8.8	17	1	ABC05018	Oligonucleotide SE	C 373	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 301	12.2	8.8	17	1	ABC05019	Oligonucleotide SE	C 374	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 302	12.2	8.8	17	1	ABC63272	Oligonucleotide SE	C 375	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 303	12.2	8.8	17	1	ABF24344	Oligonucleotide SE	C 376	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 304	12.2	8.8	17	1	ABH47624	Oligonucleotide SE	C 377	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 305	12.2	8.8	17	1	ABF95705	Oligonucleotide SE	C 378	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 306	12.2	8.8	17	1	AAAD26061	Human apolipoprote	C 379	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 307	12.2	8.8	17	1	AAV98750	Colony stimulating	C 380	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 308	12.2	8.8	17	1	ABL52231	Human PHK22 allele	C 381	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 309	12.2	8.8	17	1	AAV44022	Human cytochrome P	C 382	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 310	12.2	8.8	17	1	AAV02799	Hammerhead ribozym	C 383	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 311	12.2	8.8	17	1	ABV90232	Human POSHL1 scann	C 384	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 312	12.2	8.8	17	1	ABV90236	Human POSHL1 scann	C 385	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 313	12.2	8.8	17	1	ABV90234	Human POSHL1 scann	C 386	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 314	12.2	8.8	17	1	ABV90235	Human POSHL1 scann	C 387	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 315	12.2	8.8	17	1	ABV90233	Human POSHL1 scann	C 388	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 316	12.2	8.8	17	1	ABV90237	Human POSHL1 scann	C 389	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 317	12.2	8.8	17	1	ACC64298	Murine oligonucleo	C 390	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 318	12.2	8.8	17	1	AAV82250	PCR primer for M.	C 391	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 319	12.2	8.8	17	1	AAV82250	Influenza virus PA	C 392	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 320	12.2	8.8	17	1	AAV46979	Bcl-Xl mRNA specif	C 393	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 321	12.2	8.8	17	1	ABZ10839	Haematopoietic cel	C 394	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 322	11.8	8.5	15	1	AAQ050548	Human chromosome 6	C 395	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 323	11.8	8.5	15	1	AAAT89133	Lutetium texaphyr	C 396	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 324	11.8	8.5	15	1	AAAT65005	Human chromosome 6	C 397	11.8	8.5	15	1	AAV99795	Human pPKF22 allel
C 325	11.8	8.5	15	1	AAAT98897	Probe 41w19 for HI	C 398	11.8	8.5	15	1	AAV99795	Human pPKF22 allel

C 399	11.8	8.5	17	1	ABZ64791	Human HER2 DNAzyme	472	11.4	8.2	13	1	ABC62590	Oligonucleotide SE
C 400	11.8	8.5	17	1	ACD62967	HCV minus strand D	473	11.4	8.2	13	1	ABF42171	Oligonucleotide SE
C 401	11.8	8.5	17	1	ACD52213	HBV inozyme substr	C 474	11.4	8.2	13	1	ABH33146	Oligonucleotide SE
C 402	11.8	8.5	17	1	ACD59647	HBV DNAzyme substr	C 475	11.4	8.2	13	1	ABF15452	Oligonucleotide SE
C 403	11.8	8.5	17	1	ACD62966	HCV minus strand D	C 476	11.4	8.2	13	1	ABF62159	Oligonucleotide SE
C 404	11.8	8.5	17	1	ACC65896	Murine oligonucleo	C 477	11.4	8.2	13	1	ABF49591	Oligonucleotide SE
C 405	11.8	8.5	17	1	ACC67445	Murine oligonucleo	C 478	11.4	8.2	13	1	ABC25065	Oligonucleotide SE
C 406	11.8	8.5	17	1	ACC63689	Murine oligonucleo	C 479	11.4	8.2	13	1	ABC08446	Oligonucleotide SE
C 407	11.8	8.5	17	1	ACC63888	Murine oligonucleo	C 480	11.4	8.2	13	1	ABC84786	Oligonucleotide SE
C 408	11.8	8.5	17	1	ABX04768	Thymidine kinase (	C 481	11.4	8.2	13	1	ABF10343	Oligonucleotide SE
C 409	11.8	8.5	17	1	ADC37712	Human AMLPLA scann	C 482	11.4	8.2	13	1	ABC62760	Oligonucleotide SE
C 410	11.8	8.5	18	1	AAQ20431	Debrisoquine polym	C 483	11.4	8.2	13	1	ABC38204	Oligonucleotide SE
C 411	11.8	8.5	18	1	AAQ05428	Primer B (Group 3,	C 484	11.4	8.2	13	1	ABF36186	Oligonucleotide SE
C 412	11.8	8.5	18	1	AAV49520	Mycobacterium sp.	C 485	11.4	8.2	13	1	ABF42170	Oligonucleotide SE
C 413	11.8	8.5	18	1	AAV49618	AlaDH derived olig	C 486	11.4	8.2	13	1	ABC26849	Oligonucleotide SE
C 414	11.8	8.5	18	1	AAV47637	Primer 1, located	C 487	11.4	8.2	13	1	ABC62591	Oligonucleotide SE
C 415	11.8	8.5	18	1	AAV60911	Angiogenin antisen	C 488	11.4	8.2	13	1	ABC65199	Oligonucleotide SE
C 416	11.8	8.5	18	1	AAV60919	Angiogenin sense o	C 489	11.4	8.2	13	1	ABC08447	Oligonucleotide SE
C 417	11.8	8.5	18	1	AAH86530	Primer rb21 used f	C 490	11.4	8.2	13	1	ABH57117	Oligonucleotide SE
C 418	11.8	8.5	18	1	AAH74957	PCR primer used to	C 491	11.4	8.2	13	1	ABC84686	Oligonucleotide SE
C 419	11.8	8.5	18	1	AAZ65415	Human CD71 phospho	C 492	11.4	8.2	13	1	ABC93116	Oligonucleotide SE
C 420	11.8	8.5	18	1	AAZ71696	Human biallelic ma	C 493	11.4	8.2	13	1	ABC25064	Oligonucleotide SE
C 421	11.8	8.5	18	1	AAH63106	Antisense oligonuc	C 494	11.4	8.2	13	1	ABF19170	Oligonucleotide SE
C 422	11.8	8.5	18	1	AAH84596	Probe and primer f	C 495	11.4	8.2	13	1	ABF19306	Oligonucleotide SE
C 423	11.8	8.5	18	1	AAH03672	PCR primer rb21, u	C 496	11.4	8.2	13	1	ABH33147	Oligonucleotide SE
C 424	11.8	8.5	18	1	ABZ72191	Gene 216 SSCP sequ	C 497	11.4	8.2	13	1	ABF19307	Oligonucleotide SE
C 425	11.8	8.5	18	1	ABH88792	HIV-1 related bind	C 498	11.4	8.2	13	1	ABF42169	Oligonucleotide SE
C 426	11.8	8.5	18	1	ABH88799	HIV-1 related bind	C 499	11.4	8.2	13	1	ABC93115	Oligonucleotide SE
C 427	11.8	8.5	18	1	ABA97098	Human cathepsin B	C 500	11.4	8.2	13	1	ABC23224	Oligonucleotide SE
C 428	11.8	8.5	18	1	ABJ44660	Human chromosome 1	C 501	11.4	8.2	13	1	ABC93113	Oligonucleotide SE
C 429	11.8	8.5	18	1	ABK94528	Human BRCA1 gene r	C 502	11.4	8.2	13	1	ABC84687	Oligonucleotide SE
C 430	11.8	8.5	18	1	ABH97959	Human urokinase ge	C 503	11.4	8.2	13	1	ABC38205	Oligonucleotide SE
C 431	11.8	8.5	18	1	ABH98011	Human urokinase ge	C 504	11.4	8.2	13	1	ABF36187	Oligonucleotide SE
C 432	11.8	8.5	18	1	ABJ30541	Human HLA genotypi	C 505	11.4	8.2	13	1	ABH57116	Oligonucleotide SE
C 433	11.8	8.5	18	1	ABZ76994	Bovine DGAT PCR pr	C 506	11.4	8.2	13	1	ABH62557	Oligonucleotide SE
C 434	11.8	8.5	18	1	ABX75044	Human gene 216 pol	C 507	11.4	8.2	14	1	AAQ74479	Primer based on pl
C 435	11.8	8.5	18	1	ABZ58715	Human HAM cDNA fra	C 508	11.4	8.2	15	1	AAQ74479	G. oxydans T100 L-
C 436	11.8	8.5	18	1	ADC59461	Human precutin PCR	C 509	11.4	8.2	15	1	AAQ080594	M.tuberculosis 16S
C 437	11.8	8.5	18	1	ADH13404	HLA class I allele	C 510	11.4	8.2	15	1	AAQ80594	Substrate for HH r
C 438	11.8	8.5	20	1	AAH78641	Probe for mechanic	C 511	11.4	8.2	15	1	AAZ62841	IGFBP3 oligonucleo
C 439	11.6	8.3	13	1	ABH66153	Oligonucleotide SE	C 512	11.4	8.2	15	1	AAZ47175	IGF-I oligonucleot
C 440	11.6	8.3	13	1	ABH66152	Oligonucleotide SE	C 513	11.4	8.2	15	1	AAZ51493	IGF-I oligonucleot
C 441	11.6	8.3	15	1	AAZ44834	H. annuus slidi hom	C 514	11.4	8.2	15	1	AAZ53421	IGF-I oligonucleot
C 442	11.6	8.3	15	1	ABN81456	Human HPA1P allele	C 515	11.4	8.2	15	1	AAZ53420	IGF-I oligonucleot
C 443	11.6	8.3	15	1	ABJ36320	Human lysosomal ac	C 516	11.4	8.2	15	1	AAZ53669	IGF-I oligonucleot
C 444	11.4	8.2	13	1	AAH06017	CFTR gene analysis	C 517	11.4	8.2	15	1	AAZ51495	IGF-I oligonucleot
C 445	11.4	8.2	13	1	ABC25859	Oligonucleotide SE	C 518	11.4	8.2	15	1	AAZ53670	IGF-I oligonucleot
C 446	11.4	8.2	13	1	ABC26848	Oligonucleotide SE	C 519	11.4	8.2	15	1	AAZ53671	IGF-I oligonucleot
C 447	11.4	8.2	13	1	ABF15453	Oligonucleotide SE	C 520	11.4	8.2	15	1	AAZ51494	IGF-I oligonucleot
C 448	11.4	8.2	13	1	ABC93112	Oligonucleotide SE	C 521	11.4	8.2	15	1	AAZ53419	Human KGNB1 gene a
C 449	11.4	8.2	13	1	ABC93117	Oligonucleotide SE	C 522	11.4	8.2	15	1	AAZ45302	Human GNRH2 gene p
C 450	11.4	8.2	13	1	ABC70351	Oligonucleotide SE	C 523	11.4	8.2	15	1	AAZ25425	Human PBR1 allele
C 451	11.4	8.2	13	1	ABC84787	Oligonucleotide SE	C 524	11.4	8.2	15	1	ABJ52104	Human AKR1B1 gene
C 452	11.4	8.2	13	1	ABF19171	Oligonucleotide SE	C 525	11.4	8.2	15	1	ABJ01115	ASO probe #1, used
C 453	11.4	8.2	13	1	ABC47949	Oligonucleotide SE	C 526	11.4	8.2	15	1	ABK12736	SCYA20 allele spec
C 454	11.4	8.2	13	1	ABC49590	Oligonucleotide SE	C 527	11.4	8.2	15	1	ABK81430	Human PKFB2 allele
C 455	11.4	8.2	13	1	ABF10345	Oligonucleotide SE	C 528	11.4	8.2	15	1	ABV99783	RDG1 gene allele-s
C 456	11.4	8.2	13	1	ABF16692	Oligonucleotide SE	C 529	11.4	8.2	15	1	ABK96301	Human APOA4 allele
C 457	11.4	8.2	13	1	ABF16653	Oligonucleotide SE	C 530	11.4	8.2	15	1	ABJ16721	Hepatitis C virus
C 458	11.4	8.2	13	1	ABC47948	Oligonucleotide SE	C 531	11.4	8.2	15	1	ABX00652	Hepatitis B virus
C 459	11.4	8.2	13	1	ABC23225	Oligonucleotide SE	C 532	11.4	8.2	15	1	ABK29978	Human GNRH2 gene p
C 460	11.4	8.2	13	1	ABC62761	Oligonucleotide SE	C 533	11.4	8.2	15	1	AAQ53520	B allele probe SN2
C 461	11.4	8.2	13	1	ABC65198	Oligonucleotide SE	C 534	11.4	8.2	16	1	AAQ29804	Hypervariable regi
C 462	11.4	8.2	13	1	ABF62158	Oligonucleotide SE	C 535	11.4	8.2	16	1	AAQ40622	LDLR mutation corr
C 463	11.4	8.2	13	1	ABF16693	Oligonucleotide SE	C 536	11.4	8.2	17	1	ABA81112	LDLR mutation corr
C 464	11.4	8.2	13	1	ABF16652	Oligonucleotide SE	C 537	11.4	8.2	17	1	ABA81113	Primer for human s
C 465	11.4	8.2	13	1	ABF42168	Oligonucleotide SE	C 538	11.4	8.2	17	1	AAQ77730	Human flt1 VEGF re
C 466	11.4	8.2	13	1	ABH62596	Oligonucleotide SE	C 539	11.4	8.2	17	1	AAZ70103	Human flt1 VEGF re
C 467	11.4	8.2	13	1	ABC93114	Oligonucleotide SE	C 540	11.4	8.2	17	1	AAZ70102	Granule bound star
C 468	11.4	8.2	13	1	ABC70350	Oligonucleotide SE	C 541	11.4	8.2	17	1	AAZ62178	Human EGF-R target
C 469	11.4	8.2	13	1	ABC25858	Oligonucleotide SE	C 542	11.4	8.2	17	1	AAV97519	Human TIE-2 subutr
C 470	11.4	8.2	13	1	ABF10342	Oligonucleotide SE	C 543	11.4	8.2	17	1	AAJ18625	Human TIE-2 subutr
C 471	11.4	8.2	13	1	ABF10344	Oligonucleotide SE	C 544	11.4	8.2	17	1	AAJ18519	Human TIE-2 subutr

C 545	11.4	8.2	17	1	RAV92465	Human A-Raf substr	C 618	11.2	8.1	17	1	ABZ65014	Human HER2 DNAzyme
C 546	11.4	8.2	17	1	AAV92632	Human A-Raf substr	619	11.2	8.1	17	1	ADA99592	Human MD23 scannin
C 547	11.4	8.2	17	1	AAV72307	Human blood bacter	C 620	11.2	8.1	17	1	AAQ29810	C allele probe VP1
C 548	11.4	8.2	17	1	AAA60267	Mouse HPC2 cDNA ex	621	11.2	8.1	17	1	AAQ29815	C allele probe VP4
C 549	11.4	8.2	17	1	AAF02259	Hammerhead ribozym	622	11.2	8.1	17	1	AAQ29814	C allele probe VP4
C 550	11.4	8.2	17	1	ABL46650	Human GRID NCH rib	C 623	11.2	8.1	17	1	AAQ29789	C allele probe VP1
C 551	11.4	8.2	17	1	ABL46649	Human GRID NCH rib	C 624	11.2	8.1	17	1	AAQ29812	C allele probe VP2
C 552	11.4	8.2	17	1	ABL46463	Human GRID hammerh	C 625	11.2	8.1	17	1	AAQ29788	C allele probe VP1
C 553	11.4	8.2	17	1	ABL46651	Human GRID NCH rib	C 626	11.2	8.1	17	1	AAQ29811	C allele probe VP1
C 554	11.4	8.2	17	1	ABL92148	Long human Tumour	C 627	11.2	8.1	17	1	AAQ66711	Primer to amplify
C 555	11.4	8.2	17	1	ABN07835	Human GDMLP-1 17-m	C 628	11.2	8.1	17	1	AAT53734	Rat ICAM hammerhea
C 556	11.4	8.2	17	1	ABN07836	Human GDMLP-1 17-m	C 629	11.2	8.1	17	1	AAT53501	Rat ICAM hammerhea
C 557	11.4	8.2	17	1	RA599002	Mouse prostate can	630	11.2	8.1	17	1	AAT60652	Antisense oligonuc
C 558	11.4	8.2	17	1	RAV78964	Human HTPL scannin	631	11.2	8.1	17	1	AAT70570	Haemoglobin G gamm
C 559	11.4	8.2	17	1	ABV79490	Human HTPL scannin	C 632	11.2	8.1	17	1	AA68727	Human flk-1 VEGF r
C 560	11.4	8.2	17	1	ABV79494	Human HTPL scannin	C 633	11.2	8.1	17	1	AA68727	Mouse flk-1 VEGF r
C 561	11.4	8.2	17	1	ABV79491	Human HTPL scannin	C 634	11.2	8.1	17	1	AA6872948	Mouse flk-1 VEGF r
C 562	11.4	8.2	17	1	ABV79492	Human HTPL scannin	C 635	11.2	8.1	17	1	AA6873306	Mouse flk-1 VEGF r
C 563	11.4	8.2	17	1	ABV79493	Human HTPL scannin	C 636	11.2	8.1	17	1	AA6873324	Human flk1 VEGF re
C 564	11.4	8.2	17	1	ABV78968	Human HTPL scannin	C 637	11.2	8.1	17	1	AA6873305	Mouse flk-1 VEGF r
C 565	11.4	8.2	17	1	ABV78963	Human HTPL scannin	638	11.2	8.1	17	1	AAT95345	Treatment of human
C 566	11.4	8.2	17	1	ABV78969	Human HTPL scannin	C 639	11.2	8.1	17	1	AAV14126	Probe HBPr42 for p
C 567	11.4	8.2	17	1	ABV91046	Human POSHL1 scann	C 640	11.2	8.1	17	1	AA6872812	Delta-9 desaturase
C 568	11.4	8.2	17	1	ABV90586	Human POSHL1 scann	C 641	11.2	8.1	17	1	AAV44920	Promoter molecule
C 569	11.4	8.2	17	1	ABV90585	Human POSHL1 scann	C 642	11.2	8.1	17	1	AAV97520	Human EGF-R target
C 570	11.4	8.2	17	1	ABV91045	Human POSHL1 scann	C 643	11.2	8.1	17	1	AAV97591	Human EGF-R target
C 571	11.4	8.2	17	1	ABV90583	Human POSHL1 scann	C 644	11.2	8.1	17	1	AAV49878	Myo-D E-box muscle
C 572	11.4	8.2	17	1	ABV90587	Human POSHL1 scann	C 645	11.2	8.1	17	1	AAV43831	Artificial promote
C 573	11.4	8.2	17	1	ABV90584	Human POSHL1 scann	C 646	11.2	8.1	17	1	AAV44681	Bromoctranphan-sp
C 574	11.4	8.2	17	1	ABL31671	Human HLA genotypi	C 647	11.2	8.1	17	1	AAV42344	E box nucleotide s
C 575	11.4	8.2	17	1	ABL31564	Human HLA genotypi	648	11.2	8.1	17	1	AAV80328	Phage lambda PCR p
C 576	11.4	8.2	17	1	ABX72073	Human tumour endot	C 649	11.2	8.1	17	1	AAA20626	Integrin alpha 6 s
C 577	11.4	8.2	17	1	ABZ69604	Human telomerase c	650	11.2	8.1	17	1	AAA18708	Human TIE-2 substr
C 578	11.4	8.2	17	1	ABT35614	Tumour suppression	C 651	11.2	8.1	17	1	AAA18921	Human TIE-2 substr
C 579	11.4	8.2	17	1	ABT36109	Tumour suppression	C 652	11.2	8.1	17	1	AAV91363	Human C-raf target
C 580	11.4	8.2	17	1	ABT38378	Tumour suppression	653	11.2	8.1	17	1	AAV92631	Human A-Raf substr
C 581	11.4	8.2	17	1	ACA06206	NFKB sub-unit modu	654	11.2	8.1	17	1	AAV91075	Human C-raf target
C 582	11.4	8.2	17	1	ACA06207	NFKB sub-unit modu	C 655	11.2	8.1	17	1	AA688523	Conus radiatus con
C 583	11.4	8.2	17	1	ACA07619	NFKB sub-unit modu	C 656	11.2	8.1	17	1	AA6832865	HBV pre-S gene pro
C 584	11.4	8.2	17	1	ACA08196	NFKB sub-unit modu	C 657	11.2	8.1	17	1	AA6876849	PCR primer for T66
C 585	11.4	8.2	17	1	ADB03601	Human MD27 scannin	C 658	11.2	8.1	17	1	AA6877880	HLH protein DNA bi
C 586	11.4	8.2	17	1	ADA99413	Human MD23 scannin	C 659	11.2	8.1	17	1	AA68723521	MyoD E box DNA mot
C 587	11.4	8.2	17	1	ADA99414	Human MD23 scannin	C 660	11.2	8.1	17	1	AA68724146	HLH protein E box
C 588	11.4	8.2	17	1	ADA99411	Human MD23 scannin	661	11.2	8.1	17	1	AA68729110	Antisense primer s
C 589	11.4	8.2	17	1	ADB03600	Human MD27 scannin	C 662	11.2	8.1	17	1	AA68728531	MyoD E-box muscle-
C 590	11.4	8.2	17	1	ADB03601	Human MD27 scannin	663	11.2	8.1	17	1	AA68747108	Rat AGRP mRNA PCR
C 591	11.4	8.2	17	1	ADB03603	Human MD27 scannin	664	11.2	8.1	17	1	AAA24961	Oestrogen receptor
C 592	11.4	8.2	17	1	ADA99412	Human MD23 scannin	C 665	11.2	8.1	17	1	AA6872991	Hammerhead ribozym
C 593	11.4	8.2	17	1	ADB03599	Human MD27 scannin	C 666	11.2	8.1	17	1	AA68701814	Hammerhead ribozym
C 594	11.4	8.2	17	1	ABZ65291	Human HER2 DNAzyme	C 667	11.2	8.1	17	1	ABK00575	Human NOGO Hammerh
C 595	11.4	8.2	17	1	ABZ65290	Human HER2 DNAzyme	C 668	11.2	8.1	17	1	ABK03212	Human CD20 Inozyme
C 596	11.4	8.2	17	1	ACD63408	HCV minus strand D	C 669	11.2	8.1	17	1	ABK03213	Human CD20 Inozyme
C 597	11.4	8.2	17	1	ACD55657	HBV amberyzyme subs	C 670	11.2	8.1	17	1	ABK02836	Human CD20 Hammerh
C 598	11.4	8.2	17	1	ACD59262	HCV DNAzyme subutr	C 671	11.2	8.1	17	1	ABK01445	Human NOGO Inozyme
C 599	11.4	8.2	17	1	ACD59261	HCV DNAzyme subutr	C 672	11.2	8.1	17	1	ABK02837	Human CD20 Hammerh
C 600	11.4	8.2	17	1	ACC66380	Murine oligonucleo	C 673	11.2	8.1	17	1	ABA78857	APC mutation corre
C 601	11.4	8.2	17	1	ACC66764	Murine oligonucleo	674	11.2	8.1	17	1	ABA78858	APC mutation corre
C 602	11.4	8.2	17	1	ABZ65290	LRP5 mutagenic PCR	C 675	11.2	8.1	17	1	AA6874608	Human endometrium
C 603	11.4	8.2	17	1	ADB42129	Tumour suppression	C 676	11.2	8.1	17	1	AA68716612	Gastric acid produ
C 604	11.4	8.2	17	1	ADB39940	Tumour suppression	C 677	11.2	8.1	17	1	ABL46487	Human GRID hammerh
C 605	11.4	8.2	17	1	ADB39941	Tumour suppression	C 678	11.2	8.1	17	1	ABL46970	Human GRID zinzyme
C 606	11.4	8.2	17	1	ADC37717	Human AMLP1a scann	C 679	11.2	8.1	17	1	ABL46776	Human GRID NCH rib
C 607	11.4	8.2	17	1	ADB44320	Tumour suppression	C 680	11.2	8.1	17	1	ABL46486	Human GRID hammerh
C 608	11.4	8.2	20	1	AA6876085	Plasminogen activa	681	11.2	8.1	17	1	ABL92165	Long human Tumour
C 609	11.2	8.1	16	1	AAQ29795	A allele probe VP5	682	11.2	8.1	17	1	ABN10216	Human GDMLP-1 17-m
C 610	11.2	8.1	16	1	AAQ29793	A allele probe VP5	683	11.2	8.1	17	1	ABN00537	Human GDMLP-1 17-m
C 611	11.2	8.1	16	1	AAQ52859	Cytomegalovirus ta	C 684	11.2	8.1	17	1	ABN01271	Human GDMLP-1 17-m
C 612	11.2	8.1	16	1	AAA74719	Mycobacterium BCG	C 685	11.2	8.1	17	1	ABN01293	Human GDMLP-1 17-m
C 613	11.2	8.1	16	1	AAA56873	Validation ribozym	C 686	11.2	8.1	17	1	ABN01293	Human GDMLP-1 17-m
C 614	11.2	8.1	16	1	AAI68609	ICAM-1 triple heli	C 687	11.2	8.1	17	1	ABN09665	Human GDMLP-1 17-m
C 615	11.2	8.1	16	1	ABZ34019	HIV-1 reverse tran	C 688	11.2	8.1	17	1	ABN01294	Human GDMLP-1 17-m
C 616	11.2	8.1	16	1	ADE14208	Optineurin promote	C 689	11.2	8.1	17	1	ABN01273	Human GDMLP-1 17-m
C 617	11.2	8.1	17	1	ADA99593	Human MD23 scannin	690	11.2	8.1	17	1	ABN07992	Human GDMLP-1 17-m

691	11.2	8.1	17	1	ABN07993	Human GDMPLP-1 17-m	764	11.2	8.1	17	1	ACD58497	HCV DNazyme substr
c 692	11.2	8.1	17	1	ABN09667	Human GDMPLP-1 17-m	765	11.2	8.1	17	1	ACD53921	HBV zinyzyme substr
693	11.2	8.1	17	1	ABN07840	Human GDMPLP-1 17-m	c 766	11.2	8.1	17	1	ACD55653	HBV amberzyme subs
694	11.2	8.1	17	1	ABQ63738	Human KTM1a porti	767	11.2	8.1	17	1	ACD51378	HBV hammerhead rib
695	11.2	8.1	17	1	ABQ63739	Human KTM1a porti	768	11.2	8.1	17	1	ACD57917	HCV DNazyme substr
696	11.2	8.1	17	1	ABK13146	Oligonucleotide us	769	11.2	8.1	17	1	ACD51053	HBV hammerhead rib
697	11.2	8.1	17	1	AAD42386	A. ochraceus il al	770	11.2	8.1	17	1	ACD64268	HCV minus strand D
698	11.2	8.1	17	1	ABK27291	Reduced linolenic	c 771	11.2	8.1	17	1	ACD64752	HCV minus strand D
c 699	11.2	8.1	17	1	ABK27292	Reduced linolenic	c 772	11.2	8.1	17	1	ACC67762	Murine oligonucleo
700	11.2	8.1	17	1	ABV79505	Human HTPL scannin	c 773	11.2	8.1	17	1	ACC64522	Murine oligonucleo
701	11.2	8.1	17	1	ABV79023	Human HTPL scannin	c 774	11.2	8.1	17	1	ACC66061	Murine oligonucleo
702	11.2	8.1	17	1	ABV79024	Human HTPL scannin	775	11.2	8.1	17	1	ACC67106	Murine oligonucleo
703	11.2	8.1	17	1	ABK19420	Human ERG Amberzym	c 776	11.2	8.1	17	1	ACC67588	Murine oligonucleo
704	11.2	8.1	17	1	ABK19419	Human ERG Amberzym	777	11.2	8.1	17	1	ACC65714	Murine oligonucleo
705	11.2	8.1	17	1	ABV90072	Human POSHL1 scann	c 778	11.2	8.1	17	1	ACC64616	Murine oligonucleo
706	11.2	8.1	17	1	ABV91247	Human POSHL1 scann	c 779	11.2	8.1	17	1	ACC64238	Murine oligonucleo
707	11.2	8.1	17	1	ABV90073	Human POSHL1 scann	780	11.2	8.1	17	1	ACC83620	Escherichia coli d
708	11.2	8.1	17	1	ABV90892	Human POSHL1 scann	c 781	11.2	8.1	17	1	ADB40118	Tumour suppression
709	11.2	8.1	17	1	ABV91245	Human POSHL1 scann	782	11.2	8.1	17	1	ADB40655	Tumour suppression
c 710	11.2	8.1	17	1	ABV91051	Human POSHL1 scann	783	11.2	8.1	17	1	ADB40250	Tumour suppression
c 711	11.2	8.1	17	1	ABV91071	Human POSHL1 scann	784	11.2	8.1	17	1	ADB39772	Tumour suppression
712	11.2	8.1	17	1	ABV91248	Human POSHL1 scann	c 785	11.2	8.1	17	1	ADC04842	Tumour suppression
713	11.2	8.1	17	1	ABV90896	Human POSHL1 scann	786	11.2	8.1	17	1	ADC04230	Human Na/H exchang
714	11.2	8.1	17	1	ABV90900	Human POSHL1 scann	787	11.2	8.1	17	1	ADC04229	Human Na/H exchang
c 715	11.2	8.1	17	1	ABV91072	Human POSHL1 scann	c 788	11.2	8.1	17	1	ADC04843	Human Na/H exchang
716	11.2	8.1	17	1	ABV91244	Human POSHL1 scann	c 789	11.2	8.1	17	1	ADB45742	Tumour suppression
717	11.2	8.1	17	1	ABV91246	Human POSHL1 scann	790	11.2	8.1	17	1	ADB45372	Tumour suppression
718	11.2	8.1	17	1	ABV91249	Human POSHL1 scann	c 791	11.2	8.1	17	1	ADB44858	Tumour suppression
719	11.2	8.1	17	1	ABV90898	Human POSHL1 scann	c 792	11.2	8.1	17	1	ADB48000	Human NOVX reverse
720	11.2	8.1	17	1	ABL30789	Human HLA genotyp1	c 793	11.2	8.1	18	1	AAA92575	Antisense oligonuc
c 721	11.2	8.1	17	1	ABL31672	Human HLA genotyp1	c 794	11.2	8.1	19	1	AC58274	Human PRO212 rever
722	11.2	8.1	17	1	ABK56128	Human CLC1A1 gene e	c 795	11.2	8.1	20	1	ADB66783	Human E2A-Pbx1 ant
723	11.2	8.1	17	1	ABK56803	Human CLC1A1 gene e	796	11	7.9	11	1	ABV69782	Human skin EST 756
c 724	11.2	8.1	17	1	ACA61316	Human cytochrome p	797	11	7.9	11	1	ABV62361	Human skin EST 147
725	11.2	8.1	17	1	ACA61317	Human cytochrome p	798	11	7.9	12	1	ABV08693	Oligonucleotide pr
726	11.2	8.1	17	1	ACC52643	Human tumour suppr	c 799	11	7.9	12	1	AB158915	Oligonucleotide pr
727	11.2	8.1	17	1	ACC52645	Human tumour suppr	800	11	7.9	12	1	AB101113	Oligonucleotide pr
728	11.2	8.1	17	1	ACC51350	Human tumour suppr	801	11	7.9	12	1	AB153626	Oligonucleotide pr
729	11.2	8.1	17	1	ACC52642	Human tumour suppr	c 802	11	7.9	12	1	AB165852	Oligonucleotide pr
c 730	11.2	8.1	17	1	ACC51413	Human tumour suppr	c 803	11	7.9	12	1	AB133606	Oligonucleotide pr
731	11.2	8.1	17	1	ABX72090	Human tumour endot	c 804	11	7.9	12	1	AB181002	Oligonucleotide pr
732	11.2	8.1	17	1	ABT40040	Tumour suppression	805	11	7.9	12	1	AB168036	Oligonucleotide pr
c 733	11.2	8.1	17	1	ABT34526	Tumour suppression	806	11	7.9	12	1	AB159814	Oligonucleotide pr
c 734	11.2	8.1	17	1	ABT37658	Tumour suppression	c 807	11	7.9	12	1	AB177791	Oligonucleotide pr
c 735	11.2	8.1	17	1	ABT38730	Tumour suppression	808	11	7.9	12	1	ABH98049	Oligonucleotide pr
c 736	11.2	8.1	17	1	ABT37668	Tumour suppression	809	11	7.9	12	1	ABH74564	Oligonucleotide pr
737	11.2	8.1	17	1	ABT37550	Tumour suppression	810	11	7.9	12	1	AB140118	Oligonucleotide pr
c 738	11.2	8.1	17	1	ABT40013	Tumour suppression	811	11	7.9	13	1	ABC37623	Oligonucleotide SE
c 739	11.2	8.1	17	1	ACA09101	NFKB sub-unit modu	812	11	7.9	13	1	ABF98563	Oligonucleotide SE
740	11.2	8.1	17	1	ACA06383	NFKB sub-unit modu	813	11	7.9	13	1	ABH01585	Oligonucleotide SE
c 741	11.2	8.1	17	1	ACA09104	NFKB sub-unit modu	c 814	11	7.9	13	1	ABH30529	Oligonucleotide SE
742	11.2	8.1	17	1	ACA06384	NFKB sub-unit modu	815	11	7.9	13	1	ABC21702	Oligonucleotide SE
c 743	11.2	8.1	17	1	ADB04487	Human MDZ7 scannin	816	11	7.9	13	1	ABF22699	Oligonucleotide SE
c 744	11.2	8.1	17	1	ADA99556	Human MDZ3 scannin	c 817	11	7.9	13	1	ABF28976	Oligonucleotide SE
c 745	11.2	8.1	17	1	ADB04488	Human MDZ7 scannin	c 818	11	7.9	13	1	ABH01584	Oligonucleotide SE
c 746	11.2	8.1	17	1	ADA99485	Human MDZ3 scannin	c 819	11	7.9	13	1	ABH31314	Oligonucleotide SE
747	11.2	8.1	17	1	ADB03481	Human MDZ7 scannin	820	11	7.9	13	1	ABH08492	Oligonucleotide SE
c 748	11.2	8.1	17	1	ADA99486	Human MDZ3 scannin	821	11	7.9	13	1	ABH22016	Oligonucleotide SE
749	11.2	8.1	17	1	ADB03480	Human MDZ7 scannin	c 822	11	7.9	13	1	ABH35639	Oligonucleotide SE
c 750	11.2	8.1	17	1	ADA99594	Human MDZ3 scannin	823	11	7.9	13	1	ABF86040	Oligonucleotide SE
c 751	11.2	8.1	17	1	ADA99555	Human MDZ3 scannin	c 824	11	7.9	13	1	ABF86041	Oligonucleotide SE
752	11.2	8.1	17	1	ADA99409	Human MDZ3 scannin	825	11	7.9	13	1	ABC82521	Oligonucleotide SE
c 753	11.2	8.1	17	1	AB261824	Human H-Ras DNazym	826	11	7.9	13	1	ABF35842	Oligonucleotide SE
c 754	11.2	8.1	17	1	AB264589	Human HER2 DNazyme	827	11	7.9	13	1	ABH30528	Oligonucleotide SE
c 755	11.2	8.1	17	1	ABZ60463	Human K-Ras DNazym	828	11	7.9	13	1	ABH31315	Oligonucleotide SE
756	11.2	8.1	17	1	ABZ65103	Human HER2 DNazyme	c 829	11	7.9	13	1	ABC82520	Oligonucleotide SE
757	11.2	8.1	17	1	ABZ65446	Human HER2 DNazyme	c 830	11	7.9	13	1	ABF15181	Oligonucleotide SE
c 758	11.2	8.1	17	1	ABZ60977	Human K-Ras DNazym	831	11	7.9	13	1	ABC33136	Oligonucleotide SE
c 759	11.2	8.1	17	1	ACD64172	HCV minus strand D	832	11	7.9	13	1	ABF15180	Oligonucleotide SE
760	11.2	8.1	17	1	ACD56568	HBV amberzyme subs	c 833	11	7.9	13	1	ABF35843	Oligonucleotide SE
c 761	11.2	8.1	17	1	ACD58401	HCV DNazyme substr	c 834	11	7.9	13	1	ABF46427	Oligonucleotide SE
762	11.2	8.1	17	1	ACD51379	HBV hammerhead rib	c 835	11	7.9	13	1	ABH05407	Oligonucleotide SE
763	11.2	8.1	17	1	ACD55659	HBV amberzyme subs	836	11	7.9	13	1	ABH35638	Oligonucleotide SE

C 837	11	7.9	13	1	ABC46634	Oligonucleotide SE	C 910	10.8	7.8	15	1	AAF51599	IGF-I oligonucleot
C 838	11	7.9	13	1	ABC21703	Oligonucleotide SE	C 911	10.8	7.8	15	1	AAF47177	IGFBP3 oligonucleo
C 839	11	7.9	13	1	ABC37622	Oligonucleotide SE	C 912	10.8	7.8	15	1	AAF51266	IGF-I oligonucleot
C 840	11	7.9	13	1	ABF35840	Oligonucleotide SE	C 913	10.8	7.8	15	1	AAF47173	IGFBP3 oligonucleo
C 841	11	7.9	13	1	ABH08493	Oligonucleotide SE	C 914	10.8	7.8	15	1	AAF51501	IGF-I oligonucleot
C 842	11	7.9	13	1	ABC61029	Oligonucleotide SE	C 915	10.8	7.8	15	1	AAF45992	IGFBP2 oligonucleo
C 843	11	7.9	13	1	ABH19250	Oligonucleotide SE	C 916	10.8	7.8	15	1	AAF51598	IGF-I oligonucleot
C 844	11	7.9	13	1	ABH21128	Oligonucleotide SE	C 917	10.8	7.8	15	1	AAF51268	IGF-I oligonucleot
C 845	11	7.9	13	1	ABF98562	Oligonucleotide SE	C 918	10.8	7.8	15	1	AAF51502	IGF-I oligonucleot
C 846	11	7.9	13	1	ABF84271	Oligonucleotide SE	C 919	10.8	7.8	15	1	AAF51269	IGF-I oligonucleot
C 847	11	7.9	13	1	ABF46426	Oligonucleotide SE	C 920	10.8	7.8	15	1	AAF69956	Human TNFRSF11B ge
C 848	11	7.9	13	1	ABF15421	Oligonucleotide SE	C 921	10.8	7.8	15	1	AAF69487	Human ILARalpha ge
C 849	11	7.9	13	1	ABH21129	Oligonucleotide SE	C 922	10.8	7.8	15	1	AAH49214	Anti-c-Ha-ras olig
C 850	11	7.9	13	1	ABH05406	Oligonucleotide SE	C 923	10.8	7.8	15	1	ABL01599	c-Ha-ras targeted
C 851	11	7.9	13	1	ABC33137	Oligonucleotide SE	C 924	10.8	7.8	15	1	ABA97499	c-Ha-ras targeted
C 852	11	7.9	13	1	ABF84270	Oligonucleotide SE	C 925	10.8	7.8	15	1	ABS97484	Human epoxide hydr
C 853	11	7.9	13	1	ABC61028	Oligonucleotide SE	C 926	10.8	7.8	15	1	AAI46735	c-Ha-ras antisense
C 854	11	7.9	13	1	ABF22698	Oligonucleotide SE	C 927	10.8	7.8	15	1	ACD82348	Nucleic acid cloni
C 855	11	7.9	13	1	ABF35841	Oligonucleotide SE	C 928	10.8	7.8	15	1	ADC84126	Human papillomavir
C 856	11	7.9	13	1	ABC46635	Oligonucleotide SE	C 929	10.8	7.8	15	1	AAQ29796	A allele probe VP6
C 857	11	7.9	13	1	ABF28977	Oligonucleotide SE	C 930	10.8	7.8	16	1	AAQ29791	A allele probe VP4
C 858	11	7.9	13	1	ABF15420	Oligonucleotide SE	C 931	10.8	7.8	16	1	AAQ29787	A allele probe RS2
C 859	11	7.9	13	1	ABH19251	Oligonucleotide SE	C 932	10.8	7.8	16	1	AAQ29809	C allele probe RS3
C 860	11	7.9	13	1	ABH22017	Oligonucleotide SE	C 933	10.8	7.8	16	1	AAQ29809	Rat ICAM hairpin r
C 861	11	7.9	14	1	AAF22395	Oligonucleotide pr	C 934	10.8	7.8	16	1	AAT53422	Haemoglobin G gamm
C 862	11	7.9	15	1	AAV31919	Peptide nucleic ac	C 935	10.8	7.8	16	1	AAT70568	FMR2 gene exon 11-
C 863	11	7.9	15	1	AAV31800	Transcript tag seq	C 936	10.8	7.8	16	1	AAT85750	p53 exon 7 PCR pri
C 864	11	7.9	15	1	AAV31164	Tag sequence of a	C 937	10.8	7.8	16	1	AAZ09804	HIV-1 protease gen
C 865	11	7.9	15	1	AAI67293	Human FKBP8 allele	C 938	10.8	7.8	16	1	AAZ97659	SNP containing pro
C 866	11	7.9	15	1	AAF50722	IGF-I oligonucleot	C 939	10.8	7.8	16	1	AAS06834	Human ribosomal pr
C 867	11	7.9	15	1	AAF50724	IGF-I oligonucleot	C 940	10.8	7.8	16	1	ABL46301	RNA binding peptid
C 868	11	7.9	15	1	AAF50721	IGF-I oligonucleot	C 941	10.8	7.8	16	1	AAA92609	Antisense oligonuc
C 869	11	7.9	15	1	AAF50725	IGF-I oligonucleot	C 942	10.6	7.6	15	1	ABN81420	Human HTARIP allel
C 870	11	7.9	15	1	AAF50723	IGF-I oligonucleot	C 943	10.6	7.6	15	1	ABN80551	Human P450(cytochr
C 871	11	7.9	15	1	AAV98658	Colony stimulating	C 944	10.6	7.6	17	1	ACD55655	HBV amberyzyme subs
C 872	11	7.9	15	1	ABK92567	ASO primer #4 to d	C 945	10.6	7.6	17	1	ABV91247	Human POSHL1 scann
C 873	11	7.9	15	1	ABK92619	ASO primer #17 to	C 946	10.6	7.6	17	1	ABV91248	Human POSHL1 scann
C 874	11	7.9	15	1	ABK32117	Human colon cancer	C 947	10.4	7.5	12	1	AAV28522	Blackcurrant rever
C 875	11	7.9	15	1	ABK32754	Human colorectal a	C 948	10.4	7.5	12	1	ABH71060	Oligonucleotide pr
C 876	11	7.9	15	1	AAI39485	CCBP2 detecting AS	C 949	10.4	7.5	12	1	ABH84710	Oligonucleotide pr
C 877	11	7.9	16	1	AAQ89557	Rat CYP7 gene ster	C 950	10.4	7.5	12	1	ABH13903	Oligonucleotide pr
C 878	11	7.9	16	1	AAV9026	Human SAPI40 exon	C 951	10.4	7.5	12	1	ABH71789	Oligonucleotide pr
C 879	10.8	7.8	14	1	AAQ74120	Platelet derived g	C 952	10.4	7.5	12	1	ABI22425	Oligonucleotide pr
C 880	10.8	7.8	14	1	AAV98896	Probe 4lw18 for HI	C 953	10.4	7.5	12	1	ABI24271	Oligonucleotide pr
C 881	10.8	7.8	14	1	AAV55199	Multiple antisense	C 954	10.4	7.5	12	1	ABH77659	Oligonucleotide pr
C 882	10.8	7.8	14	1	AAI14792	Triple helix formi	C 955	10.4	7.5	12	1	ABI03913	Oligonucleotide pr
C 883	10.8	7.8	14	1	AAA34646	Human adenosine re	C 956	10.4	7.5	12	1	ABI16026	Oligonucleotide pr
C 884	10.8	7.8	14	1	AAF20768	Human multiple tar	C 957	10.4	7.5	12	1	ABI71584	Oligonucleotide pr
C 885	10.8	7.8	14	1	AAF21471	Human multiple tar	C 958	10.4	7.5	12	1	ABI73215	Oligonucleotide pr
C 886	10.8	7.8	14	1	ABZ96462	Human nucleic acid	C 959	10.4	7.5	12	1	ABI18149	Oligonucleotide pr
C 887	10.8	7.8	14	1	ABZ97165	Human MTA oligonuc	C 960	10.4	7.5	12	1	ABH72659	Oligonucleotide pr
C 888	10.8	7.8	15	1	AAQ22446	Probe (6) for DNA	C 961	10.4	7.5	12	1	ABI02394	Oligonucleotide pr
C 889	10.8	7.8	15	1	AAQ45774	Human prostate tra	C 962	10.4	7.5	12	1	ABI07435	Oligonucleotide pr
C 890	10.8	7.8	15	1	AAQ88720	c-Ha-ras modified	C 963	10.4	7.5	12	1	ABI13369	Oligonucleotide pr
C 891	10.8	7.8	15	1	AAV56203	Mouse TNF-a hammer	C 964	10.4	7.5	12	1	ABI16174	Oligonucleotide pr
C 892	10.8	7.8	15	1	AAQ97685	Biotinylated antic	C 965	10.4	7.5	12	1	ABI41618	Oligonucleotide pr
C 893	10.8	7.8	15	1	AAAT4432	Antisense oligonuc	C 966	10.4	7.5	12	1	ABI46964	Oligonucleotide pr
C 894	10.8	7.8	15	1	AAAT44237	c-Ha-ras antisense	C 967	10.4	7.5	12	1	ABI18906	Oligonucleotide pr
C 895	10.8	7.8	15	1	AAV33907	c-Ha-ras expressio	C 968	10.4	7.5	12	1	ABI08058	Oligonucleotide pr
C 896	10.8	7.8	15	1	AAT14843	Human prostatic tr	C 969	10.4	7.5	12	1	ABI46421	Oligonucleotide pr
C 897	10.8	7.8	15	1	AAV66553	Human CD40 hammerh	C 970	10.4	7.5	12	1	ABI50037	Oligonucleotide pr
C 898	10.8	7.8	15	1	AAV24191	Phosphononoester	C 971	10.4	7.5	12	1	ABI55710	Oligonucleotide pr
C 899	10.8	7.8	15	1	AAT50231	Rabbit CTRP HH rib	C 972	10.4	7.5	12	1	ABI66750	Oligonucleotide pr
C 900	10.8	7.8	15	1	AAT50229	Rabbit CTRP HH rib	C 973	10.4	7.5	12	1	ABI30472	Oligonucleotide pr
C 901	10.8	7.8	15	1	AAV48892	c-fos gene antisen	C 974	10.4	7.5	12	1	ABI07173	Oligonucleotide pr
C 902	10.8	7.8	15	1	AAZ10279	Primer ZC4048 used	C 975	10.4	7.5	12	1	ABI13408	Oligonucleotide pr
C 903	10.8	7.8	15	1	AAV60907	Anti-c-Ha-ras olig	C 976	10.4	7.5	12	1	ABH92015	Oligonucleotide pr
C 904	10.8	7.8	15	1	AAV04348	Human DAXX DNA all	C 977	10.4	7.5	12	1	ABI18788	Oligonucleotide pr
C 905	10.8	7.8	15	1	AAV04346	Human DAXX DNA all	C 978	10.4	7.5	12	1	ABH94245	Oligonucleotide pr
C 906	10.8	7.8	15	1	AAV51267	IGF-I oligonucleot	C 979	10.4	7.5	12	1	ABH73848	Oligonucleotide pr
C 907	10.8	7.8	15	1	AAV52888	IGF-I oligonucleot	C 980	10.4	7.5	12	1	ABI03256	Oligonucleotide pr
C 908	10.8	7.8	15	1	AAV45991	IGFBP2 oligonucleo	C 981	10.4	7.5	12	1	ABI11679	Oligonucleotide pr
C 909	10.8	7.8	15	1	AAV52892	IGF-I oligonucleot	C 982	10.4	7.5	12	1	ABI66422	Oligonucleotide pr

983	10.4	7.5	12	1	AB118936	Oligonucleotide pr	1056	10.4	7.5	13	1	ABR46002	Oligonucleotide SE
c 984	10.4	7.5	12	1	AB125117	Oligonucleotide pr	1057	10.4	7.5	13	1	ABR55622	Oligonucleotide SE
c 985	10.4	7.5	12	1	AB100532	Oligonucleotide pr	c1058	10.4	7.5	13	1	ABH47623	Oligonucleotide SE
c 986	10.4	7.5	12	1	AB103600	Oligonucleotide pr	c1059	10.4	7.5	13	1	ABC69427	Oligonucleotide SE
987	10.4	7.5	12	1	AB106503	Oligonucleotide pr	c1060	10.4	7.5	13	1	ABC00339	Oligonucleotide SE
988	10.4	7.5	12	1	ABH85010	Oligonucleotide pr	c1061	10.4	7.5	13	1	ABC31788	Oligonucleotide SE
c 989	10.4	7.5	12	1	ABH87531	Oligonucleotide pr	c1062	10.4	7.5	13	1	ABC31801	Oligonucleotide SE
990	10.4	7.5	12	1	AB151466	Oligonucleotide pr	c1063	10.4	7.5	13	1	ABC31809	Oligonucleotide SE
991	10.4	7.5	12	1	AB168217	Oligonucleotide pr	c1064	10.4	7.5	13	1	ABC11715	Oligonucleotide SE
992	10.4	7.5	12	1	AB169091	Oligonucleotide pr	c1065	10.4	7.5	13	1	ABF20795	Oligonucleotide SE
993	10.4	7.5	12	1	ABR95646	Oligonucleotide pr	c1066	10.4	7.5	13	1	ABF24349	Oligonucleotide SE
c 994	10.4	7.5	12	1	AB1000799	Oligonucleotide pr	c1067	10.4	7.5	13	1	ABF25383	Oligonucleotide SE
995	10.4	7.5	12	1	AB116484	Oligonucleotide pr	c1068	10.4	7.5	13	1	ABF43730	Oligonucleotide SE
996	10.4	7.5	12	1	ABH91477	Oligonucleotide pr	c1069	10.4	7.5	13	1	ABF73145	Oligonucleotide SE
c 997	10.4	7.5	12	1	AB142917	Oligonucleotide pr	c1070	10.4	7.5	13	1	ABF74436	Oligonucleotide SE
998	10.4	7.5	12	1	AB143245	Oligonucleotide pr	c1071	10.4	7.5	13	1	ABH37503	Oligonucleotide SE
999	10.4	7.5	12	1	AB168275	Oligonucleotide pr	c1072	10.4	7.5	13	1	ABH47423	Oligonucleotide SE
1000	10.4	7.5	12	1	AB180271	Oligonucleotide pr	c1073	10.4	7.5	13	1	ABH49575	Oligonucleotide SE
c1001	10.4	7.5	12	1	AB166749	Oligonucleotide pr	c1074	10.4	7.5	13	1	ABC00211	Oligonucleotide SE
1002	10.4	7.5	12	1	ABH98561	Oligonucleotide pr	c1075	10.4	7.5	13	1	ABC31792	Oligonucleotide SE
c1003	10.4	7.5	12	1	ABH98748	Oligonucleotide pr	c1076	10.4	7.5	13	1	ABF11506	Oligonucleotide SE
1004	10.4	7.5	12	1	ABH76068	Oligonucleotide pr	c1077	10.4	7.5	13	1	ABF25379	Oligonucleotide SE
1005	10.4	7.5	12	1	AB106534	Oligonucleotide pr	c1078	10.4	7.5	13	1	ABF25943	Oligonucleotide SE
c1006	10.4	7.5	12	1	ABH91284	Oligonucleotide pr	c1079	10.4	7.5	13	1	ABF39732	Oligonucleotide SE
c1007	10.4	7.5	12	1	AB181369	Oligonucleotide pr	c1080	10.4	7.5	13	1	ABH00390	Oligonucleotide SE
c1008	10.4	7.5	12	1	ABH78792	Oligonucleotide pr	c1081	10.4	7.5	13	1	ABF53254	Oligonucleotide SE
c1009	10.4	7.5	12	1	AB169250	Oligonucleotide pr	c1082	10.4	7.5	13	1	ABF79386	Oligonucleotide SE
1010	10.4	7.5	12	1	AB170895	Oligonucleotide pr	c1083	10.4	7.5	13	1	ABH13558	Oligonucleotide SE
c1011	10.4	7.5	12	1	AB179557	Oligonucleotide pr	c1084	10.4	7.5	13	1	ABH42003	Oligonucleotide SE
c1012	10.4	7.5	12	1	ABH74230	Oligonucleotide pr	c1085	10.4	7.5	13	1	ABH63203	Oligonucleotide SE
1013	10.4	7.5	12	1	AB174324	Oligonucleotide pr	c1086	10.4	7.5	13	1	ABC44244	Oligonucleotide SE
1014	10.4	7.5	12	1	AB125200	Oligonucleotide pr	c1087	10.4	7.5	13	1	ABC19753	Oligonucleotide SE
c1015	10.4	7.5	12	1	AB127537	Oligonucleotide pr	c1088	10.4	7.5	13	1	ABC24273	Oligonucleotide SE
1016	10.4	7.5	12	1	AB105067	Oligonucleotide pr	c1089	10.4	7.5	13	1	ABC00210	Oligonucleotide SE
c1017	10.4	7.5	12	1	AB113679	Oligonucleotide pr	c1090	10.4	7.5	13	1	ABC88050	Oligonucleotide SE
c1018	10.4	7.5	12	1	AB174121	Oligonucleotide pr	c1091	10.4	7.5	13	1	ABF40889	Oligonucleotide SE
c1019	10.4	7.5	12	1	AB176760	Oligonucleotide pr	c1092	10.4	7.5	13	1	ABF25378	Oligonucleotide SE
c1020	10.4	7.5	12	1	ABH93219	Oligonucleotide pr	c1093	10.4	7.5	13	1	ABF25382	Oligonucleotide SE
c1021	10.4	7.5	12	1	AB145848	Oligonucleotide pr	c1094	10.4	7.5	13	1	ABF28968	Oligonucleotide SE
1022	10.4	7.5	12	1	AB148545	Oligonucleotide pr	c1095	10.4	7.5	13	1	ABF28969	Oligonucleotide SE
c1023	10.4	7.5	12	1	AB167505	Oligonucleotide pr	c1096	10.4	7.5	13	1	ABF33958	Oligonucleotide SE
1024	10.4	7.5	12	1	AB154852	Oligonucleotide pr	c1097	10.4	7.5	13	1	ABF92684	Oligonucleotide SE
1025	10.4	7.5	12	1	AB155339	Oligonucleotide pr	c1098	10.4	7.5	13	1	ABF46003	Oligonucleotide SE
1026	10.4	7.5	12	1	AB163114	Oligonucleotide pr	c1099	10.4	7.5	13	1	ABF73144	Oligonucleotide SE
c1027	10.4	7.5	12	1	AB128532	Oligonucleotide pr	c1100	10.4	7.5	13	1	ABH00760	Oligonucleotide SE
c1028	10.4	7.5	12	1	AB150660	Oligonucleotide pr	c1101	10.4	7.5	13	1	ABH00761	Oligonucleotide SE
c1029	10.4	7.5	12	1	AB171189	Oligonucleotide pr	c1102	10.4	7.5	13	1	ABF55723	Oligonucleotide SE
1030	10.4	7.5	12	1	AB181529	Oligonucleotide pr	c1103	10.4	7.5	13	1	ABF66103	Oligonucleotide SE
c1031	10.4	7.5	12	1	ABH92917	Oligonucleotide pr	c1104	10.4	7.5	13	1	ABC46628	Oligonucleotide SE
c1032	10.4	7.5	12	1	ABH96992	Oligonucleotide pr	c1105	10.4	7.5	13	1	ABC52598	Oligonucleotide SE
c1033	10.4	7.5	12	1	ABH77660	Oligonucleotide pr	c1106	10.4	7.5	13	1	ABC57208	Oligonucleotide SE
1034	10.4	7.5	12	1	AB128296	Oligonucleotide pr	c1107	10.4	7.5	13	1	ABC57209	Oligonucleotide SE
c1035	10.4	7.5	12	1	AB134755	Oligonucleotide pr	c1108	10.4	7.5	13	1	ABC84791	Oligonucleotide SE
c1036	10.4	7.5	12	1	ABH86312	Oligonucleotide pr	c1109	10.4	7.5	13	1	ABC14558	Oligonucleotide SE
c1037	10.4	7.5	12	1	AB158975	Oligonucleotide pr	c1110	10.4	7.5	13	1	ABF18155	Oligonucleotide SE
c1038	10.4	7.5	12	1	AB161446	Oligonucleotide pr	c1111	10.4	7.5	13	1	ABF20794	Oligonucleotide SE
1039	10.4	7.5	12	1	ABH67931	Oligonucleotide pr	c1112	10.4	7.5	13	1	ABF33959	Oligonucleotide SE
c1040	10.4	7.5	12	1	ABH69474	Oligonucleotide pr	c1113	10.4	7.5	13	1	ABH61554	Oligonucleotide SE
c1041	10.4	7.5	12	1	ABH96180	Oligonucleotide pr	c1114	10.4	7.5	13	1	ABC46625	Oligonucleotide SE
1042	10.4	7.5	12	1	AB105053	Oligonucleotide pr	c1115	10.4	7.5	13	1	ABC77643	Oligonucleotide SE
1043	10.4	7.5	12	1	AB132594	Oligonucleotide pr	c1116	10.4	7.5	13	1	ABC31789	Oligonucleotide SE
c1044	10.4	7.5	12	1	ABH90089	Oligonucleotide pr	c1117	10.4	7.5	13	1	ABC31793	Oligonucleotide SE
c1045	10.4	7.5	12	1	ABH93470	Oligonucleotide pr	c1118	10.4	7.5	13	1	ABC32493	Oligonucleotide SE
c1046	10.4	7.5	12	1	ABH78187	Oligonucleotide pr	c1119	10.4	7.5	13	1	ABC84790	Oligonucleotide SE
1047	10.4	7.5	12	1	ABH28998	Oligonucleotide pr	c1120	10.4	7.5	13	1	ABC66988	Oligonucleotide SE
c1048	10.4	7.5	12	1	ABH81163	Oligonucleotide pr	c1121	10.4	7.5	13	1	ABF53255	Oligonucleotide SE
1049	10.4	7.5	12	1	ABH90546	Oligonucleotide pr	c1122	10.4	7.5	13	1	ABH15230	Oligonucleotide SE
c1050	10.4	7.5	12	1	AB145398	Oligonucleotide pr	c1123	10.4	7.5	13	1	ABF90783	Oligonucleotide SE
c1051	10.4	7.5	12	1	AB163218	Oligonucleotide pr	c1124	10.4	7.5	13	1	ABC46629	Oligonucleotide SE
1052	10.4	7.5	13	1	AA293102	5'UTR sequence use	c1125	10.4	7.5	13	1	ABC49574	Oligonucleotide SE
1053	10.4	7.5	13	1	ABC69426	Oligonucleotide SE	c1126	10.4	7.5	13	1	ABC02829	Oligonucleotide SE
1054	10.4	7.5	13	1	ABF18044	Oligonucleotide SE	c1127	10.4	7.5	13	1	ABC53246	Oligonucleotide SE
1055	10.4	7.5	13	1	ABF25942	Oligonucleotide SE	c1128	10.4	7.5	13	1	ABC53247	Oligonucleotide SE

c1129	10.4	7.5	13	1	ABC04730	Oligonucleotide SE	1202	10.4	7.5	13	1	ABF54762	Oligonucleotide SE
1130	10.4	7.5	13	1	ABC80341	Oligonucleotide SE	1203	10.4	7.5	13	1	ABF61036	Oligonucleotide SE
1131	10.4	7.5	13	1	ABC31002	Oligonucleotide SE	c1204	10.4	7.5	13	1	ABH36660	Oligonucleotide SE
1132	10.4	7.5	13	1	ABF24348	Oligonucleotide SE	1205	10.4	7.5	13	1	ABH36661	Oligonucleotide SE
1133	10.4	7.5	13	1	ABF32774	Oligonucleotide SE	1206	10.4	7.5	13	1	ABF65198	Oligonucleotide SE
1134	10.4	7.5	13	1	ABF32776	Oligonucleotide SE	1207	10.4	7.5	13	1	ABH50619	Oligonucleotide SE
c1135	10.4	7.5	13	1	ABF39733	Oligonucleotide SE	c1208	10.4	7.5	13	1	ABF05796	Oligonucleotide SE
1136	10.4	7.5	13	1	ABF51621	Oligonucleotide SE	c1209	10.4	7.5	13	1	ABC33106	Oligonucleotide SE
c1137	10.4	7.5	13	1	ABC44245	Oligonucleotide SE	1210	10.4	7.5	13	1	ABC33107	Oligonucleotide SE
c1138	10.4	7.5	13	1	ABC46624	Oligonucleotide SE	1211	10.4	7.5	13	1	ABC40066	Oligonucleotide SE
1139	10.4	7.5	13	1	ABF38495	Oligonucleotide SE	1212	10.4	7.5	13	1	ABC66989	Oligonucleotide SE
1140	10.4	7.5	13	1	ABF41114	Oligonucleotide SE	c1213	10.4	7.5	13	1	ABH26444	Oligonucleotide SE
c1141	10.4	7.5	13	1	ABF95707	Oligonucleotide SE	c1214	10.4	7.5	13	1	ABH35974	Oligonucleotide SE
c1142	10.4	7.5	13	1	ABF95709	Oligonucleotide SE	1215	10.4	7.5	13	1	ABC24272	Oligonucleotide SE
1143	10.4	7.5	13	1	ABF73141	Oligonucleotide SE	1216	10.4	7.5	13	1	ABC52599	Oligonucleotide SE
c1144	10.4	7.5	13	1	ABH00391	Oligonucleotide SE	1217	10.4	7.5	13	1	ABC05020	Oligonucleotide SE
1145	10.4	7.5	13	1	ABF55722	Oligonucleotide SE	c1218	10.4	7.5	13	1	ABC80340	Oligonucleotide SE
1146	10.4	7.5	13	1	ABF82123	Oligonucleotide SE	1219	10.4	7.5	13	1	ABC31800	Oligonucleotide SE
1147	10.4	7.5	13	1	ABH12820	Oligonucleotide SE	1220	10.4	7.5	13	1	ABC82527	Oligonucleotide SE
1148	10.4	7.5	13	1	ABF90782	Oligonucleotide SE	1221	10.4	7.5	13	1	ABC11714	Oligonucleotide SE
1149	10.4	7.5	13	1	ABF66102	Oligonucleotide SE	c1222	10.4	7.5	13	1	ABC63275	Oligonucleotide SE
c1150	10.4	7.5	13	1	ABC05021	Oligonucleotide SE	1223	10.4	7.5	13	1	ABC14559	Oligonucleotide SE
c1151	10.4	7.5	13	1	ABC31005	Oligonucleotide SE	1224	10.4	7.5	13	1	ABC40888	Oligonucleotide SE
1152	10.4	7.5	13	1	ABC32492	Oligonucleotide SE	1225	10.4	7.5	13	1	ABF32046	Oligonucleotide SE
1153	10.4	7.5	13	1	ABC84322	Oligonucleotide SE	c1226	10.4	7.5	13	1	ABF32775	Oligonucleotide SE
1154	10.4	7.5	13	1	ABC87616	Oligonucleotide SE	c1227	10.4	7.5	13	1	ABF92685	Oligonucleotide SE
1155	10.4	7.5	13	1	ABC63274	Oligonucleotide SE	c1228	10.4	7.5	13	1	ABF54763	Oligonucleotide SE
1156	10.4	7.5	13	1	ABC16398	Oligonucleotide SE	c1229	10.4	7.5	13	1	ABF55623	Oligonucleotide SE
c1157	10.4	7.5	13	1	ABC66449	Oligonucleotide SE	c1230	10.4	7.5	13	1	ABF02122	Oligonucleotide SE
c1158	10.4	7.5	13	1	ABF20156	Oligonucleotide SE	c1231	10.4	7.5	13	1	ABH36975	Oligonucleotide SE
1159	10.4	7.5	13	1	ABF20157	Oligonucleotide SE	1232	10.4	7.5	13	1	ABH13559	Oligonucleotide SE
1160	10.4	7.5	13	1	ABF30620	Oligonucleotide SE	c1233	10.4	7.5	13	1	ABF63800	Oligonucleotide SE
c1161	10.4	7.5	13	1	ABF32047	Oligonucleotide SE	c1234	10.4	7.5	13	1	ABC47685	Oligonucleotide SE
c1162	10.4	7.5	13	1	ABF32777	Oligonucleotide SE	1235	10.4	7.5	13	1	ABC31004	Oligonucleotide SE
c1163	10.4	7.5	13	1	ABF74437	Oligonucleotide SE	c1236	10.4	7.5	13	1	ABC57211	Oligonucleotide SE
c1164	10.4	7.5	13	1	ABH00387	Oligonucleotide SE	c1237	10.4	7.5	13	1	ABC82526	Oligonucleotide SE
1165	10.4	7.5	13	1	ABF79387	Oligonucleotide SE	c1238	10.4	7.5	13	1	ABC84323	Oligonucleotide SE
1166	10.4	7.5	13	1	ABF58666	Oligonucleotide SE	1239	10.4	7.5	13	1	ABF16774	Oligonucleotide SE
1167	10.4	7.5	13	1	ABH35975	Oligonucleotide SE	1240	10.4	7.5	13	1	ABF18154	Oligonucleotide SE
1168	10.4	7.5	13	1	ABF87483	Oligonucleotide SE	c1241	10.4	7.5	13	1	ABF38484	Oligonucleotide SE
c1169	10.4	7.5	13	1	ABH13554	Oligonucleotide SE	1242	10.4	7.5	13	1	ABF43731	Oligonucleotide SE
c1170	10.4	7.5	13	1	ABH50618	Oligonucleotide SE	c1243	10.4	7.5	13	1	ABF51620	Oligonucleotide SE
1171	10.4	7.5	13	1	ABH61555	Oligonucleotide SE	c1244	10.4	7.5	13	1	ABF53251	Oligonucleotide SE
1172	10.4	7.5	13	1	ABH63202	Oligonucleotide SE	c1245	10.4	7.5	13	1	ABF61037	Oligonucleotide SE
1173	10.4	7.5	13	1	ABC00338	Oligonucleotide SE	1246	10.4	7.5	13	1	ABH36974	Oligonucleotide SE
c1174	10.4	7.5	13	1	ABC77733	Oligonucleotide SE	c1247	10.4	7.5	13	1	ABH13555	Oligonucleotide SE
1175	10.4	7.5	13	1	ABC04731	Oligonucleotide SE	c1248	10.4	7.5	13	1	ABC47422	Oligonucleotide SE
1176	10.4	7.5	13	1	ABC31808	Oligonucleotide SE	1249	10.4	7.5	13	1	ABC47684	Oligonucleotide SE
1177	10.4	7.5	13	1	ABC57210	Oligonucleotide SE	c1250	10.4	7.5	13	1	ABC75934	Oligonucleotide SE
1178	10.4	7.5	13	1	ABC40890	Oligonucleotide SE	1251	10.4	7.5	13	1	ABC77732	Oligonucleotide SE
c1179	10.4	7.5	13	1	ABC40891	Oligonucleotide SE	1252	10.4	7.5	13	1	ABF05797	Oligonucleotide SE
c1180	10.4	7.5	13	1	ABF18045	Oligonucleotide SE	c1253	10.4	7.5	13	1	ABC31003	Oligonucleotide SE
1181	10.4	7.5	13	1	ABF24346	Oligonucleotide SE	1254	10.4	7.5	13	1	ABC09989	Oligonucleotide SE
c1182	10.4	7.5	13	1	ABF24347	Oligonucleotide SE	c1255	10.4	7.5	13	1	ABF16775	Oligonucleotide SE
c1183	10.4	7.5	13	1	ABF36621	Oligonucleotide SE	c1256	10.4	7.5	13	1	ABF34099	Oligonucleotide SE
1184	10.4	7.5	13	1	ABF34098	Oligonucleotide SE	c1257	10.4	7.5	13	1	ABF41115	Oligonucleotide SE
1185	10.4	7.5	13	1	ABF95706	Oligonucleotide SE	1258	10.4	7.5	13	1	ABH00386	Oligonucleotide SE
1186	10.4	7.5	13	1	ABH26445	Oligonucleotide SE	1259	10.4	7.5	13	1	ABF53250	Oligonucleotide SE
1187	10.4	7.5	13	1	ABF58667	Oligonucleotide SE	1260	10.4	7.5	13	1	ABH15231	Oligonucleotide SE
c1188	10.4	7.5	13	1	ABH37502	Oligonucleotide SE	c1261	10.4	7.5	13	1	ABF65199	Oligonucleotide SE
c1189	10.4	7.5	13	1	ABF74482	Oligonucleotide SE	1262	10.4	7.5	13	1	ABH47622	Oligonucleotide SE
c1190	10.4	7.5	13	1	ABH12821	Oligonucleotide SE	c1263	10.4	7.5	13	1	ABC19752	Oligonucleotide SE
1191	10.4	7.5	13	1	ABF66672	Oligonucleotide SE	1264	10.4	7.5	13	1	ABC75935	Oligonucleotide SE
c1192	10.4	7.5	13	1	ABF66673	Oligonucleotide SE	c1265	10.4	7.5	13	1	ABC02828	Oligonucleotide SE
c1193	10.4	7.5	13	1	ABH42002	Oligonucleotide SE	c1266	10.4	7.5	13	1	ABF11507	Oligonucleotide SE
1194	10.4	7.5	13	1	ABC77642	Oligonucleotide SE	c1267	10.4	7.5	13	1	ABC87617	Oligonucleotide SE
c1195	10.4	7.5	13	1	ABC09988	Oligonucleotide SE	1268	10.4	7.5	13	1	ABC66448	Oligonucleotide SE
c1196	10.4	7.5	13	1	ABC86051	Oligonucleotide SE	1269	10.4	7.5	13	1	ABF43820	Oligonucleotide SE
c1197	10.4	7.5	13	1	ABC40067	Oligonucleotide SE	1270	10.4	7.5	13	1	ABF63801	Oligonucleotide SE
c1198	10.4	7.5	13	1	ABC16399	Oligonucleotide SE	1271	10.4	7.5	13	1	AAI56800	Oligonucleotide SE
c1199	10.4	7.5	13	1	ABF43821	Oligonucleotide SE	c1272	10.4	7.5	14	1	AAQ78441	Oligonucleotide SE
1200	10.4	7.5	13	1	ABF95708	Oligonucleotide SE	c1273	10.4	7.5	14	1	AAV99069	Oligonucleotide SE
c1201	10.4	7.5	13	1	ABF73140	Oligonucleotide SE	1274	10.4	7.5	14	1	AAAL7659	Oligonucleotide SE

Aryl hydrocarbon n





XX 24-MAR-2000; 2000JP-00084264.  
XX (BMLB-) BML INC.  
XX Nagano M, Ito M, Sagehashi Y, Hattori H, Egashira T, Yamashita S;  
XX Matsuzawa Y;  
XX WPI; 2001-611516/70.  
XX Determining a risk factor for arteriosclerosis comprises detecting  
XX mutations in genes for cholesterol ester transfer protein.  
XX Disclosure; Page 21; 59pp; Japanese.  
XX The invention relates to detecting the risk factor for arteriosclerosis  
XX in a subject that involves detecting mutations in the gene for  
XX cholesterol ester transfer protein (CETP) related to the degree of risk  
XX of arteriosclerosis. The mutant proteins alter the level of HDL in the  
XX blood. The high frequency mutations can be detected for prevention and  
XX treatment of arteriosclerosis. Sequences AA16655-91 represent PCR  
XX primers related to the human CETP DNA, used during the course of the  
XX invention  
XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;  
Query Match 15.1%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1665 TCACAGCTGGAAACCTGGTGT 1685  
DB 21 TCACAGCTGGAAACCTGGTGT 1  
RESULT 3  
ABT13031/c  
ID ABT13031 standard; DNA; 20 BP.  
XX AC ABT13031;  
XX 30-JAN-2003 (first entry)  
XX Human cholesterol ester transfer protein PCR primer (SNP specific) #12.  
XX Human; PCR; primer; ss; gene therapy; single nucleotide polymorphism;  
XX cytochrome C oxidase subunit VIB; COX6B; high serum cholesterol; GPI-1;  
XX N-acetylglucosaminyl transferase component; cardiovascular disease; HDL;  
XX glycosylphosphatidylinositol-1; SNP; low serum high density lipoprotein.  
XX Homo sapiens.  
XX WO200272604-A2.  
XX 19-SEP-2002.  
XX 05-MAR-2002; 2002WO-US006728.  
XX 09-MAR-2001; 2001US-00802640.  
XX (SEQU-) SEQUENOM INC.  
XX Braun A, Bansal A, Kieyn FW;  
XX WPI; 2002-750478/81.  
XX Detecting the presence or absence of an allelic variant of a polymorphic  
XX region of COX6B and/or GPI-1 gene, useful for detecting a predisposition  
XX to high serum cholesterol, low serum HDL and cardiovascular disease.  
XX Disclosure; Page 30; 199pp; English.  
XX The invention comprises methods of detecting the presence or absence of

CC at least one allelic variant of a polymorphic region of a gene associated  
CC with cardiovascular disease. The invention specifically relates to  
CC detecting the region of a cytochrome C oxidase subunit VIB (COX6B) gene  
CC that is associated with high serum cholesterol, or the region of the N-  
CC acetylglucosaminyl transferase component glycosylphosphatidylinositol-1  
CC (GPI-1) gene that is associated with low serum high density lipoprotein  
CC (HDL). The methods of the invention are useful for detecting a  
CC predisposition to high serum cholesterol, low serum HDL and  
CC cardiovascular disease. The methods are also useful for elucidating  
CC pathological pathways, developing diagnostic assays and new drug  
CC therapies for such disorders. The present DNA sequence represents a PCR  
CC primer used to amplify a human gene that is associated with high serum  
CC cholesterol, low serum HDL and/or cardiovascular disease  
XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;  
Query Match 14.4%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1639 CTTGTAGCAGAGCAAGCA 1658  
DB 20 CTTGTAGCAGAGCAAGCA 1  
RESULT 4  
ABX12200/c  
ID ABX12200 standard; DNA; 20 BP.  
XX AC ABX12200;  
XX 16-MAY-2003 (first entry)  
XX Human cholesteryl ester transfer protein, antisense oligo #21.  
XX Human; cholesteryl ester transfer protein; lipid metabolism;  
XX cholesterol metabolism; atherosclerosis; cardiovascular disease;  
XX antisense; probe; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX modified\_base 1..20  
XX /mod\_base= OTHER  
XX /note= "Phosphorothioate nucleotides; all cytidine  
XX residues are 5-methylcytidines"  
XX modified\_base 1..6  
XX /mod\_base= OTHER  
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
XX modified\_base 15..20  
XX /mod\_base= OTHER  
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
XX WO2003014306-A2.  
XX 20-FEB-2003.  
XX 05-AUG-2002; 2002WO-US024919.  
XX 08-AUG-2001; 2001US-00925139.  
XX (ISIS-) ISIS PHARM INC.  
XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;  
XX WPI; 2003-256564/25.  
XX New antisense compound, useful for preparing a composition for treating  
XX abnormal lipid or cholesterol metabolism, atherosclerosis or  
XX cardiovascular disease.  
XX Claim 3; Page 96; 114pp; English.

CC The invention relates to new antisense compounds targeted to a nucleic  
CC acid molecule encoding human cholesteryl ester transfer protein,  
CC specifically hybridises with it and inhibits the expression of human  
CC cholesteryl ester transfer protein. The compound is useful for preparing  
CC a composition for treating abnormal lipid or cholesterol metabolism,  
CC atherosclerosis or cardiovascular disease. The present sequence  
CC represents a human cholesteryl ester transfer protein, antisense  
CC oligonucleotide of the invention  
XX Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 U; 0 Other;  
SQ Query Match 14.4%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1701 GGAAGTGGGTTAGGAGTAC 1720  
DB 20 GGAAGTGGGTTAGGAGTAC 1

RESULT 5  
ABX12198/c  
ID ABX12198 standard; DNA; 20 BP.  
XX AC ABX12198;  
XX 16-MAY-2003 (first entry)  
XX Human cholesteryl ester transfer protein, antisense oligo #19.  
XX Human; cholesteryl ester transfer protein; lipid metabolism;  
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;  
KW antisense; probe; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH modified\_base 1..20  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate nucleotides; all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..6  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
FT modified\_base 15..20  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
XX WO2003014306-A2.  
XX 20-FEB-2003.  
XX 05-AUG-2002; 2002WO-US024919.  
XX 08-AUG-2001; 2001US-00925139.  
XX (ISIS-) ISIS PHARM INC.  
XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;  
XX WPI; 2003-256564/25.  
XX New antisense compound, useful for preparing a composition for treating  
PT abnormal lipid or cholesterol metabolism, atherosclerosis or  
PT cardiovascular disease.  
XX Claim 3; Page 96; 114pp; English.  
XX The invention relates to new antisense compounds targeted to a nucleic  
CC acid molecule encoding human cholesteryl ester transfer protein,  
CC specifically hybridises with it and inhibits the expression of human  
CC cholesteryl ester transfer protein. The compound is useful for preparing  
CC a composition for treating abnormal lipid or cholesterol metabolism,  
CC atherosclerosis or cardiovascular disease. The present sequence  
CC represents a human cholesteryl ester transfer protein, antisense  
CC oligonucleotide of the invention  
XX Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 U; 0 Other;  
SQ Query Match 14.4%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1701 GGAAGTGGGTTAGGAGTAC 1720  
DB 20 GGAAGTGGGTTAGGAGTAC 1

RESULT 5  
ABX12198/c  
ID ABX12198 standard; DNA; 20 BP.  
XX AC ABX12198;  
XX 16-MAY-2003 (first entry)  
XX Human cholesteryl ester transfer protein, antisense oligo #19.  
XX Human; cholesteryl ester transfer protein; lipid metabolism;  
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;  
KW antisense; probe; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH modified\_base 1..20  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate nucleotides; all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..6  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
FT modified\_base 15..20  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
XX WO2003014306-A2.  
XX 20-FEB-2003.  
XX 05-AUG-2002; 2002WO-US024919.  
XX 08-AUG-2001; 2001US-00925139.  
XX (ISIS-) ISIS PHARM INC.  
XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;  
XX WPI; 2003-256564/25.  
XX New antisense compound, useful for preparing a composition for treating  
PT abnormal lipid or cholesterol metabolism, atherosclerosis or  
PT cardiovascular disease.  
XX Claim 3; Page 96; 114pp; English.  
XX The invention relates to new antisense compounds targeted to a nucleic  
CC acid molecule encoding human cholesteryl ester transfer protein,  
CC specifically hybridises with it and inhibits the expression of human  
CC cholesteryl ester transfer protein. The compound is useful for preparing  
CC a composition for treating abnormal lipid or cholesterol metabolism,  
CC atherosclerosis or cardiovascular disease. The present sequence  
CC represents a human cholesteryl ester transfer protein, antisense  
CC oligonucleotide of the invention  
XX Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 U; 0 Other;  
SQ Query Match 14.4%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC atherosclerosis or cardiovascular disease. The present sequence  
CC represents a human cholesteryl ester transfer protein, antisense  
CC oligonucleotide of the invention  
XX Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 U; 0 Other;  
SQ Query Match 14.4%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1631 GGATGGGCTTGTAGCAGAA 1650  
DB 20 GGATGGGCTTGTAGCAGAA 1

RESULT 6  
ABX12217/c  
ID ABX12217 standard; DNA; 20 BP.  
XX AC ABX12217;  
XX 16-MAY-2003 (first entry)  
XX Human cholesteryl ester transfer protein, antisense oligo #38.  
XX Human; cholesteryl ester transfer protein; lipid metabolism;  
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;  
KW antisense; probe; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH modified\_base 1..20  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate nucleotides; all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..6  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
FT modified\_base 15..20  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
XX WO2003014306-A2.  
XX 20-FEB-2003.  
XX 05-AUG-2002; 2002WO-US024919.  
XX 08-AUG-2001; 2001US-00925139.  
XX (ISIS-) ISIS PHARM INC.  
XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;  
XX WPI; 2003-256564/25.  
XX New antisense compound, useful for preparing a composition for treating  
PT abnormal lipid or cholesterol metabolism, atherosclerosis or  
PT cardiovascular disease.  
XX Claim 3; Page 97; 114pp; English.  
XX The invention relates to new antisense compounds targeted to a nucleic  
CC acid molecule encoding human cholesteryl ester transfer protein,  
CC specifically hybridises with it and inhibits the expression of human  
CC cholesteryl ester transfer protein. The compound is useful for preparing  
CC a composition for treating abnormal lipid or cholesterol metabolism,  
CC atherosclerosis or cardiovascular disease. The present sequence  
CC represents a human cholesteryl ester transfer protein, antisense  
CC oligonucleotide of the invention  
XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;  
SQ

Query Match 14.4%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 7.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1638 GCTTGTAGCAGGCAAGC 1657  
Db 20 GCTTGTAGCAGGCAAGC 1

RESULT 7  
ABX12175/c  
ID ABX12175 standard; DNA; 20 BP.  
XX  
AC ABX12175;  
XX  
DT 16-MAY-2003 (first entry)  
XX  
DE Human cholesteryl ester transfer protein, reverse PCR primer.  
XX  
KW Human; cholesteryl ester transfer protein; lipid metabolism;  
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;  
KW antisense; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003014306-A2.  
XX  
PD 20-FEB-2003.  
XX  
PF 05-AUG-2002; 2002WO-US024919.  
XX  
PR 08-AUG-2001; 2001US-00925139.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Crooke RM, Graham MJ, Nero PS, Wancewicz E;  
XX  
DR WPI; 2003-256564/25.

New antisense compound, useful for preparing a composition for treating abnormal lipid or cholesterol metabolism, atherosclerosis or cardiovascular disease.  
XX  
PS Example 13; Page 93; 114pp; English.  
XX  
CC The invention relates to new antisense compounds targeted to a nucleic acid molecule encoding human cholesteryl ester transfer protein, specifically hybridizes with it and inhibits the expression of human cholesteryl ester transfer protein. The compound is useful for preparing a composition for treating abnormal lipid or cholesterol metabolism, atherosclerosis or cardiovascular disease. The present sequence represents a human cholesteryl ester transfer protein, PCR primer  
XX  
SQ Sequence 20 BP; 6 A; 10 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 14.4%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 7.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1695 CGTGTGGAAGTTGGTTAG 1714  
Db 20 CGTGTGGAAGTTGGTTAG 1

RESULT 8  
ABX12219/c  
ID ABX12219 standard; DNA; 20 BP.  
XX  
AC ABX12219;  
XX  
DT 16-MAY-2003 (first entry)  
XX

DE Human cholesteryl ester transfer protein, antisense oligo #40.  
XX  
KW Human; cholesteryl ester transfer protein; lipid metabolism;  
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;  
KW antisense; probe; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate nucleotides; all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..6  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
FT modified\_base 15..20  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
XX  
PN WO2003014306-A2.  
XX  
PD 20-FEB-2003.  
XX  
PF 05-AUG-2002; 2002WO-US024919.  
XX  
PR 08-AUG-2001; 2001US-00925139.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Crooke RM, Graham MJ, Nero PS, Wancewicz E;  
XX  
DR WPI; 2003-256564/25.  
XX  
New antisense compound, useful for preparing a composition for treating abnormal lipid or cholesterol metabolism, atherosclerosis or cardiovascular disease.  
XX  
PS Claim 3; Page 97; 114pp; English.

The invention relates to new antisense compounds targeted to a nucleic acid molecule encoding human cholesteryl ester transfer protein, specifically hybridizes with it and inhibits the expression of human cholesteryl ester transfer protein. The compound is useful for preparing a composition for treating abnormal lipid or cholesterol metabolism, atherosclerosis or cardiovascular disease. The present sequence represents a human cholesteryl ester transfer protein, antisense oligonucleotide of the invention  
XX  
SQ Sequence 20 BP; 4 A; 9 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 14.4%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 7.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1714 GGAGTACGAGATGGAGATT 1733  
Db 20 GGAGTACGAGATGGAGATT 1

RESULT 9  
ABX12220/c  
ID ABX12220 standard; DNA; 20 BP.  
XX  
AC ABX12220;  
XX  
DT 16-MAY-2003 (first entry)  
XX  
DE Human cholesteryl ester transfer protein, antisense oligo #41.  
XX  
KW Human; cholesteryl ester transfer protein; lipid metabolism;  
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;  
KW antisense; probe; ss.

```

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate nucleotides; all cytidine
XX FT residues are 5-methylcytidines"
XX FT modified_base 1..6
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX FT modified_base 15..20
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX PN WO2003014306-A2.
XX PD 20-FEB-2003.
XX PF 05-AUG-2002; 2002WO-US024919.
XX PR 08-AUG-2001; 2001US-00925139.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Crooke RM, Graham MJ, Nero PS, Wancewicz E;
XX DR WPI; 2003-256564/25.
XX PT New antisense compound, useful for preparing a composition for treating
XX PT abnormal lipid or cholesterol metabolism, atherosclerosis or
XX PT cardiovascular disease.
XX PS Claim 3; Page 97; 114pp; English.
XX CC The invention relates to new antisense compounds targeted to a nucleic
XX CC acid molecule encoding human cholesteryl ester transfer protein,
XX CC specifically hybridises with it and inhibits the expression of human
XX CC cholesteryl ester transfer protein. The compound is useful for preparing
XX CC a composition for treating abnormal lipid or cholesterol metabolism,
XX CC atherosclerosis or cardiovascular disease. The present sequence
XX CC represents a human cholesteryl ester transfer protein, antisense
XX CC oligonucleotide of the invention
XX SQ Sequence 20 BP; 4 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 14.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1750 CTATCCTAAAGGCCCACTGG 1769
DB 20 CTATCCTAAAGGCCCACTGG 1

RESULT 10
ABX12199/c
ID ABX12199 standard; DNA; 20 BP.
XX AC ABX12199;
XX XX
XX DT 16-MAY-2003 (first entry)
XX DE Human cholesteryl ester transfer protein, antisense oligo #20.
XX KW Human; cholesteryl ester transfer protein; lipid metabolism;
XX KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
XX KW antisense; probe; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20

```

```

XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate nucleotides; all cytidine
XX FT residues are 5-methylcytidines"
XX FT modified_base 1..6
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX FT modified_base 15..20
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX PN WO2003014306-A2.
XX PD 20-FEB-2003.
XX PF 05-AUG-2002; 2002WO-US024919.
XX PR 08-AUG-2001; 2001US-00925139.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Crooke RM, Graham MJ, Nero PS, Wancewicz E;
XX DR WPI; 2003-256564/25.
XX PT New antisense compound, useful for preparing a composition for treating
XX PT abnormal lipid or cholesterol metabolism, atherosclerosis or
XX PT cardiovascular disease.
XX PS Claim 3; Page 96; 114pp; English.
XX CC The invention relates to new antisense compounds targeted to a nucleic
XX CC acid molecule encoding human cholesteryl ester transfer protein,
XX CC specifically hybridises with it and inhibits the expression of human
XX CC cholesteryl ester transfer protein. The compound is useful for preparing
XX CC a composition for treating abnormal lipid or cholesterol metabolism,
XX CC atherosclerosis or cardiovascular disease. The present sequence
XX CC represents a human cholesteryl ester transfer protein, antisense
XX CC oligonucleotide of the invention
XX SQ Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 14.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1671 CTGGAACCCCTGGTGTCTCT 1690
DB 20 CTGGAACCCCTGGTGTCTCT 1

RESULT 11
ABX12218/c
ID ABX12218 standard; DNA; 20 BP.
XX AC ABX12218;
XX XX
XX DT 16-MAY-2003 (first entry)
XX DE Human cholesteryl ester transfer protein, antisense oligo #39.
XX KW Human; cholesteryl ester transfer protein; lipid metabolism;
XX KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
XX KW antisense; probe; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate nucleotides; all cytidine
XX FT residues are 5-methylcytidines"
XX FT modified_base 1..6
XX FT /mod_base= OTHER

```

```

FT modified_base /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT 15..20
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
PN WO2003014306-A2.
XX
XX
PD 20-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-US024919.
XX
XX 08-AUG-2001; 2001US-00925139.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;
XX WPI; 2003-256564/25.
XX
XX New antisense compound, useful for preparing a composition for treating
XX abnormal lipid or cholesterol metabolism, atherosclerosis or
XX cardiovascular disease.
XX
XX Claim 3; Page 97; 114pp; English.
XX
XX The invention relates to new antisense compounds targeted to a nucleic
XX acid molecule encoding human cholesteryl ester transfer protein,
XX specifically hybridises with it and inhibits the expression of human
XX cholesteryl ester transfer protein. The compound is useful for preparing
XX a composition for treating abnormal lipid or cholesterol metabolism,
XX atherosclerosis or cardiovascular disease. The present sequence
XX represents a human cholesteryl ester transfer protein, antisense
XX oligonucleotide of the invention
XX
XX Sequence 20 BP; 6 A; 10 C; 1 G; 3 T; 0 U; 0 Other;
XX
Query Match 14.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1693 AGCGTGGTGAAGTTGGTT 1712
DB 20 AGCGTGGTGAAGTTGGTT 1
RESULT 12
AAT50642
ID AAT50642 standard; RNA; 18 BP.
XX
XX AAT50642;
XX
XX 10-MAR-1997 (first entry)
XX
XX Human CETP hairpin ribozyme target sequence #1669.
XX
XX Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
XX neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
XX reverse cholesterol transport; high density lipoprotein; therapy; CETP;
XX familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
XX peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
XX angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
XX LDL; ss.
XX
XX Homo sapiens.
XX
XX WO9620279-A1.
XX
XX 04-JUL-1996.
XX
XX 11-DEC-1995; 95WO-US016000.
XX
XX 23-DEC-1994; 94US-00363240.
XX

```

```

PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN ) WARNER LAMBERT CO.
XX
XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;
XX WPI; 1996-321852/32.
XX
XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX useful for preventing or treating initial development, progression or
XX regression of vascular diseases, esp. familial hypercholesterolaemia.
XX
XX Claim 4; Page 54; 72pp; English.
XX
XX AAT50595-T50642 represent target sequences for the human cholesterol
XX ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).
XX CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
XX between plasma lipoproteins. The numbering of the targets refers to the
XX position of the cleavage site in full length CETP. The ribozyme then
XX binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
XX ribozymes are able to cleave mRNA from the gene encoding CETP, thereby
XX blocking synthesis and/or expression of the mRNA. By inhibiting CETP, the
XX reverse cholesterol transport (RCT) pathway can be inhibited (or
XX eliminated) thereby preventing the reduction in size density of the high
XX density lipoproteins (HDL), prolonging HDL half life, and therefore
XX associated with abnormal levels of CETP, specifically atherosclerosis,
XX peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
XX familial hypercholesterolaemia, hypoalphalipoproteinaemia, vascular
XX complications of diabetes, transplant, atherectomy and angioplastic
XX restenosis. By inhibiting CETP, the levels of HDL and low density
XX lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
XX decrease in LDL levels, and a corresponding increase in HDL levels). The
XX ribozymes can also be used diagnostically to study genetic drift and
XX mutations in diseased cells, and to detect CETP mRNA. As the ribozymes
XX target specific regions of the CETP gene, they have low non-specific
XX activity
XX
XX Sequence 18 BP; 4 A; 7 C; 4 G; 0 T; 3 U; 0 Other;
XX
Query Match 12.9%; Score 18; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1663 GCTCAGCTGGGAACCCCT 1680
DB 1 GCUCACAGCUGGAACCCU 18
RESULT 13
AAX37644
ID AAX37644 standard; DNA; 22 BP.
XX
XX AAX37644;
XX
XX 08-JUL-1999 (first entry)
XX
XX HBV detecting primer 8.
XX
XX Detection; HBV; real time; PCR; reporter; fluorescent; primer; quencher;
XX fluorescence resonance energy transfer; ss.
XX
XX Synthetic.
XX
XX Hepatitis B virus.
XX
XX JP11103897-A.
XX
XX 20-APR-1999.
XX
XX 30-SEP-1997; 97JP-00282612.
XX
XX 30-SEP-1997; 97JP-00282612.
XX
XX (SRLS-) SRL KK.
XX

```

XX WPI; 1999-305860/26.  
 XX New primers and probes - for measurement of an Herpes B Virus (HBV) gene  
 PT by a real time detecting PCR.  
 XX  
 XX Example 2; Page 8; 12pp; Japanese.  
 XX  
 CC This invention describes a method for the measurement of an HBV gene by a  
 CC real time detecting PCR. The invention also describes a method for the  
 CC measurement of an HBV gene by a real time detecting PCR in which a  
 CC reporter fluorescent colour and a quencher fluorescent colour are  
 CC combined to an oligonucleotide, the fluorescence of said reporter  
 CC fluorescent colour is controlled by fluorescence resonance energy  
 CC transfer when reporter fluorescent colour is combined to the same probe  
 CC as quencher fluorescent colour. The method can measure an HBV exactly in  
 CC a high sensitivity  
 XX  
 SQ Sequence 22 BP; 5 A; 11 C; 1 G; 5 T; 0 U; 0 Other;  
 Query Match 12.4%; Score 17.2; DB 1; Length 22;  
 Best Local Similarity 86.4%; Pred. No. 37;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1738 CCCAATCTCTCCCTATCTCTAA 1759  
 Db 1 CCCAATCTCTCCAGTCTCTAA 22  
 RESULT 14  
 AAX22550/c  
 ID AAX22550 standard; mRNA; 17 BP.  
 XX  
 AC AAX22550;  
 XX  
 DT 21-MAY-1999 (first entry)  
 XX  
 DE Human CETP RNA fragment #5.  
 XX  
 KW CETP; cholesteryl ester transfer protein; inhibitor; therapy; treatment;  
 KW surface plasmon resonance; vascular disease; pathogenic; atherosclerosis;  
 KW human; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE19731609-A1.  
 XX  
 PD 18-FEB-1999.  
 XX  
 PF 23-JUL-1997; 97DE-01031609.  
 XX  
 PR 23-JUL-1997; 97DE-01031609.  
 XX  
 PA (BOEH) BOEHRINGER INGELHEIM PHARMA KG.  
 XX  
 PI Budzinski R, Krist B, Mark M, Mueller P;  
 XX  
 DR WPI; 1999-143775/13.  
 XX  
 PT RNA transcript of human cholesteryl ester transfer protein gene - useful  
 PT in drug screening assays, especially for atherosclerosis.  
 XX  
 PS Disclosure; Page 13; 24pp; German.  
 XX  
 CC This invention describes the isolation of a transcript of the human  
 CC cholesteryl ester transfer protein (CETP) gene having a 5' untranslated  
 CC region including a regulatory sequence. The invention also describes a  
 CC method (a) for identifying substances capable of inhibiting CETP gene  
 CC expression, comprising measuring the translation rate of the above  
 CC transcript in the presence of a test substance, (2) a test substance  
 CC capable of inhibiting CETP gene expression, (3) an antisense  
 CC oligonucleotide capable of binding to the 5' untranslated region of the  
 CC above transcript and (4) a method based on surface plasmon resonance for

CC measuring the binding of a substance to a nucleic acid. The test  
 CC substance of (2) and the oligonucleotide of (3) are useful for  
 CC prophylactic or therapeutic treatment of vascular diseases in which CETP  
 CC has a pathogenic role, especially atherosclerosis  
 XX  
 SQ Sequence 17 BP; 2 A; 8 C; 1 G; 0 T; 6 U; 0 Other;  
 Query Match 12.2%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1715 GAGTACGGAGATGGAGA 1731  
 Db 17 GAGTACGGAGATGGAGA 1  
 RESULT 15  
 AAI99829  
 ID AAI99829 standard; DNA; 21 BP.  
 XX  
 AC AAI99829;  
 XX  
 DT 28-JAN-2002 (first entry)  
 XX  
 DE Human G protein-coupled receptor protein TGR5 PCR primer SEQ ID NO 5.  
 XX  
 KW Human; TGR5; G protein-coupled receptor protein; cerebroprotective;  
 KW cardiant; immunomodulator; cytostatic; antiinflammatory; antidiabetic;  
 KW cancer; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177325-A1.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 12-APR-2001; 2001WO-JP003143.  
 XX  
 PR 12-APR-2000; 2000JP-00110765.  
 XX  
 PA (TAKE) TAKEDA CHEM IND LTD.  
 XX  
 PI Miwa M, Matsui H, Shintani Y;  
 XX  
 DR WPI; 2002-010910/01.  
 XX  
 PT Human brain-originated G protein-coupled receptor protein TGR5,  
 PT applicable in diagnosis and developing drugs for diseases of e.g. central  
 PT nervous system and digestive organs, inflammation, cancer and diabetes.  
 XX  
 PS Example 2; Page 98; 104pp; Japanese.  
 XX  
 CC The invention relates to a novel human G protein-coupled receptor protein  
 CC TGR5 and the encoding cDNA with cerebroprotective, cardiant,  
 CC immunomodulator, cytostatic, antiinflammatory and antidiabetic activity.  
 CC The protein, encoded DNA and anti-TGR5 antibody are applicable in  
 CC diagnosis and developing drugs for diseases of central nervous system and  
 CC circulatory organs, inflammation, cancer and diabetes. The present  
 CC sequence is that of a TGR5 PCR primer of the invention  
 XX  
 SQ Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 U; 0 Other;  
 Query Match 12.1%; Score 16.8; DB 1; Length 21;  
 Best Local Similarity 90.0%; Pred. No. 42;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1732 TTGGCTCCCACTCTCTCTT 1751  
 Db 1 TTGGCTCCCACTCTCTCTT 20  
 RESULT 16  
 ADB66783

```

ID  ADB66783 standard; DNA; 20 BP.
XX
AC  ADB66783;
XX
XX  04-DEC-2003 (first entry)
XX
DE  Human E2A-Pbx1 antisense phosphorothioate oligonucleotide ISIS No. 16123.
XX
XX  Human; E2A-Pbx1; antisense; phosphorothioate;
XX  pre-B-cell acute lymphocytic leukaemia; sarcomatous cancer; E2A-HLA;
KW  E2A-HLF; cytostatic; ss.
XX
OS  Synthetic.
OS  Homo sapiens.
XX
XX  Key      Location/Qualifiers
FH  modified_base 1..20
FT  /*tag= a
FT  /mod_base= OTHER
FT  /note= "Phosphorothioate internucleotide linkages"
XX
XX  US6607915-B1.
XX
XX  19-AUG-2003.
XX
XX  25-JUL-2000; 2000US-00624945.
XX
XX  30-SEP-1999; 99US-0156836P.
XX
XX  (ISIS-) ISIS PHARM INC.
XX
XX  Monia BP, Wanciewicz E;
PI  WPI; 2003-707866/67.
XX
XX  New antisense compounds targeted to nucleic acids encoding E2A-Pbx1,
PT  useful for inhibiting the expression of E2A-Pbx1, and for treating or
PT  diagnosing a disease associated with overexpression of E2A-Pbx1, e.g.
PT  sarcomatous cancer.
XX
XX  Example 2; Col 24; 20pp; English.
XX
XX  The present invention relates to antisense compounds targeted to
CC  polynucleotide sequences encoding human E2A-Pbx1. The antisense compounds
CC  comprise antisense phosphorothioate oligonucleotides. The antisense
CC  compounds are useful for inhibiting the expression of E2A-Pbx1, and for
CC  treating or diagnosing a disease or condition associated with the
CC  overexpression or constitutive activation of E2A-Pbx1, e.g. pre-B-cell
CC  acute lymphocytic leukaemia or sarcomatous cancer. The compounds are also
CC  useful as research reagents and tools, e.g. for detecting and determining
CC  the role of E2-Pbx1 in various cell functions and physiological
CC  processes. The present sequence represents a human E2A-Pbx1 antisense
CC  phosphorothioate oligonucleotide.
XX
XX  Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
SQ
Query Match      11.8%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 48;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1658 ACCAGGCTCAGCTGGA 1675
    |||||
Db  1 ACCAGGCTGACAGCTGGA 18

RESULT 17
AAV52705
ID  AAV52705 standard; DNA; 22 BP.
XX
XX  AAV52705;
AC
XX
XX  21-DEC-1998 (first entry)
DT
XX

```

```

DE  Hepatocyte nuclear factor 1 beta gene exon 4-2 forward PCR primer.
XX
XX  Hepatocyte nuclear factor 1 beta; HNF-1 beta; MODY4; human;
KW  transcription factor; maturity onset diabetes of the young; TCF2;
KW  diabetes; NIDDM; diagnosis; therapy; PCR; primer; ss.
XX
OS  Synthetic.
OS  Homo sapiens.
XX
XX  WO9811254-A1.
PN
XX
XX  19-MAR-1998.
PD
XX
XX  10-SEP-1997; 97WO-US016037.
PF
XX
XX  10-SEP-1996; 96US-0025719P.
PR
XX  02-OCT-1996; 96US-0028056P.
PR
XX  30-OCT-1996; 96US-0029679P.
PR
XX
XX  (ARCH-) ARCH DEV CORP.
PA
XX
XX  Bell GI, Yamagata K, Oda N, Kaisaki PJ, Furuta H, Menzel S;
PI  Horikawa Y;
PI
XX
XX  WPI; 1998-271667/24.
DR
XX
XX  Isolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and 1-
PT  beta - useful for detecting susceptibility for non-insulin dependent
PT  diabetes, especially maturity-onset diabetes of the young.
XX
XX  Example 8; Page 146; 363pp; English.
XX
XX  This is a forward PCR primer designed for use with a reverse primer (see
CC  AAV52706) in the PCR amplification of the 4-2 exon of the human
CC  hepatocyte nuclear factor-1 beta (HNF-1 beta) TCF2 gene (see AAV52730).
CC  Mutations of the HNF-1 beta gene have been identified by amplifying (see
CC  AAV5293-716) and sequencing the appropriate exon. The invention concerns
CC  the identification of genes responsible for non-insulin dependent
CC  diabetes mellitus (NIDDM) for use in diagnostics and therapeutics. It
CC  demonstrates that the MODY4 (maturity-onset diabetes of the young) locus
CC  is the HNF-1 beta gene. Analysis of mutations in the HNF-1 beta gene can
CC  be diagnostic for diabetes
XX
XX  Sequence 22 BP; 8 A; 9 C; 3 G; 2 T; 0 U; 0 Other;
SQ
Query Match      11.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1658 ACCAGGCTCAGCTGGAACC 1678
    |||||
Db  2 ACCAGACTCAGCTGAACC 22

RESULT 18
ABZ57102/C
ID  ABZ57102 standard; DNA; 24 BP.
XX
XX  ABZ57102;
AC
XX
XX  24-MAR-2003 (first entry)
DT
XX
XX  Human zinc finger protein 12.76 RT-PCR primer, SEQ ID NO:3.
DE
XX
XX  Human; zinc finger protein 12.76; recombinant production; gene therapy;
KW  cancer; tumour; development disorder; cytostatic;
KW  reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS  Homo sapiens.
OS
XX
XX  CN1355206-A.
PN
XX
XX  26-JUN-2002.
PD

```





```

Query Match      10.9%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1713 AGGAGTACGGAGATGGAGAT 1732
      ||||| ||||| ||||| |||||
DB 4 AGGAGGAGGGAGATGGACAT 23

RESULT 21
AAT49837
XX AC AAT49837;
XX DT 07-MAR-1997 (first entry)
XX DE Human CETP HH ribozyme target sequence #1752.
XX KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX OS Homo sapiens.
XX PN WO9620279-A1.
XX PD 04-JUL-1996.
XX PF 11-DEC-1995; 95WO-US016000.
XX PR 23-DEC-1994; 94US-00363240.
XX PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN ) WARNER LAMBERT CO.
XX PI Couture L, Stinchcomb D, Meswigen J, Bisgaier C, Pape M;
XX WPI; 1996-321852/32.
XX PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
PT useful for preventing or treating initial development, progression or
PT regression of vascular diseases, esp. familial hypercholesterolaemia.
PS Claim 4; Page 32; 72pp; English.
XX AAT49608-T49863 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT4981-
CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
CC transfer between plasma lipoproteins. The numbering of the targets refers
CC to the position of the cleavage site in full length CETP. The ribozyme
CC binds to 5 nucleotides either side of this site, provided the sequence
CC is immediately upstream. The ribozymes are able to cleave mRNA from the
CC gene encoding CETP, thereby blocking synthesis and/or expression of the
CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
CC can be inhibited (or eliminated) thereby preventing the reduction in size
CC density of the high density lipoproteins (HDL), prolonging HDL half life,
CC and therefore increasing HDL levels. The ribozymes can be used to treat
CC conditions associated with abnormal levels of CETP, specifically familial
CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
CC hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
CC vascular complications of diabetes, transplant, atherectomy and
CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
CC (a decrease in LDL levels), and a corresponding increase in HDL levels).
CC The HH ribozymes can also be used diagnostically to study genetic drift
CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
CC ribozymes target specific regions of the CETP gene, they have low non-
CC specific activity
```

```

XX SQ Sequence 15 BP; 4 A; 7 C; 0 G; 0 T; 4 U; 0 Other;
Query Match      10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 65;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1745 CTTCCCTATCCTTAAA 1759
      ||:||||:|||||
DB 1 CCUCCCUAUCUAAA 15

RESULT 22
AAT49841
XX ID AAT49841 standard; RNA; 15 BP.
XX AC AAT49841;
XX DT 07-MAR-1997 (first entry)
XX DE Human CETP HH ribozyme target sequence #1757.
XX KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX OS Homo sapiens.
XX PN WO9620279-A1.
XX PD 04-JUL-1996.
XX PF 11-DEC-1995; 95WO-US016000.
XX PR 23-DEC-1994; 94US-00363240.
XX PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN ) WARNER LAMBERT CO.
XX PI Couture L, Stinchcomb D, Meswigen J, Bisgaier C, Pape M;
XX WPI; 1996-321852/32.
XX PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
PT useful for preventing or treating initial development, progression or
PT regression of vascular diseases, esp. familial hypercholesterolaemia.
PS Claim 4; Page 32; 72pp; English.
XX AAT49608-T49863 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT4981-
CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
CC transfer between plasma lipoproteins. The numbering of the targets refers
CC to the position of the cleavage site in full length CETP. The ribozyme
CC binds to 5 nucleotides either side of this site, provided the sequence
CC is immediately upstream. The ribozymes are able to cleave mRNA from the
CC gene encoding CETP, thereby blocking synthesis and/or expression of the
CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
CC can be inhibited (or eliminated) thereby preventing the reduction in size
CC density of the high density lipoproteins (HDL), prolonging HDL half life,
CC and therefore increasing HDL levels. The ribozymes can be used to treat
CC conditions associated with abnormal levels of CETP, specifically familial
CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
CC hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
CC vascular complications of diabetes, transplant, atherectomy and
CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
CC (a decrease in LDL levels), and a corresponding increase in HDL levels).
CC The HH ribozymes can also be used diagnostically to study genetic drift
CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
CC ribozymes target specific regions of the CETP gene, they have low non-
CC specific activity
```



CC hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia, and therefore increasing HDL levels. The ribozymes can be used to treat conditions associated with abnormal levels of CETP, specifically familial hypercholesterolaemia, atherosclerosis, peripheral vascular disease, angioplastic restenosis. By inhibiting CETP, the levels of HDL and low density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a decrease in LDL levels, and a corresponding increase in HDL levels). The HH ribozymes can also be used diagnostically to study genetic drift and mutations in diseased cells, and to detect CETP mRNA. As the HH ribozymes target specific regions of the CETP gene, they have low non-specific activity

XX Sequence 15 BP; 3 A; 1 C; 6 G; 0 T; 5 U; 0 Other;

SQ Query Match 10.8%; Score 15; DB 1; Length 15;  
Best Local Similarity 66.7%; Pred. No. 65;  
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1706 TTGGGTTAGGATAC 1720  
Db 1 UUGGUUAGGAGUAC 15

RESULT 25  
AAT49811  
ID AAT49811 standard; RNA; 15 BP.  
XX AC AAT49811;  
XX 18-MAR-1997 (first entry)  
DT Human CETP HH ribozyme target sequence #1644.  
DE Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;  
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;  
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;  
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;  
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;  
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;  
KW LDL; ss.  
XX Homo sapiens.  
XX OS  
XX WO9620279-A1.  
XX PN  
XX PD 04-JUL-1996.  
XX PF 11-DEC-1995; 95WO-US016000.  
XX PR 23-DEC-1994; 94US-00363240.  
XX PA (RIBO-) RIBOZYME PHARM INC.  
XX PA (WARN ) WARNER LAMBERT CO.  
XX PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;  
XX WPI; 1996-321852/32.  
XX DR  
XX PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -  
XX PT useful for preventing or treating initial development, progression or  
XX PT regression of vascular diseases, esp. familial hypercholesterolaemia.  
XX PS Claim 4; Page 32; 72pp; English.  
XX AAT49608-T49863 represent target sequences for the human cholesterol  
XX CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-  
XX CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid  
XX CC transfer between plasma lipoproteins. The numbering of the targets refers  
XX CC to the position of the cleavage site in full length CETP. The ribozyme  
XX CC binds to 5 nucleotides either side of this site, provided the sequence UH  
XX CC is immediately upstream. The ribozymes are able to cleave mRNA from the  
XX CC gene encoding CETP, thereby blocking synthesis and/or expression of the  
XX CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway  
XX CC can be inhibited (or eliminated) thereby preventing the reduction in size  
XX CC density of the high density lipoproteins (HDL), prolonging HDL half life,

CC and therefore increasing HDL levels. The ribozymes can be used to treat conditions associated with abnormal levels of CETP, specifically familial hypercholesterolaemia, atherosclerosis, peripheral vascular disease, angioplastic restenosis. By inhibiting CETP, the levels of HDL and low density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a decrease in LDL levels, and a corresponding increase in HDL levels). The HH ribozymes can also be used diagnostically to study genetic drift and mutations in diseased cells, and to detect CETP mRNA. As the HH ribozymes target specific regions of the CETP gene, they have low non-specific activity

XX Sequence 15 BP; 4 A; 2 C; 6 G; 0 T; 3 U; 0 Other;

SQ Query Match 10.8%; Score 15; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 65;  
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1637 GGCTTGATAGAGAAG 1651  
Db 1 GGCUGUAGGAGAAG 15

RESULT 26  
AAT49809  
ID AAT49809 standard; RNA; 15 BP.  
XX AC AAT49809;  
XX 18-MAR-1997 (first entry)  
DT Human CETP HH ribozyme target sequence #1641.  
DE Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;  
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;  
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;  
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;  
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;  
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;  
KW LDL; ss.  
XX Homo sapiens.  
XX OS  
XX WO9620279-A1.  
XX PN  
XX PD 04-JUL-1996.  
XX PF 11-DEC-1995; 95WO-US016000.  
XX PR 23-DEC-1994; 94US-00363240.  
XX PA (RIBO-) RIBOZYME PHARM INC.  
XX PA (WARN ) WARNER LAMBERT CO.  
XX PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;  
XX WPI; 1996-321852/32.  
XX DR  
XX PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -  
XX PT useful for preventing or treating initial development, progression or  
XX PT regression of vascular diseases, esp. familial hypercholesterolaemia.  
XX PS Claim 4; Page 32; 72pp; English.  
XX AAT49608-T49863 represent target sequences for the human cholesterol  
XX CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-  
XX CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid  
XX CC transfer between plasma lipoproteins. The numbering of the targets refers  
XX CC to the position of the cleavage site in full length CETP. The ribozyme  
XX CC binds to 5 nucleotides either side of this site, provided the sequence UH  
XX CC is immediately upstream. The ribozymes are able to cleave mRNA from the  
XX CC gene encoding CETP, thereby blocking synthesis and/or expression of the  
XX CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway  
XX CC can be inhibited (or eliminated) thereby preventing the reduction in size  
XX CC density of the high density lipoproteins (HDL), prolonging HDL half life,

CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway  
 CC can be inhibited (or eliminated) thereby preventing the reduction in size  
 CC density of the high density lipoproteins (HDL), prolonging HDL half life,  
 CC and therefore increasing HDL levels. The ribozymes can be used to treat  
 CC conditions associated with abnormal levels of CETP, specifically familial  
 CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,  
 CC hyperbetalipoproteinaemia, hypopalipoproteinaemia, dyslipidaemia,  
 CC vascular complications of diabetes, transplant, atherectomy and  
 CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low  
 CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered  
 CC (a decrease in LDL levels, and a corresponding increase in HDL levels).  
 CC The HH ribozymes can also be used diagnostically to study genetic drift  
 CC and mutations in diseased cells, and to detect CETP mRNA. As the HH  
 CC ribozymes target specific regions of the CETP gene, they have low non-  
 CC specific activity

SQ Sequence 15 BP; 2 A; 2 C; 7 G; 0 T; 4 U; 0 Other;  
 Query Match 10.8%; Score 15; DB 1; Length 15;  
 Best Local Similarity 73.3%; Pred. No. 65;  
 Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1634 TCGGGCTTCTAGCAG 1648  
 :|||||:|||||  
 Db 1 UGGGGCUUGAGCAG 15

## RESULT 27

AAT49827  
 ID AAT49827 standard; RNA; 15 BP.

AC AAT49827;

XX 07-MAR-1997 (first entry)

DE Human CETP HH ribozyme target sequence #1719.

XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;  
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;  
 KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;  
 KW familial hypercholesterolaemia; dyslipidaemia; hypopalipoproteinaemia;  
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;  
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;  
 KW LDL; ss.

XX Homo sapiens.

XX WO9620279-A1.

XX 04-JUL-1996.

XX 11-DEC-1995; 95WO-US016000.

XX 23-DEC-1994; 94US-00363240.

XX (RIBO-) RIBOZYME PHARM INC.

XX (WARN ) WARNER LAMBERT CO.

XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;

XX WPI; 1996-321852/32.

XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -  
 PT useful for preventing or treating initial development, progression or  
 PT regression of vascular diseases, esp. familial hypercholesterolaemia.

XX Claim 4; Page 32; 72pp; English.

XX AAT49608-749863 represent target sequences for the human cholesterol  
 CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-  
 CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid  
 CC transfer between plasma lipoproteins. The numbering of the targets refers  
 CC to the position of the cleavage site in full length CETP. The ribozyme

CC binds to 5 nucleotides either side of this site, provided the sequence UH  
 CC is immediately upstream. The ribozymes are able to cleave mRNA from the  
 CC gene encoding CETP, thereby blocking synthesis and/or expression of the  
 CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway  
 CC can be inhibited (or eliminated) thereby preventing the reduction in size  
 CC density of the high density lipoproteins (HDL), prolonging HDL half life,  
 CC and therefore increasing HDL levels. The ribozymes can be used to treat  
 CC conditions associated with abnormal levels of CETP, specifically familial  
 CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,  
 CC hyperbetalipoproteinaemia, hypopalipoproteinaemia, dyslipidaemia,  
 CC vascular complications of diabetes, transplant, atherectomy and  
 CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low  
 CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered  
 CC (a decrease in LDL levels, and a corresponding increase in HDL levels).  
 CC The HH ribozymes can also be used diagnostically to study genetic drift  
 CC and mutations in diseased cells, and to detect CETP mRNA. As the HH  
 CC ribozymes target specific regions of the CETP gene, they have low non-  
 CC specific activity

SQ Sequence 15 BP; 5 A; 1 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 10.8%; Score 15; DB 1; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 65;  
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1712 TAGGAGTACGGAGAT 1726

Db 1 UAGGAGUACGGAGAU 15

## RESULT 28

AAT49829

ID AAT49829 standard; RNA; 15 BP.

XX AAT49829;

XX 07-MAR-1997 (first entry)

XX Human CETP HH ribozyme target sequence #1733.

XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;  
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;  
 KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;  
 KW familial hypercholesterolaemia; dyslipidaemia; hypopalipoproteinaemia;  
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;  
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;  
 KW LDL; ss.

XX Homo sapiens.

XX WO9620279-A1.

XX 04-JUL-1996.

XX 11-DEC-1995; 95WO-US016000.

XX 23-DEC-1994; 94US-00363240.

XX (RIBO-) RIBOZYME PHARM INC.

XX (WARN ) WARNER LAMBERT CO.

XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;

XX WPI; 1996-321852/32.

XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -  
 PT useful for preventing or treating initial development, progression or  
 PT regression of vascular diseases, esp. familial hypercholesterolaemia.  
 XX Claim 4; Page 32; 72pp; English.

XX AAT49608-749863 represent target sequences for the human cholesterol  
 CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-

XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -  
PT useful for preventing or treating initial development, progression or  
PT regression of vascular diseases, esp. familial hypercholesterolaemia.  
XX  
PS Claim 4; Page 32; 72pp; English.

PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -  
PT useful for preventing or treating initial development, progression or

```

PT regression of vascular diseases, esp. familial hypercholesterolaemia.
XX
PS Claim 4; Page 32; 72pp; English.
XX
CC AAT49608-T49863 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
CC transfer between plasma lipoproteins. The numbering of the targets refers
CC to the position of the cleavage site in full length CETP. The ribozyme
CC binds to 5 nucleotides either side of this site, provided the sequence UH
CC gene encoding CETP, thereby blocking synthesis and/or expression of the
CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
CC can be inhibited (or eliminated) thereby preventing the reduction in size
CC density of the high density lipoproteins (HDL), prolonging HDL half life,
CC and therefore increasing HDL levels. The ribozymes can be used to treat
CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
CC vascular complications of diabetes, transplant, atherectomy and
CC hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
CC The HH ribozymes can also be used diagnostically to study genetic drift
CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
CC ribozymes target specific regions of the CETP gene, they have low non-
CC specific activity
XX
SQ Sequence 15 BP; 3 A; 0 C; 7 G; 0 T; 5 U; 0 Other;
Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1700 TGGAACTGGGTAG 1714
DB 1 UGGAAGUUGGUUAG 15
:|||||:|||||:

RESULT 31
AAT49831
ID AAT49831 standard; RNA; 15 BP.
XX
AC AAT49831;
XX
DT 07-MAR-1997 (first entry)
XX
DE Human CETP HH ribozyme target sequence #1738.
XX
KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US016000.
XX
PR 23-DEC-1994; 94US-00363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN ) WARNER LAMBERT CO.
XX
PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;
XX WPI; 1996-321852/32.
XX

```

---

```

XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
PT useful for preventing or treating initial development, progression or
PT regression of vascular diseases, esp. familial hypercholesterolaemia.
PT
XX Claim 4; Page 32; 72pp; English.
XX
CC AAT49608-T49863 represent target sequences for the human cholesterol
CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
CC transfer between plasma lipoproteins. The numbering of the targets refers
CC to the position of the cleavage site in full length CETP. The ribozyme
CC binds to 5 nucleotides either side of this site, provided the sequence UH
CC is immediately upstream. The ribozymes are able to cleave mRNA from the
CC gene encoding CETP, thereby blocking synthesis and/or expression of the
CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
CC can be inhibited (or eliminated) thereby preventing the reduction in size
CC density of the high density lipoproteins (HDL), prolonging HDL half life,
CC and therefore increasing HDL levels. The ribozymes can be used to treat
CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
CC vascular complications of diabetes, transplant, atherectomy and
CC hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
CC The HH ribozymes can also be used diagnostically to study genetic drift
CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
CC ribozymes target specific regions of the CETP gene, they have low non-
CC specific activity
XX
SQ Sequence 15 BP; 3 A; 6 C; 2 G; 0 T; 4 U; 0 Other;
Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 65;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1731 ATTGGCTCCCACTC 1745
DB 1 AUUGGCCUCCCACTC 15
:|||||:|||||:

RESULT 32
AAT49819
ID AAT49819 standard; RNA; 15 BP.
XX
AC AAT49819;
XX
DT 07-MAR-1997 (first entry)
XX
DE Human CETP HH ribozyme target sequence #1691.
XX
KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
PN WO9620279-A1.
XX
PD 04-JUL-1996.
XX
PF 11-DEC-1995; 95WO-US016000.
XX
PR 23-DEC-1994; 94US-00363240.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN ) WARNER LAMBERT CO.
XX

```

QY 1698 GGTGAAGTTGGG 1710  
 Db 1 GGTGGTAGTTGGG 13  
 RESULT 463  
 ABC16693/c  
 ID ABC16693 standard; DNA; 13 BP.  
 XX AC ABC16693;  
 XX DT 20-FEB-2002 (first entry)  
 XX DE Oligonucleotide SEQ ID NO 16700 for detecting SNP TSC0003627.  
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.  
 XX PN WO200177384-A2.  
 XX DT 18-OCT-2001.  
 XX PF 06-APR-2001; 2001WO-IB000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPITG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 16700; 29pp + Sequence Listing; German.  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 4 A; 6 C; 1 G; 2 T; 0 U; 0 Other;  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 4 A; 6 C; 1 G; 2 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1709 GGTGAGGAGTACG 1721  
 Db 13 GGTGAGGAGTTCG 1  
 RESULT 464  
 ABF16652/c  
 ID ABF16652 standard; DNA; 13 BP.  
 XX AC ABF16652;  
 XX DT 21-FEB-2002 (first entry)  
 XX DE Oligonucleotide SEQ ID NO 142165 for detecting SNP TSC0035612.  
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.  
 XX PN WO200177384-A2.  
 XX DT 18-OCT-2001.  
 XX PF 06-APR-2001; 2001WO-IB000713.

DE Oligonucleotide SEQ ID NO 116649 for detecting SNP TSC0029189.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.  
 XX PN WO200177384-A2.  
 XX DT 18-OCT-2001.  
 XX PF 06-APR-2001; 2001WO-IB000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPITG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 116649; 29pp + Sequence Listing; German.  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1739 CCAACTCCTCCCT 1751  
 Db 13 CCAACTACTCCCT 1  
 RESULT 465  
 ABF42168/c  
 ID ABF42168 standard; DNA; 13 BP.  
 XX AC ABF42168;  
 XX DT 21-FEB-2002 (first entry)  
 XX DE Oligonucleotide SEQ ID NO 142165 for detecting SNP TSC0035612.  
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.  
 XX PN WO200177384-A2.  
 XX DT 18-OCT-2001.  
 XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 142165; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 13 BP; 2 A; 0 C; 8 G; 3 T; 0 U; 0 Other;  
  
Query Match 8.2%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1737 TCCCAACTCTCC 1749  
Db 13 TCCCAACTCTCC 1  
|||||  
|  
RESULT 466  
ABH62596  
ID ABH62596 standard; DNA; 13 BP.  
XX AC ABH62596;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 262573 for detecting SNP TSC0001590.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.

PS Claim 1; SEQ ID NO 262573; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;  
  
Query Match 8.2%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1703 AGTTGGGTAGG 1715  
Db 1 AAGTTGGGTAGG 13  
|||||  
|  
RESULT 467  
ABC93114/C  
ID ABC93114 standard; DNA; 13 BP.  
XX AC ABC93114;  
XX DT 21-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 93131 for detecting SNP TSC0023277.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX PS Claim 1; SEQ ID NO 93131; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at



```
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 9 G; 3 T; 0 U; 0 Other;

Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1738 CCAACTCTCTCCC 1750
DB 13 CCCACACTCTCC 1

RESULT 468
ABC70350/c
ID ABC70350 standard; DNA; 13 BP.
XX
AC ABC70350;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 70367 for detecting SNP TSC0018290.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 70367; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1739 CCAACTCTCTCCT 1751
DB 13 CCAACTCTCCT 1

RESULT 470
ABF10342
ID ABF10342 standard; DNA; 13 BP.
XX
AC ABF10342;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 110339 for detecting SNP TSC0027562.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
```



CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1701 GGAAGTGGGTTA 1713  
 Db 1 GGAAGTGGGTTA 13

RESULT 473  
 ABF42171  
 ID ABF42171 standard; DNA; 13 BP.

XX ABF42171;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 142168 for detecting SNP TSC0035612.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is  
 designed to detect single-nucleotide polymorphisms and cytosine  
 methylation status.

Claim 1; SEQ ID NO 142168; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic  
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 and cytosine methylation status in chemically pretreated genomic DNA. The  
 oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 range of diseases including immune system, gastrointestinal, respiratory,  
 central nervous system, cardiovascular and metabolic disorders. The  
 oligomers are also used for detecting cell type differentiation. ABC00010  
 -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 represent the oligomers described in the invention. NOTE: The sequence  
 data for this patent did not form part of the printed specification, but  
 was obtained in electronic format from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 13 BP; 2 A; 8 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1737 TCCCAACTCTCTCC 1749  
 Db 1 TCCCAACGCTCTCC 13

RESULT 474

ABH33146/C

ID ABH33146 standard; DNA; 13 BP.

XX ABH33146;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 233123 for detecting SNP TSC0056884.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is  
 designed to detect single-nucleotide polymorphisms and cytosine  
 methylation status.

Claim 1; SEQ ID NO 233123; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic  
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 and cytosine methylation status in chemically pretreated genomic DNA. The  
 oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 range of diseases including immune system, gastrointestinal, respiratory,  
 central nervous system, cardiovascular and metabolic disorders. The  
 oligomers are also used for detecting cell type differentiation. ABC00010  
 -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 represent the oligomers described in the invention. NOTE: The sequence  
 data for this patent did not form part of the printed specification, but  
 was obtained in electronic format from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1747 TCCCTATCTCTAAA 1759  
 Db 13 TACCTATCTCTAAA 1

RESULT 475

ABF15452/C

ID ABF15452 standard; DNA; 13 BP.

XX ABF15452;

```
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 115449 for detecting SNP TSC0028931.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 115449; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 0 C; 9 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1739 CCACCTCCTCCCT 1751
Db 13 CCCACTCCTCCCT 1
XX
RESULT 476
ABF62159/c
ID ABF62159 standard; DNA; 13 BP.
XX AC ABF62159;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 162156 for detecting SNP TSC0040797.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 115449; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 0 C; 9 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1739 CCACCTCCTCCCT 1751
Db 13 CCCACTCCTCCCT 1
XX
RESULT 477
ABC49591
ID ABC49591 standard; DNA; 13 BP.
XX AC ABC49591;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 49608 for detecting SNP TSC0014014.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 162156; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 8 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1698 GGTGGAAGTTGGG 1710
Db 13 GGTGGTAGTTGGG 1
XX
RESULT 477
ABC49591
ID ABC49591 standard; DNA; 13 BP.
XX AC ABC49591;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 49608 for detecting SNP TSC0014014.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 162156; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 8 C; 0 G; 1 T; 0 U; 0 Other;
```

PT designed to detect single-nucleotide polymorphisms and cytosine  
methylation status.

XX Claim 1; SEQ ID NO 49608; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
and cytosine methylation status in chemically pretreated genomic DNA. The  
oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
range of diseases including immune system, gastrointestinal, respiratory,  
central nervous system, cardiovascular and metabolic disorders. The  
oligonucleotides are also used for detecting cell type differentiation. ABC00010  
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
represent the oligomers described in the invention. NOTE: The sequence  
data for this patent did not form part of the printed specification, but  
was obtained in electronic format from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 2 A; 6 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1745 CCTCCTATCCTA 1757

Db 1 CCTCCTATCCTA 13

RESULT 478

ABC25065/c

ID ABC25065 standard; DNA; 13 BP.

XX ABC25065;

XX 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 25082 for detecting SNP TSC0006096.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
designed to detect single-nucleotide polymorphisms and cytosine  
methylation status.

XX Claim 1; SEQ ID NO 25082; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
and cytosine methylation status in chemically pretreated genomic DNA. The  
oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
range of diseases including immune system, gastrointestinal, respiratory,  
central nervous system, cardiovascular and metabolic disorders. The  
oligonucleotides are also used for detecting cell type differentiation. ABC00010  
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence  
data for this patent did not form part of the printed specification, but  
was obtained in electronic format from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1697 TGGTCGAAGTTGG 1709

Db 13 TAGTGGGAAGTTGG 1

RESULT 479

ABC08446/c

ID ABC08446 standard; DNA; 13 BP.

XX ABC08446;

XX 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 8437 for detecting SNP TSC0002329.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
designed to detect single-nucleotide polymorphisms and cytosine  
methylation status.

XX Claim 1; SEQ ID NO 8437; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
and cytosine methylation status in chemically pretreated genomic DNA. The  
oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
range of diseases including immune system, gastrointestinal, respiratory,  
central nervous system, cardiovascular and metabolic disorders. The  
oligonucleotides are also used for detecting cell type differentiation. ABC00010  
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
represent the oligomers described in the invention. NOTE: The sequence  
data for this patent did not form part of the printed specification, but  
was obtained in electronic format from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1747 TCCCTATCCTAAA 1759

|||||

```

Db      13  TCCATATCCTAAA 1
RESULT 480
ABC84786/c
ID      ABC84786 standard; DNA; 13 BP.
XX
AC      ABC84786;
XX
DT      21-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 84803 for detecting SNP TSC0021342.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
DT      21-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 84803 for detecting SNP TSC0021342.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
PI      WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 84803; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1746 CTCCTATCCTAA 1758
Db      13 CTCCTATCCTAA 1
||||| |||||
13 CTCCTATCCTAA 1

RESULT 481
ABF10343/c
ID      ABF10343 standard; DNA; 13 BP.
XX
AC      ABF10343;
XX
DT      21-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 110340 for detecting SNP TSC0027562.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
PI      WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 84803; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1701 GGAAGTGGGTTA 1713
Db      13 GGAAGTGGGTTA 1
||||| |||||
13 GGAAGTGGGTTA 1

RESULT 482
ABC62760/c
ID      ABC62760 standard; DNA; 13 BP.
XX
AC      ABC62760;
XX
DT      21-FEB-2002 (first entry)
XX
DE      Oligonucleotide SEQ ID NO 62777 for detecting SNP TSC0016623.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
PI      WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 110340; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
XX
Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1701 GGAAGTGGGTTA 1713
Db      13 GGAAGTGGGTTA 1
||||| |||||
13 GGAAGTGGGTTA 1

```

XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX XX WPI; 2001-657177/75.  
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 62777; 29pp + Sequence Listing; German.  
XX XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 13 BP; 3 A; 0 C; 8 G; 2 T; 0 U; 0 Other;  
  
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;  
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1745 CCTCCTATCCTA 1757  
DB 13 CCCCCCTATCCTA 1  
  
RESULT 483  
ABC38204/C  
ID ABC38204 standard; DNA; 13 BP.  
XX AC ABC38204;  
XX DT 20-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 38221 for detecting SNP TSC0011836.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN W0200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX XX WPI; 2001-657177/75.  
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 38221; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 13 BP; 4 A; 0 C; 8 G; 1 T; 0 U; 0 Other;  
  
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;  
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1744 TCCTCCTATCCT 1756  
DB 13 TCCCCCTATCCT 1  
  
RESULT 484  
ABF36186/C  
ID ABF36186 standard; DNA; 13 BP.  
XX AC ABF36186;  
XX DT 21-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 136183 for detecting SNP TSC0034006.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN W0200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX XX WPI; 2001-657177/75.  
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 136183; 29pp + Sequence Listing; German.  
XX XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX XX

RESULT 486  
ABC26849



XX WO200177384-A2.  
 PN 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 XX PF 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 62608; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1701 GGAAGTTGGGTTA 1713  
 Db 13 GGAAGTTGGGTTA 1  
 RESULT 488  
 ABC65199/c  
 ID ABC65199 standard; DNA; 13 BP.  
 AC ABC65199;  
 XX 21-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 65216 for detecting SNP TSC0017166.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 XX 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 XX PF 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 62608; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1701 GGAAGTTGGGTTA 1713  
 Db 13 GGAAGTTGGGTTA 1

DR WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 65216; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 4 A; 7 C; 0 G; 2 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1701 GGAAGTTGGGTTA 1713  
 Db 13 GGAAGTTGGGTTA 1  
 RESULT 489  
 ABC08447  
 ID ABC08447 standard; DNA; 13 BP.  
 XX ABC08447;  
 AC 20-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 8438 for detecting SNP TSC0002329.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 XX 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 XX PF 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 8438; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC

CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1747 TCCCTATCCTAA 1759  
 DB 1 TCCATATCCTAA 13  
 RESULT 490  
 ABH57117/C  
 ID ABH57117 standard; DNA; 13 BP.  
 XX  
 AC ABH57117;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 257094 for detecting SNP TSC0062579.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 257094; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 4 A; 6 C; 1 G; 2 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1747 TCCCTATCCTAA 1759  
 DB 1 TCCATATCCTAA 13  
 RESULT 490  
 ABH57117/C  
 ID ABH57117 standard; DNA; 13 BP.  
 XX  
 AC ABH57117;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 257094 for detecting SNP TSC0062579.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 257094; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 4 A; 6 C; 1 G; 2 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1710 GTTAGGAGTACGG 1722  
 DB 13 GTTTGGAGTACGG 1  
 RESULT 491  
 ABC84686  
 ID ABC84686 standard; DNA; 13 BP.  
 XX  
 AC ABC84686;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 84703 for detecting SNP TSC0021323.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 84703; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 5 A; 0 C; 7 G; 1 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1719 ACGGAGATGGAGA 1731  
 DB 1 AGGGAGATGGAGA 13  
 RESULT 492  
 ABC93116/C  
 ID ABC93116 standard; DNA; 13 BP.  
 XX  
 AC ABC93116;  
 XX  
 DT 21-FEB-2002 (first entry)



```
XX PS Claim 1; SEQ ID NO 119167; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 0 C; 8 G; 1 T; 0 U; 0 Other;

Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1739 CCACTCTCTCCT 1751
Db 13 CCTACTCTCTCCT 1

RESULT 495
ABF19306
ID ABF19306 standard; DNA; 13 BP.
XX AC ABF19306;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 119303 for detecting SNP TSC0029792.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX DN WO200177384-A2.
XX PT 18-OCT-2001.
XX PS 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX DN Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 119303; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1747 TCCTATCTCTTAA 1759
Db 1 TACCTATCTTAA 13

RESULT 496
ABH33147
ID ABH33147 standard; DNA; 13 BP.
XX AC ABH33147;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 233124 for detecting SNP TSC0056884.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX DN Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 233124; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1747 TCCTATCTCTTAA 1759
Db 1 TACCTATCTTAA 13
```

RESULT 497  
 ABF19307/c  
 ID ABF19307 standard; DNA; 13 BP.  
 XX  
 AC ABF19307;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 119304 for detecting SNP TSC0029792.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 119304; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 5 A; 7 C; 0 G; 1 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1699 GTGCACTGTGGGT 1711  
 DB 13 GTGCTAGTTGGGT 1  
 RESULT 498  
 ABF42169  
 ID ABF42169 standard; DNA; 13 BP.  
 XX  
 AC ABF42169;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 142166 for detecting SNP TSC0035612.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 WIPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 142166; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 8 C; 0 G; 2 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1737 TCCCAACTCTCC 1749  
 DB 1 TCCCAACACCTCC 13  
 RESULT 499  
 ABC93115  
 ID ABC93115 standard; DNA; 13 BP.  
 XX  
 AC ABC93115;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 93132 for detecting SNP TSC0023277.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.

XX FI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 93132; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 3 A; 9 C; 0 G; 1 T; 0 U; 0 Other;  
XX  
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;  
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1738 CCCAACTCCTCCC 1750  
XX | | | | | | | | | |  
XX 1 CCCAACACCTCCC 13  
XX  
XX RESULT 500  
XX ID ABC23224 standard; DNA; 13 BP.  
XX AC ABC23224;  
XX 20-FEB-2002 (first entry)  
XX Oligonucleotide SEQ ID NO 23241 for detecting SNP TSC0004727.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 23241; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 3 A; 9 C; 0 G; 1 T; 0 U; 0 Other;  
XX  
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;  
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1738 CCCAACTCCTCCC 1750  
XX | | | | | | | | | |  
XX 1 CCCAACACCTCCC 13  
XX  
XX RESULT 500  
XX ID ABC23224 standard; DNA; 13 BP.  
XX AC ABC23224;  
XX 20-FEB-2002 (first entry)  
XX Oligonucleotide SEQ ID NO 23241 for detecting SNP TSC0004727.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 23241; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;  
XX  
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;  
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1701 GGAAGTTGGTTA 1713  
XX | | | | | | | | | |  
XX 1 GGAAGTTGGTTA 13  
XX  
XX RESULT 501  
XX ID ABC93113 standard; DNA; 13 BP.  
XX AC ABC93113;  
XX 21-FEB-2002 (first entry)  
XX Oligonucleotide SEQ ID NO 93130 for detecting SNP TSC0023277.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 93130; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 2 A; 13 C; 0 G; 1 T; 0 U; 0 Other;  
XX

```

Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1738 CCCAACTCCTCCC 1750
DB 1 CCCAACCCCTCCC 13

RESULT 502
ABC84687/c
ID ABC84687 standard; DNA; 13 BP.
XX AC ABC84687;
XX DE
XX DT 21-FEB-2002 (first entry)
XX DE
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 84704; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 1 A; 7 C; 0 G; 5 T; 0 U; 0 Other;

Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1719 ACGGAGATGGAGA 1731
DB 13 ACGGAGATGGAGA 1

RESULT 503
ABC38205
ID ABC38205 standard; DNA; 13 BP.
XX AC ABC38205;
XX DE
XX DT 21-FEB-2002 (first entry)
XX DE
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 84704; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 1 A; 7 C; 0 G; 5 T; 0 U; 0 Other;

Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1744 TCCTCCCTATCCT 1756
DB 1 TCCTCCCTATCCT 13

RESULT 504
ABF36187
ID ABF36187 standard; DNA; 13 BP.
XX AC ABF36187;
XX DE
XX DT 21-FEB-2002 (first entry)
XX DE
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 38222; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 1 A; 8 C; 0 G; 4 T; 0 U; 0 Other;

Query Match      8.2%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1744 TCCTCCCTATCCT 1756
DB 1 TCCTCCCTATCCT 13

RESULT 504
ABF36187
ID ABF36187 standard; DNA; 13 BP.
XX AC ABF36187;
XX DE
XX DT 21-FEB-2002 (first entry)
XX DE
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 38222; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 1 A; 8 C; 0 G; 4 T; 0 U; 0 Other;

```





CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1703 AAGTTGGGTAGG 1715  
 |||||  
 Db 13 AAGTTGGGTAGG 1

RESULT 507  
 AAT98901  
 ID AAT98901 standard; DNA; 14 BP.  
 XX  
 AC AAT98901;  
 XX  
 DT 23-MAR-1998 (first entry)  
 XX  
 DE Probe 41w32 for HIV RT gene wild type E40M41.  
 XX  
 KW Reverse transcriptase gene; HIV; RT gene; antiviral drug susceptibility;  
 KW virus susceptibility; antiviral drug resistant viral strain; retrovirus;  
 KW Hepadnaviridae; HIV RT genotyping; probe; ss.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus 1.  
 PN WO9727332-A1.  
 XX  
 PD 31-JUL-1997.  
 XX  
 PF 17-JAN-1997; 97WO-EP000211.  
 XX  
 PR 26-JAN-1996; 96EP-00870005.  
 PR 25-JUN-1996; 96EP-00870081.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Stuyver L, Louwagie J, Rossau R;  
 XX  
 DR WPI; 1997-393716/36.  
 XX  
 PT Determining susceptibility to antiviral drugs of reverse transcriptase  
 PT containing viruses - useful for genotyping HIV RT and detecting antiviral  
 PT resistant HIV.  
 XX  
 PS Claim 13; Page 36; 59pp; English.  
 XX  
 CC This sequence represents a probe for a wild type HIV reverse  
 CC transcriptase (Rt) gene fragment. This sequence can be used in the method  
 CC of the invention for determining the susceptibility to antiviral drugs of  
 CC viruses which contain Rt genes and are present in a biological sample. It  
 CC comprises: (1) releasing, isolating or concentrating the polynucleic  
 CC acids present in a sample; (2) amplifying the relevant part of the Rt  
 CC genes present with at least one suitable primer pair; (3) hybridising the  
 CC polynucleic acids of step (1) or (2) with at least two Rt gene probes,  
 CC the probes being applied to known locations on a solid support, and are  
 CC capable of simultaneously hybridising to their respective target regions  
 CC under appropriate hybridisation and wash condition allowing the detection  
 CC of homologous targets, or with the probes hybridising specifically with a  
 CC sequence complementary to any of the target sequences; (4) detecting the  
 CC hybrids formed in step (3); and (4) inferring the nucleotide sequence at  
 CC the codons of interest (codons 38-44, 47-53, 65-72, 73-77, 148-154, 180-  
 CC 187, 212-216, and 217-220), and/or the amino acids of the codons of  
 CC interest and/or antiviral drug resistance spectrum, and possible the type  
 CC of viral isolates involved from the differential hybridisation signals

CC obtained in step (4). The method is specifically used to detect antiviral  
 CC drug resistant strains of viruses containing RT genes, especially HIV  
 CC retroviruses and Hepadnaviridae. The method can also be used for  
 CC genotyping HIV RT  
 XX  
 SQ Sequence 14 BP; 6 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 14;  
 Best Local Similarity 92.3%; Pred. No. 3.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1717 GTACGAGATGGA 1729  
 |||||  
 Db 1 GTACGAGATGGA 13

RESULT 508  
 AAQ74479  
 ID AAQ74479 standard; DNA; 15 BP.  
 XX  
 AC AAQ74479;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 28-APR-1995 (first entry)  
 XX  
 DE Primer based on plasmid constructs pSD5MRV and pSD6RRV sequences.  
 XX  
 KW L-sorbose dehydrogenase; Gluconobacter oxydans; enzyme;  
 KW L-keto-L-gulononic acid; ascorbic acid; L-sorbose dehydrogenase; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9420609-A1.  
 XX  
 PD 15-SEP-1994.  
 XX  
 PF 08-MAR-1994; 94WO-JP000369.  
 XX  
 PR 08-MAR-1993; 93GB-00004700.  
 PR 28-SEP-1993; 93JP-00241851.  
 XX  
 PA (FUJI ) FUJISAWA PHARM CO LTD.  
 XX  
 PI Niwa M, Saito Y, Ishii Y, Yoshida M, Suzuki H;  
 XX  
 DR WPI; 1994-303017/37.  
 XX  
 PT Novel dehydrogenase enzymes - used in the production of L-keto-L-gulononic  
 PT acid and L-ascorbic acid.  
 XX  
 PS Example 9; Page 23; 47pp; Japanese.  
 XX  
 CC Seven primers (AAQ74479-85) were based on sequences of the constructs  
 CC designated pSD5MRV and pSD6RRV and used in amplification reactions.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 15 BP; 4 A; 1 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 92.3%; Pred. No. 4e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1724 GATGAGATTGGC 1736  
 |||||  
 Db 2 GATGAGATTGGC 14

RESULT 509  
 AAT04287  
 ID AAT04287 standard; DNA; 15 BP.  
 XX  
 AC AAT04287;  
 XX

```

DT 09-APR-1996 (first entry)
XX
DE G. oxydans T100 L-sorbose dehydrogenase gene primer 1.
XX
KW L-sorbose dehydrogenase; 2-keto-gulonic acid; ascorbic acid; synthesis;
KW recombinant production; expression vector; primer 1; ss.
XX
OS Synthetic.
XX
PN WO9523220-A1.
XX
PD 31-AUG-1995.
XX
PF 24-FEB-1995; 95WO-JP000285.
XX
PR 25-FEB-1994; 94JP-00028612.
XX
PA (FUJII) FUJISAWA PHARM CO LTD.
XX
PI Niwa M, Saito Y, Ishii Y, Yoshida M, Hayashi H;
XX WPI; 1995-311531/40.
XX
DR Vector containing L-sorbose and L-sorbose dehydrogenase genes - used to
PT transform microorganisms for the efficient production of 2-keto-L-gulonic
PT acid.
XX
PS Example 9; Page 21; 78pp; Japanese.
XX
AAAT04287-T04293 are primers for the G. oxydans L-sorbose dehydrogenase
CC (SNDH) gene. An expression vector contg. the G. oxydans L-sorbose
CC dehydrogenase and SNDH genes arranged in sequence from a single promoter,
CC is used to transform Gluconobacter or Acetobacter spp. hosts. The hosts
CC then express the above dehydrogenases which are used in the prodn. of
CC large quantities of 2-keto-gulonic acid, an ascorbic acid synthesis
CC intermediate
XX
SQ Sequence 15 BP; 4 A; 1 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1724 GATGGAGATTGGC 1736
DB ||||| |||||
2 GATGGAGATTGGC 14

RESULT 510
AAQ80594/C
ID AAQ80594 standard; DNA; 15 BP.
XX
XX AAQ80594;
XX AC
XX 25-MAR-2003 (revised)
DT 12-OCT-1995 (first entry)
XX
XX M.tuberculosis 16S rRNA 3'-biotinylated capture probe.
DE
DE Mycobacterium tuberculosis; 16S ribosomal RNA;
KW strand displacement amplification; simultaneous detection;
KW adaptor-mediated multiplex amplification; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 15
FT /*tag= a
FT /note= "3'-biotinylated"
XX
XX EP640691-A2.
XX PN
XX 01-MAR-1995.
XX PD

16-AUG-1994; 94EP-00112741.
XX
24-AUG-1993; 93US-00111076.
XX
(BECT) BECTON DICKINSON CO.
XX
Walker GT, Nadeau JG, Spears PA, Nycz CM, Shank DD, Schram JL;
PI Jurgensen SR;
PI WPI; 1995-092337/13.
XX
Detection of Mycobacterium by multiplex nucleic acid amplification - by
PT amplification of the IS6110 insertion element of M. tuberculosis, allows
PT detection and/or identification of the M. tuberculosis complex.
XX
Example 3; Page 16; 23pp; English.
XX
A Mycobacterium tuberculosis IS6110 amplification primer (AAQ80578) is
CC used in a PCR and the extension product is then displaced and an IS6110
CC adaptor primer (AAQ80579) is hybridised to it. Following extension of the
CC adaptor primer, the second extension product is displaced and hybridised
CC to a M.tuberculosis 16S rRNA gene amplification primer (AAQ80582) which
CC is then extended. The third extension product is displaced and hybridised
CC to a 16S adaptor primer (AAQ80583) for chain extension; the fourth
CC extension product is then displaced and is amplified simultaneously with
CC the second extension product using the IS6110 and 16S amplification
CC primers. The new method allows coamplification of genus- (i.e. 16S rRNA)
CC and species- (i.e. IS6110) specific target nucleic acids by strand
CC displacement amplification. Opt. an internal control sequence (AAQ80589)
CC can be added to the sample prior to initial amplification. In this case,
CC amplified target and control sequences were captured on microwell plates
CC by hybridisation to an immobilised (via biotin-streptavidin binding)
CC capture probe. Detector probes labelled with alkaline phosphatase were
CC then used in a sandwich hybridisation assay to indirectly detect the
CC amplification products. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 15 BP; 2 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1658 ACCAGGCTCACAG 1670
DB ||||| |||||
14 ACCAGGCTCACAG 2

RESULT 511
AAZ62841
ID AAZ62841 standard; RNA; 15 BP.
XX
XX AAZ62841;
XX AC
XX 28-MAR-2000 (first entry)
DT
XX
XX Substrate for HH ribozyme HCV-8701 which cleaves HCV RNA at nt. 8701.
XX
XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
OS Hepatitis C virus.
XX
XX WO9955847-A2.
XX
XX 04-NOV-1999.
PD
XX
XX 26-APR-1999; 99WO-US009027.
PF
XX
XX 27-APR-1998; 98US-0083217P.
PR
XX 18-SEP-1998; 98US-0100842P.
PR
XX 25-FEB-1999; 99US-00257608.
PR

```

PR 23-MAR-1999; 99US-00274553.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;  
 XX WPI; 2000-062023/05.  
 XX  
 XX Novel ribozymes for the treatment of diseases and conditions related to  
 PT hepatitis C infection.  
 XX  
 XX Claim 1; Page 65; 123pp; English.  
 XX  
 CC The present sequence represents the preferred target sequence of an  
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves  
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given in  
 CC the descriptor line. The HCV sequence was screened for optimal ribozyme  
 CC target sites using a computer folding algorithm and regions of the mRNA  
 CC which did not form secondary folding structures and contained potential  
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to  
 CC target these sites and their activities optimised by either varying the  
 CC length of the binding arms or by modification to prevent degradation by  
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or  
 CC viral replication, and are used to treat diseases associated with  
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and  
 CC hepatocellular carcinoma. The ribozymes may be used in combination with  
 CC interferon to treat HCV infection, other infectious diseases, autoimmune  
 CC diseases, and cancer  
 XX  
 XX Sequence 15 BP; 2 A; 6 C; 3 G; 0 T; 4 U; 0 Other;  
 SQ

Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 69.2%; Pred. No. 4e+02;  
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCGTG 1698  
 Db 3 CUCCUCCACGUG 15  
 |||:|||||  
 |||:|||||

RESULT 512  
 AAF47175/C  
 ID AAF47175 standard; DNA; 15 BP.  
 XX  
 XX AAF47175;  
 XX  
 XX 30-MAR-2001 (first entry)  
 XX  
 XX IGFBP3 oligonucleotide #595.  
 XX  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 XX skin disorder; insulin-like growth factor 1 receptor; IGF-1; ptyriasis;  
 XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;  
 XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 XX hyperneovascular condition; hyperplasia; kidney disease;  
 XX neovascular condition of the retina; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200078341-A1.  
 XX  
 XX 28-DEC-2000.  
 XX  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX  
 XX 21-JUN-1999; 99US-0140345P.  
 XX  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 XX Wraight CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.

DR WPI; 2001-041421/05.  
 XX  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional), and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 XX Example 7; Page 48; 201pp; English.  
 PS  
 XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 XX Sequence 15 BP; 3 A; 8 C; 1 G; 3 T; 0 U; 0 Other;  
 SQ

Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 92.3%; Pred. No. 4e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1698 GGTGGAAGTTGGG 1710  
 Db 14 GGTGGAAGTTGGG 2  
 |||||  
 |||||

RESULT 513  
 AAF51493  
 ID AAF51493 standard; DNA; 15 BP.  
 XX  
 XX AAF51493;  
 XX  
 XX 30-MAR-2001 (first entry)  
 XX  
 XX IGF-I oligonucleotide #2453.  
 XX  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 XX skin disorder; insulin-like growth factor 1 receptor; IGF-1; ptyriasis;  
 XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;  
 XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 XX hyperneovascular condition; hyperplasia; kidney disease;  
 XX neovascular condition of the retina; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200078341-A1.  
 XX  
 XX 28-DEC-2000.  
 XX  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX  
 XX 21-JUN-1999; 99US-0140345P.  
 XX  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 XX Wraight CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.  
 XX  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.  
XX Example 8; Page 76; 201pp; English.  
XX  
XX The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia  
XX  
SQ Sequence 15 BP; 4 A; 7 C; 2 G; 2 T; 0 U; 0 Other;  
Query Match 8.2%; Score 11.4; DB 1; Length 15;  
Best Local Similarity 92.3%; Pred. No. 4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1666 CACAGCTGGAACC 1678  
Db 3 CACAGCTGCAACC 15  
RESULT 514  
AAF53421/c  
ID AAF53421 standard; DNA; 15 BP.  
XX  
XX AAF53421;  
XX  
XX 30-MAR-2001 (first entry)  
XX  
XX IGF-I oligonucleotide #4381.  
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.  
XX  
XX Homo sapiens.  
XX WO200078341-A1.  
XX  
XX 28-DEC-2000.  
XX  
XX 21-JUN-2000; 2000WO-AU000693.  
XX  
XX 21-JUN-1999; 99US-0140345P.  
XX (MURD-) MURDOCH CHILDRENS RES INST.  
XX  
XX Wright CJ, Werther GA, Edmondson SR;  
XX WPI; 2001-041421/05.  
XX  
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.  
XX  
XX Example 8; Page 89; 201pp; English.

XX  
CC The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia  
XX  
SQ Sequence 15 BP; 4 A; 3 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 8.2%; Score 11.4; DB 1; Length 15;  
Best Local Similarity 92.3%; Pred. No. 4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1753 TCCTAAAGGCCCA 1765  
Db 13 TCCTTAAGGCCCA 1  
RESULT 515  
AAF53420/c  
ID AAF53420 standard; DNA; 15 BP.  
XX  
XX AAF53420;  
XX  
XX 30-MAR-2001 (first entry)  
XX  
XX IGF-I oligonucleotide #4380.  
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.  
XX  
XX Homo sapiens.  
XX WO200078341-A1.  
XX  
XX 28-DEC-2000.  
XX  
XX 21-JUN-2000; 2000WO-AU000693.  
XX  
XX 21-JUN-1999; 99US-0140345P.  
XX (MURD-) MURDOCH CHILDRENS RES INST.  
XX  
XX Wright CJ, Werther GA, Edmondson SR;  
XX WPI; 2001-041421/05.  
XX  
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.  
XX  
XX Example 8; Page 89; 201pp; English.  
XX The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 5 A; 2 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 92.3%; Pred. No. 4e+02; Mismatches 0; Gaps 0;  
 Matches 12; Conservative 0; Indels 1; Indels 0; Gaps 0;  
 QY 1753 TCCTAAGGCCCA 1765  
 Db 14 TCCTAAGGCCCA 2  
 RESULT 516  
 AAF53669  
 ID AAF53669 standard; DNA; 15 BP.  
 XX  
 AC AAF53669;  
 XX  
 DT 30-MAR-2001 (first entry)  
 DE  
 DE IGF-I oligonucleotide #4629.  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; insulin-like growth factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200078341-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 PR 21-JUN-1999; 99US-0140345P.  
 XX  
 PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PI Wraight CJ, Werther GA, Edmondson SR;  
 XX  
 DR WPI, 2001-041421/05.  
 XX  
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 PS Example 8; Page 91; 201pp; English.  
 XX  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for insulin-like Growth factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 5 A; 0 C; 6 G; 4 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 92.3%; Pred. No. 4e+02; Mismatches 0; Gaps 0;  
 Matches 12; Conservative 0; Indels 1; Indels 0; Gaps 0;  
 QY 1721 GGAGATGGAGATT 1733  
 Db 3 GGAGATGGAAATT 15  
 RESULT 517  
 AAF51495  
 ID AAF51495 standard; DNA; 15 BP.  
 XX  
 AC AAF51495;  
 XX  
 DT 30-MAR-2001 (first entry)  
 DE  
 DE IGF-I oligonucleotide #2455.  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; insulin-like growth factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200078341-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 PR 21-JUN-1999; 99US-0140345P.  
 XX  
 PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PI Wraight CJ, Werther GA, Edmondson SR;  
 XX  
 DR WPI, 2001-041421/05.  
 XX  
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 PS Example 8; Page 76; 201pp; English.  
 XX  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for insulin-like Growth factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 5 A; 7 C; 2 G; 1 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 92.3%; Pred. No. 4e+02; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1666 CACAGCTGGACC 1678  
 |||||  
 1 CACAGCTGGACC 13

RESULT 518  
 AAF53670  
 ID AAF53670 standard; DNA; 15 BP.

XX AC AAF53670;  
 XX DT 30-MAR-2001 (first entry)  
 XX DE IGF-I oligonucleotide #4630.  
 XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition of the retina; ss.  
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX FN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU000693.

XX PR 21-JUN-1999; 99US-0140345P.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wright CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 UV (ultra-violet) treatment (optional), and an antisense nucleic acid that  
 inhibits or reduces growth factor mediated cell proliferation and/or  
 inflammation.

XX PS Example 8; Page 91; 201pp; English.

XX CC The present invention relates to a method for ameliorating the effects of  
 skin disorders. The method comprises contacting the skin with an  
 antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 inhibiting or reducing growth factor mediated cell proliferation,  
 inflammation and/or other disorders. The present sequence is an  
 oligonucleotide which can be used to design the antisense  
 oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 F45161). The method is useful for ameliorating the effects of psoriasis,  
 ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 hyperneovascular condition such as a neovascular condition of the retina,  
 brain or skin, growth factor-mediated malignancies, other sclerotic  
 disease, kidney disease, hyperproliferation of the inside of blood  
 vessels or any other hyperplasia

XX SQ Sequence 15 BP; 5 A; 0 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 92.3%; Pred. No. 4e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATT 1733  
 |||||  
 2 GGAGATGGAGATT 14

RESULT 519  
 AAF53671  
 ID AAF53671 standard; DNA; 15 BP.

XX AC AAF53671;  
 XX DT 30-MAR-2001 (first entry)  
 XX DE IGF-I oligonucleotide #4631.  
 XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX FN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU000693.

XX PR 21-JUN-1999; 99US-0140345P.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wright CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 inhibits or reduces growth factor mediated cell proliferation and/or  
 inflammation.

XX PS Example 8; Page 91; 201pp; English.

XX CC The present invention relates to a method for ameliorating the effects of  
 skin disorders. The method comprises contacting the skin with an  
 antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 inhibiting or reducing growth factor mediated cell proliferation,  
 inflammation and/or other disorders. The present sequence is an  
 oligonucleotide which can be used to design the antisense  
 oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 F45161). The method is useful for ameliorating the effects of psoriasis,  
 ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 hyperneovascular condition such as a neovascular condition of the retina,  
 brain or skin, growth factor-mediated malignancies, other sclerotic  
 disease, kidney disease, hyperproliferation of the inside of blood  
 vessels or any other hyperplasia

XX SQ Sequence 15 BP; 5 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 15;

```
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATT 1733
Db 1 GGAGATGGAAATT 13
|||||
|

RESULT 520
AAF51494
ID AAF51494 standard; DNA; 15 BP.
XX AC AAF51494;
XX 30-MAR-2001 (first entry)
XX IGF-I oligonucleotide #2454.
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX Homo sapiens.
XX WO200078341-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000WO-AU000693.
XX 21-JUN-1999; 99US-0140345P.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX Example 8; Page 76; 201pp; English.
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX Sequence 15 BP; 5 A; 7 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1666 CACAGCTGCAACC 1678
Db 1 CACAGCTGCAACC 14
|||||
|

RESULT 521
AAF53419/C
ID AAF53419 standard; DNA; 15 BP.
XX AC AAF53419;
XX 30-MAR-2001 (first entry)
XX IGF-I oligonucleotide #4379.
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX Homo sapiens.
XX WO200078341-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000WO-AU000693.
XX 21-JUN-1999; 99US-0140345P.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX Example 8; Page 89; 201pp; English.
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX Sequence 15 BP; 4 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1753 TCCTAAAGGCCCA 1765
Db 15 TCCTAAAGGCCCA 3
|||||
|
```

RESULT 522  
 AAL45302/c  
 ID AAL45302 standard; DNA; 15 BP.  
 XX  
 AC AAL45302;  
 XX  
 DT 29-MAY-2002 (first entry)  
 XX  
 DE Human KCNB1 gene allele-specific primer SEQ ID NO: 16.  
 XX  
 KW Human; KCNB1; single nucleotide polymorphism; SNP; gene therapy;  
 KW potassium voltage-gated channel; Shab-related subfamily, member 1;  
 KW isogene; arrhythmia; seizures; allele-specific oligonucleotide; PCR;  
 KW primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200204675-A1.  
 XX  
 PD 17-JAN-2002.  
 XX  
 PF 05-JUL-2001; 2001WO-US021307.  
 XX  
 PR 05-JUL-2000; 2000US-0215885P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Chew A, Choi JY, Koshy B;  
 XX  
 DR WPI; 2002-188469/24.  
 XX  
 PT Isolated polymorphic variants of potassium voltage-gated channel, Shab-  
 PT related subfamily, member 1 (KCNB1) gene useful for expressing KCNB1  
 PT protein isoform to screen drugs to treat KCNB1 activity-related disease.  
 XX  
 PS Claim 16; Page 13; 180pp; English.  
 XX  
 CC The present invention provides the protein, gene and cDNA sequences of  
 CC the human potassium voltage-gated channel, Shab-related subfamily, member  
 CC 1 (KCNB1) isogene and polymorphisms identified within these sequences.  
 CC The sequences can be used to screen drugs, which involves contacting the  
 CC polypeptide with a candidate agent, and to assay for binding activity as  
 CC a target for drugs to treat arrhythmia and seizures. The present sequence  
 CC is an allele-specific oligonucleotide primer for the gene of the  
 CC invention  
 XX  
 SQ Sequence 15 BP; 1 A; 5 C; 7 G; 1 T; 0 U; 1 Other;  
 XX  
 Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 4e+02;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 1660 CAGGCTCACAGCTGG 1674  
 |:|||||:|||||  
 Db 15 CRGGCTCCAGCCGG 1  
 XX  
 RESULT 523  
 AAD25425  
 ID AAD25425 standard; DNA; 15 BP.  
 XX  
 AC AAD25425;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human GNRH2 gene polymorphism detecting ASO primer #12.  
 XX  
 KW Human; gonadotropin-releasing hormone 2; GNRH2 gene; haplotyping;  
 KW genotyping; gene therapy; reproductive disorder; polymorphism;  
 KW allele specific oligonucleotide; ASO; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX

PN WO200187910-A2.  
 XX  
 PD 22-NOV-2001.  
 XX  
 PF 18-MAY-2001; 2001WO-US016353.  
 XX  
 PR 18-MAY-2000; 2000US-0205187P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Duda A, Klieh SE, Nandabalan K, Sausker EA;  
 XX  
 DR WPI; 2002-055683/07.  
 XX  
 PT New genetic variants of gonadotropin-releasing hormone 2 isogene, useful  
 PT in studying expression and function of protein and for screening drugs to  
 PT treat diseases e.g. reproduction disorders.  
 XX  
 PS Claim 16; Page 13; 64pp; English.  
 XX  
 CC The invention relates to genetic variants of human gonadotropin-  
 CC releasing hormone 2 (GNRH2) gene. The invention also relates to  
 CC compositions and methods for haplotyping and/or genotyping the GNRH2 gene  
 CC in an individual. Polynucleotides of the invention are useful for  
 CC studying the expression and function of GNRH2 and in expressing GNRH2  
 CC proteins for use in screening candidate drugs to treat diseases related  
 CC to GNRH2 activity. They are also used in gene therapy. The methods of the  
 CC invention are useful in determining whether an individual has a haplotype  
 CC or haplotype pairs. The haplotyping method is useful for improving the  
 CC efficiency and reliability of several steps in the discovery and  
 CC development of drugs for treating diseases associated with GNRH2  
 CC activity, e.g., reproductive disorders. The present sequence is an allele  
 CC specific oligonucleotide (ASO) primer used for detecting human GNRH2 gene  
 CC polymorphisms  
 XX  
 SQ Sequence 15 BP; 2 A; 9 C; 0 G; 3 T; 0 U; 1 Other;  
 XX  
 Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 4e+02;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 1744 TCCTCCCTATCCTAA 1758  
 |||||:|||||:  
 Db 1 TCCTCCCTATCCCTAA 15  
 XX  
 RESULT 524  
 ABL52104/c  
 ID ABL52104 standard; DNA; 15 BP.  
 XX  
 AC ABL52104;  
 XX  
 DT 12-JUL-2002 (first entry)  
 XX  
 DE Human PER1 allele specific oligonucleotide probe SEQ ID NO:29.  
 XX  
 KW Human; period (Drosophila) homologue 1; PER1; polymorphic variant;  
 KW polymorphic site; genotyping; haplotyping; circadian rhythm regulation;  
 KW single nucleotide polymorphism; SNP; gene; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 8  
 FT /\*tag= a  
 FT /note= "polymorphic site indicated by an ambiguity base"  
 XX  
 PN WO200222650-A2.  
 XX  
 PD 21-MAR-2002.  
 XX  
 PF 13-SEP-2001; 2001WO-US028780.  
 XX



PR 13-SEP-2000; 2000US-0232468P.  
 XX (GENA-) GENAISSANCE PHARM INC.  
 PA Duda A, Kliem SE, Koshy B;  
 XX WPI; 2002-393941/42.  
 DR  
 XX  
 XX  
 PT Novel isolated human period Drosophila homolog 1 polynucleotide, useful  
 PT for therapeutic purposes, for studying the expression and function of the  
 PT polynucleotide, and for expressing the homolog.  
 XX  
 XX  
 PS Claim 17; Page 14; 162pp; English.  
 XX  
 XX The present invention describes an isolated human period (Drosophila)  
 CC homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a  
 CC polymorphic variant for a reference sequence (ABL52077) for the PER1 gene  
 CC or its fragment, or a polymorphic variant of a reference sequence  
 CC (ABL52078) for a PER1 cDNA or its fragment. The present invention also  
 CC describes methods for genotyping and haplotyping the PER1 gene of an  
 CC individual. (I) is useful in studying the expression and function of  
 CC PER1, and in expressing PER1 protein for use in screening for candidate  
 CC drugs to treat diseases related to PER1 activity. (I) is useful for  
 CC therapeutic purposes. A recombinant non-human organism transformed or  
 CC transfected with (I) can be used for studying expression of the PER1  
 CC isogenes in vivo, for in vivo screening and testing of drugs targeted  
 CC against PER1 protein, and for testing the efficacy of therapeutic agents  
 CC and compounds for disorders associated with circadian rhythm regulation.  
 CC The present sequence represents an allele specific oligonucleotide probe  
 CC for human PER1, which is used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 15 BP; 2 A; 3 C; 9 G; 0 T; 0 U; 1 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 4e+02;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1734 GGCTCCCACTCCCTC 1748  
 Db |||||: |||||  
 15 GGCTCCCGCTCCCC 1  
 RESULT 525  
 ABL01115/c  
 ID ABL01115 standard; DNA; 15 BP.  
 XX ABL01115;  
 AC  
 XX 12-MAR-2002 (first entry)  
 DT Human AKR1B1 gene polymorphism detection ASO probe SEQ ID NO:12.  
 DE  
 XX Human; aldo-keto reductase family 1 member B1; aldose reductase; ss;  
 XX AKR1B1; chromosome 7q35; detection; polymorphism; ASO; probe; primer;  
 KW allele-specific oligonucleotide; antidiabetic; gene therapy; diabetes.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200179223-A2.  
 PN  
 XX 25-OCT-2001.  
 PD  
 XX 12-APR-2001; 2001WO-US011944.  
 PF  
 XX 12-APR-2000; 2000US-0196315P.  
 PR (GENA-) GENAISSANCE PHARM INC.  
 XX  
 XX Choi JY, Nandabalan K, Rounds E, Sanchis A;  
 PI WPI; 2002-075056/10.  
 XX  
 DR  
 XX

PT Novel polymorphic variants of aldo-keto reductase family 1, member b1  
 PT gene useful in studying expression and function of the protein, useful  
 PT for screening drugs to treat diseases e.g. diabetes.  
 XX  
 PS Claim 16; Page 14; 103pp; English.  
 XX  
 CC The present invention describes an isolated polynucleotide (I) comprising  
 CC a sequence which is a polymorphic variant (PV) of a reference sequence  
 CC for aldo-keto reductase family 1, member B1 (AKR1B1) gene or its  
 CC fragment, having the 22214 base pair sequence given in ABL01105. AKR1B1  
 CC has antidiabetic activity and can be used in gene therapy. AKR1B1 can be  
 CC used in the treatment of diabetes. The human AKR1B1 gene is located on  
 CC chromosome 7q35. ABL01107 to ABL01129 represent allele-specific  
 CC oligonucleotide (ASO) probes used in the detection of polymorphisms in  
 CC the human AKR1B1 gene; ABL01130 to ABL01175 represent ASO primers used in  
 CC the detection of polymorphisms in the human AKR1B1 gene; and ABL01176 to  
 CC ABL01221 represent preferred primers used in the detection of  
 CC polymorphisms in the human AKR1B1 gene  
 XX  
 SQ Sequence 15 BP; 3 A; 3 C; 5 G; 3 T; 0 U; 1 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 4e+02;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1662 GGCTCACAGCTGGAA 1676  
 Db |||||: |||||  
 15 GGCTCACRCCTGTAA 1  
 RESULT 526  
 ABLK12736/c  
 ID ABLK12736 standard; DNA; 15 BP.  
 XX  
 AC ABLK12736;  
 XX  
 XX 18-JUN-2002 (first entry)  
 DT  
 XX ASO probe #1, used to detect human IFNG gene polymorphisms.  
 DE  
 XX Human; interferon-gamma; IFNG; polymorphic variant; isogene; ss;  
 KW type I diabetes; multiple sclerosis; asthma; immune-related disorder;  
 KW haplotyping; single nucleotide polymorphism; SNP; probe; ASO;  
 KW allele-specific oligonucleotide.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200216631-A1.  
 PN  
 XX 28-FEB-2002.  
 PD  
 XX 27-AUG-2001; 2001WO-US026678.  
 PF  
 XX 25-AUG-2000; 2000US-0227842P.  
 PR  
 XX (GENA-) GENAISSANCE PHARM INC.  
 PA  
 XX Chew A, Denton RR, Finkel K, Nandabalan K;  
 PI WPI; 2002-280945/32.  
 DR  
 XX Novel isolated human interferon, gamma polynucleotide, useful for  
 PT therapeutic purposes, for studying the expression and function of the  
 PT polynucleotide, and for expressing the interferon, gamma protein.  
 XX  
 PS Claim 16; Page 13; 58pp; English.  
 XX  
 CC The present invention relates to a new human interferon-gamma (IFNG)  
 CC polynucleotide comprising a sequence which is a polymorphic variant for a  
 CC reference sequence for the IFNG gene or its fragment. The invention is  
 CC useful in studying the expression and function of IFNG and in expressing  
 CC IFNG protein for use in screening for candidate drugs to treat diseases  
 CC related to IFNG activity. The polynucleotide of the invention is useful

CC for therapeutic purposes. The invention is also useful for studying  
 CC expression of the IFNG isogenes in vivo, for in vivo screening and  
 CC testing of drugs targeted against IFNG protein, and for testing the  
 CC efficacy of therapeutic agents and compounds for type I diabetes,  
 CC multiple sclerosis, asthma and immune-related disorders, in a biological  
 CC system. The present nucleic acid sequence represents ASO (allele-specific  
 CC oligonucleotide) probe #1 that was used in the methods of the invention  
 CC to detect polymorphisms in the human IFNG gene  
 XX  
 XX Sequence 15 BP; 0 A; 4 C; 3 G; 7 T; 0 U; 1 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 4e+02; 2; Indels 0; Gaps 0;  
 Matches 12; Conservative 1; Mismatches 0; Gaps 0;  
 QY 1648 GAAGGCAAGCACCAG 1662  
 Db 15 GAAGCARGCAACAG 1  
 RESULT 527  
 ABK81430/c  
 ID ABK81430 standard; DNA; 15 BP.  
 XX  
 AC ABK81430;  
 XX  
 DT 13-AUG-2002 (first entry)  
 XX  
 DE SCYA20 allele specific oligonucleotide primer #10.  
 XX  
 KW Small inducible cytokine subfamily A (Cys-Cys) member 20; SCYA20;  
 KW polymorphism; haplotype; psoriasis; gene expression; ASO;  
 KW allele specific oligonucleotide; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200232927-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 19-OCT-2001; 2001WO-US046093.  
 XX  
 PR 19-OCT-2000; 2000US-0241725P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Bieglecki KM, Chew A, Russo DP, Sausker EA;  
 XX  
 DR WPI; 2002-435525/46.  
 XX  
 PT New genetic variants comprising haplotypes of the small inducible  
 PT cytokine subfamily A, member 20 (SCYA20) gene, useful in improving the  
 PT efficiency drug screening protocols for compounds (e.g. antipsoriatic  
 PT drug) targeting SCYA20.  
 XX  
 PS Claim 14; Page 13; 62pp; English.  
 XX  
 CC The invention describes an isolated polynucleotide, which comprises genes  
 CC and haplotypes of the small inducible cytokine subfamily A (Cys-Cys),  
 CC member 20 (SCYA20) gene. The polynucleotide comprises polymorphic sites  
 CC referred to as PS1-9 to designate the order in which they are located in  
 CC the gene. The polymorphisms and haplotypes of SCYA20 gene are useful for  
 CC validating whether SCYA20 is a suitable target for drugs to treat  
 CC psoriasis and disorders associated with its abnormal expression or  
 CC function, screening for such drugs and reducing bias in clinical trials  
 CC of such drugs. Haplotype information would be useful in improving the  
 CC efficiency and output of several steps in the drug discovery and  
 CC development process, including target validation, identifying lead  
 CC compounds, early phase clinical trials. The methods are useful in  
 CC screening for compounds targeting SCYA20 to treat a specific condition or  
 CC disease predicted to be associated with SCYA20 activity, e.g. psoriasis.  
 CC This sequence represents an allele specific oligonucleotide (ASO) primer  
 CC used to identify polymorphisms in the SCYA20 gene

XX  
 SQ Sequence 15 BP; 5 A; 6 C; 0 G; 3 T; 0 U; 1 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 92.3%; Pred. No. 4e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1696 CTGGTGAAGTTG 1708  
 Db 13 GTGATGGAAGTTG 1  
 RESULT 528  
 ABV99783  
 ID ABV99783 standard; DNA; 15 BP.  
 XX  
 AC ABV99783;  
 XX  
 DT 24-FEB-2003 (first entry)  
 XX  
 DE Human PFKFB2 allele specific oligonucleotide primer #9.  
 XX  
 KW Human; 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2; PFKFB2;  
 KW cytosolic; antidiabetic; gene therapy; cancer; diabetes; ss; ASO;  
 KW allele specific oligonucleotide; primer; polymorphism.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200194363-A2.  
 XX  
 PD 13-DEC-2001.  
 XX  
 PF 07-JUN-2001; 2001WO-US018458.  
 XX  
 PR 07-JUN-2000; 2000US-0209935P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Duda A, Kazemi A, Koshy B;  
 XX  
 DR WPI; 2002-566434/60.  
 XX  
 PT New 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 (PFKFB2) gene  
 PT variants, for improving efficiency and reliability in the development of  
 PT drugs for treating diseases associated with PFKFB2 activity e.g. cancer.  
 XX  
 PS Claim 16; Page 13; 95pp; English.  
 XX  
 CC The invention relates to a novel human 6-phosphofructo-2-kinase/ fructose  
 CC -2,6-bisphosphatase 2 (PFKFB2) isogene. The PFKFB2 of the invention has  
 CC cytosolic and antidiabetic activity. The polynucleotides may have a use  
 CC in gene therapy. The identified candidate agents targeting PFKFB2, are  
 CC useful for treating cancer and diabetes. The methods of the invention are  
 CC useful for improving the efficiency and reliability of several steps in  
 CC the discovery and development of drugs for treating diseases associated  
 CC with PFKFB2 activity. The present sequence represents an allele specific  
 CC oligonucleotide (ASO) primer used in the invention to detect PFKFB2 gene  
 CC polymorphisms  
 XX  
 SQ Sequence 15 BP; 2 A; 5 C; 4 G; 3 T; 0 U; 1 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 4e+02; 2; Indels 0; Gaps 0;  
 Matches 12; Conservative 1; Mismatches 0; Gaps 0;  
 QY 1687 TCTCCAGCGCTGGT 1701  
 Db 1 TACTCCAGCGCTGGT 15  
 RESULT 529  
 ABK96301/c  
 ID ABK96301 standard; DNA; 15 BP.

XX ABX96301;  
AC  
XX  
XX 24-SEP-2002 (first entry)  
XX  
XX  
XX EDG1 gene allele-specific oligonucleotide #16.  
XX  
XX EDG1; human; haplotyping; vascular developmental disorder; PCR; primer;  
KW endothelial differentiation sphingolipid G protein-coupled receptor 1;  
KW ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200244200-A2.  
XX  
XX 06-JUN-2002.  
XX  
XX 03-DEC-2001; 2001WO-US046946.  
XX  
XX 01-DEC-2000; 2000US-0250606P.  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
PA  
XX Bieglecki KM, Kazemi A, Shah N;  
XX  
XX WPI; 2002-519581/55.  
XX  
XX Novel genetic variants of Endothelial Differentiation, Sphingolipid G  
XX Protein-Coupled Receptor 1 isogenes, useful for improving efficiency and  
XX reliability in drug development for treating vascular developmental  
XX disorders.  
XX  
XX Claim 14; Page 13; 68pp; English.  
XX  
XX The invention relates to an isolated polynucleotide (I) encoding  
XX endothelial differentiation, sphingolipid G protein-coupled receptor 1  
XX (EDG1) (II). Also described are methods for haplotyping or genotyping  
XX EDG1 gene of an individual by identifying single nucleotide polymorphisms  
XX (SNPs) of the gene. (II) is useful in screening for drugs targeting (II)  
XX that are useful for treating vascular developmental disorders. The  
XX methods are useful for improving the efficiency and reliability of  
XX several steps in the discovery and development of drugs for treating  
XX diseases associated with EDG1 activity. The haplotyping method is also  
XX used in pharmaceutical research to validate EDG1 as a candidate target  
XX for treating a specific condition or disease predicted to be associated  
XX with EDG1 activity, e.g. vascular developmental disorders, and in the  
XX design of clinical trials for treating a specific condition of disease  
XX associated with EDG1 activity. The methods are also useful for screening  
XX compounds targeting EDG1. ABX96286-ABX96332 represent EDG1 gene allele-  
XX specific oligonucleotides, primer extension oligonucleotides and related  
XX PCR primers of the invention  
XX  
SQ Sequence 15 BP; 2 A; 5 C; 4 G; 3 T; 0 U; 1 Other;  
  
Query Match 8.2%; Score 11.4; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 4e+02;  
Matches 12; Conservative 1; Mismatches 0; Gaps 0;  
  
Qy 1725 ATGAGATGGCTCC 1739  
| : ||||| |||||  
Db 15 AYCAGATGGCTCC 1  
  
RESULT 530  
AAS16721/c  
ID AAS16721 standard; DNA; 15 BP.  
XX  
AC AAS16721;  
XX  
XX 14-FEB-2002 (first entry)  
DT  
XX  
XX Human APOA4 allele specific oligonucleotide, ASO, probe #4.

Human; ss; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;  
KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;  
KW atherosclerosis; probe.  
XX  
XX Homo sapiens.  
OS  
XX WO200177124-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 03-APR-2001; 2001WO-US010670.  
XX  
XX 05-APR-2000; 2000US-0194362P.  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
PA  
XX Bentivegna SC, Choi JY, Kliem SE, Koshy B;  
XX  
XX WPI; 2002-041281/05.  
XX  
XX New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose  
XX and treat disorders associated with its abnormal expression or function  
XX such as coronary artery disease.  
XX  
XX Claim 16; Page 15; 71pp; English.  
XX  
XX The invention relates to haplotyping the human apolipoprotein A-IV  
XX (APOA4) gene of an individual, comprising determining if the individual  
XX has one of the APOA4 haplotypes or haplotype pairs fully defined in the  
XX specification. Also disclosed are genotyping oligonucleotides (or allele  
XX specific oligonucleotides, ASO) as well as methods for correlating a  
XX particular haplotype pair with a trait e.g. obesity, in a population. The  
XX APOA4 gene is located on chromosome 11q23-qter. The methods of the  
XX invention are useful to diagnose and develop treatment for disorders  
XX associated with abnormal APOA4 expression or function, for example  
XX coronary heart disease and atherosclerosis. The APOA4 isogenes and  
XX screened compounds are useful for the treatment of disorders associated  
XX with abnormal APOA4 expression or function such as coronary artery  
XX disease. The present sequence is an APOA4 allele specific  
XX oligonucleotide, ASO, probe used to detect an APOA4 polymorphism  
XX  
SQ Sequence 15 BP; 3 A; 1 C; 9 G; 1 T; 0 U; 1 Other;  
  
Query Match 8.2%; Score 11.4; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 4e+02;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1735 GCTCCCAACTCCTCC 1749  
| : ||||| |||||  
Db 15 GCCCTCARTCTCTCC 1  
  
RESULT 531  
ABX00692  
ID ABX00692 standard; RNA; 15 BP.  
XX  
XX AC ABX00692;  
XX  
XX 23-DEC-2002 (first entry)  
DT  
XX  
XX Hepatitis C virus substrate #474 for HCV hammerhead ribozyme #474.  
XX  
XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;  
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
KW type I interferon; interferon alpha; interferon beta; cytostatic;  
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;  
KW substrate; hammerhead ribozyme; HH ribozyme; ss.  
XX  
XX Hepatitis C virus.  
OS  
XX  
XX US2002082225-A1.  
XX

```

PD 27-JUN-2002.
XX
XX
PF 23-MAR-1999; 99US-00274553.
XX
XX
PR 23-MAR-1999; 99US-00274553.
XX
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS B.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
XX
PI Blatt L, McSwiggen JA, Roberts B, Pavco PA, Macejack D;
XX
XX
DR WPI; 2002-617759/66.
XX
XX
PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.
XX
XX
PS Claim 1; Page 34; 80pp; English.
XX
XX
CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipSIDEntry.html
XX
XX
SQ Sequence 15 BP; 2 A; 6 C; 3 G; 0 T; 4 U; 0 Other;

Query Match      8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 69.2%; Pred. No. 4e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1686 CTCCTCCACGCGTG 1698
DB 3 CUCCUCCACGUG 15

RESULT 532
ABK29978/c
ID ABK29978 standard; DNA; 15 BP.
XX
XX
AC ABK29978;
XX
XX
DT 23-APR-2002 (first entry)
XX
XX
DE Hepatitis B virus (HBV) domain 10 wild type.
XX
XX
KW Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
KW vanH promoter; androgen receptor promoter; AR promoter;
KW human epidermal growth factor receptor 2 promoter; her2 promoter;
KW beta lactamase promoter; B1a promoter; transgene; cancer; breast cancer;
KW colon cancer; immunological disorder; prostate cancer; cytostatic;
KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;
KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;
KW gene expression modulator; multiple sclerosis; MS;
KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
KW systemic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
KW transgenic; ds.

Hepatitis B virus.
WO200194600-A2.
13-DEC-2001.
06-JUN-2001; 2001WO-US018343.
06-JUN-2000; 2000US-0209549P.
(GENE-) GENELABS TECHNOLOGIES INC.
Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;
Velligan MD, Latour DR, Thomas RL, Kongsachith A, Sheppard LT;
Lim MY, Bruice IW;
WPI; 2002-130595/17.
New nucleic acid regulatory sequences, which are able to regulate
expression of a gene operably linked to a promoter, useful for regulating
the expression of transgenes and for treating e.g., cancer and
immunological diseases.
Example 3; Page 43; 95pp; English.
The invention describes an isolated nucleic acid regulatory sequence for
a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci
(VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
(B1a) promoter. Transcription regulatory sequences may be used to
regulate expression of the endogenous, autologous or heterologous genes
operably linked to the promoter, and may be incorporated into
heterologous nucleic acid constructs for use in regulated expression of
transgenes. Regulated expression of cyclin D1 can be used in cancer
therapies, such as breast, colon or pancreatic cancers and familial
adenomatous polyposis. Regulation of the activity of CD40L gene promoter
may be used in the treatment of immunological disorders, such as
autoimmune diseases e.g. multiple sclerosis (MS), systemic lupus
erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
arthritis. Regulated expression of genes under the control of the HBV
(hepatitis B)-specific core, pre-S and X promoters can be used in the
therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
hepatocellular carcinoma, and in the regulated expression of liver cell-
specific genes. Regulated expression of the vanH gene promoter can be
used in treatment of Enterococcus infection, while regulated expression
of the androgen receptor gene can be used in the treatment of prostate
cancer. This represents the wild type sequence of a promoter region used
in the invention to create mutant promoter fragments to determine the
regulatory regions involved in gene expression, described in the method
of the invention
Sequence 15 BP; 3 A; 0 C; 10 G; 2 T; 0 U; 0 Other;

Query Match      8.2%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 CTCCTCACTCTCTC 1748
DB 13 CCCCAACTCTCTC 1

RESULT 533
AAD53520
ID AAD53520 standard; DNA; 15 BP.
XX
XX
AC AAD53520;
XX
XX
DT 28-MAY-2003 (first entry)
XX
XX
DE Human GNRH2 gene polymorphism detecting ASO primer #12.
XX

```

KW Human; gonadotropin-releasing hormone 2; GNRH2; reproductive disorder;  
 KW gynaecological; cytostatic; hormonal; target validation; gene therapy;  
 KW drug screening; lead compound; allele-specific oligonucleotide; ASO;  
 KW primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 PN WO200294850-A2.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PF 01-NOV-2001; 2001WO-US050630.  
 XX  
 PF 18-MAY-2001; 2001WO-US016353.  
 XX  
 PR (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PA Duda A, Kliem SE, Nandabalan K, Sausker EA;  
 XX  
 PI WPI; 2003-148454/14.  
 XX  
 DR  
 XX  
 XX New gonadotropin-releasing hormone 2 (GNRH2) polypeptide encoded by  
 PT genetic variants having polymorphisms in the GNRH2 gene, for studying the  
 PT function of, and treating disorders, such as, reproductive disorders.  
 XX  
 PT  
 XX  
 PS Claim 14; Col 13; 33pp; English.  
 XX  
 CC The invention relates to gonadotropin-releasing hormone 2 (GNRH2) and its  
 CC nucleic acid sequence. Polymorphic variants of the GNRH2 gene are useful  
 CC in studying the expression and function of GNRH2, and in expressing GNRH2  
 CC proteins for use in screening candidate drugs for treating diseases  
 CC associated with GNRH2 activity, such as reproductive disorders.  
 CC Polynucleotides comprising a polymorphic gene variant or fragment may be  
 CC used for therapeutic purposes, where a patient could benefit from  
 CC expression or increased expression of a particular GNRH2 protein isoform,  
 CC or an expression vector encoding the isoform may be administered to the  
 CC patient. Haplotype information is useful in improving the efficiency and  
 CC output of several steps in a drug discovery and development process,  
 CC including target validation, identifying lead compounds, and early phase  
 CC clinical trials. GNRH2 gene is used in gene therapy. The present sequence  
 CC is an allele-specific oligonucleotide (ASO) primer used for detecting  
 CC human GNRH2 gene polymorphisms  
 XX  
 SQ Sequence 15 BP; 2 A; 9 C; 0 G; 3 T; 0 U; 1 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 4e+02;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1744 TCCCTCCCTATCCTAA 1758  
 |||||  
 Db 1 TCCCTCCCTACCCCA 15  
 RESULT 534  
 AAQ29804/C  
 ID AAQ29804 standard; DNA; 16 BP.  
 XX  
 AC AAQ29804;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 19-MAR-1993 (first entry)  
 XX  
 XX B allele probe SN26.  
 DE  
 XX  
 XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;  
 KW paternity; forensic; ss.  
 KW  
 XX  
 OS Synthetic.  
 XX  
 PN EP512342-A2.  
 XX  
 PD 11-NOV-1992.

XX 25-APR-1992; 92EP-00107084.  
 PF  
 XX 07-MAY-1991; 91US-00696793.  
 PR  
 XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA  
 XX Saiki RK, Nasarabadi SL;  
 PI WPI; 1992-374679/46.  
 XX  
 DR  
 XX  
 XX Determn. of an individuals genotype at the gamma-globin locus - using  
 PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.  
 XX  
 XX Disclosure; Page 17; 29pp; English.  
 PS  
 XX The sequences given in AAQ29787-816 are probes which were used within the  
 CC method of the invention for detecting the presence of a variant sequence  
 CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be  
 CC distinguished from one another by the polymorphic sequence corresponding  
 CC to the HindIII site of the A allele. The sequences of the three alleles  
 CC are given in AAQ29842-44. The methods for determining an individuals  
 CC genotype at the GGG locus with respect to a set of alleles improves the  
 CC discriminatory power of GGG typing methodology compared to previous  
 CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 16 BP; 4 A; 9 C; 1 G; 2 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 16;  
 Best Local Similarity 92.3%; Pred. No. 4.4e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1699 GTGGAAGTTGGGT 1711  
 |||||  
 Db 16 GTGGAAGCTGGGT 4  
 RESULT 535  
 AAQ40622  
 ID AAQ40622 standard; DNA; 16 BP.  
 XX  
 AC AAQ40622;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 10-AUG-1993 (first entry)  
 XX  
 XX Hypervariable region detection probe 16C17.  
 XX  
 KW HVR; human; animal; forensic science; paternity testing; diagnosis;  
 KW animal breeding; hereditary diseases; tumours; allele; loss;  
 KW chromosomal regions; tumour region identification; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX FR2680520-A1.  
 PN  
 XX 26-FEB-1993.  
 PD  
 XX 22-AUG-1991; 91FR-00010516.  
 PF  
 XX 22-AUG-1991; 91FR-00010516.  
 PR  
 XX (ETFR ) ETAT FRANCAIS.  
 PA  
 XX Vergnaud G;  
 PI  
 XX WPI; 1993-136548/17.  
 DR  
 XX  
 XX Detecting the hypervariable regions of DNA for diagnosing hereditary  
 PT illnesses and tumours - by hybridising labelled polynucleotides and  
 PT analysing genomic DNA of individuals which react with restriction  
 PT fragments.  
 XX

PS Example; Page 13; 46pp; French.

XX The sequence is that of a polynucleotide probe which may be used in the

CC detection of new hypervariable regions (HVR) in a DNA sequence. HVR

CC represent a fingerprint useful in e.g. forensic science, paternity

CC testing, animal breeding, etc. The probe may be used as part of a method

CC for the efficient detection in humans or other animals, without the use

CC of mini-satellites or primary enrichment. (Updated on 25-MAR-2003 to

CC correct EN field.)

XX

SQ Sequence 16 BP; 5 A; 4 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 16;

Best Local Similarity 92.3%; Pred. No. 4.4e+02;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCA 1667

DB 1 AGACACAGGCTCA 13

RESULT 536

ABA81112/c

ID ABA81112 standard; DNA; 17 BP.

XX

AC ABA81112;

XX

DT 24-JAN-2002 (first entry)

XX

DE LDLR mutation correcting oligonucleotide SEQ ID NO: 3958.

XX

KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;

KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;

KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;

KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;

KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;

KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;

KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;

KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;

KW Alzheimer's disease; cytostatic; antickling; antianaemic; haemostatic;

KW antilipemic; ss.

XX

OS Homo sapiens.

XX

PN WO200173002-A2.

XX

PD 04-OCT-2001.

XX

PF 27-MAR-2001; 2001WO-US009761.

XX

PR 27-MAR-2000; 2000US-0192176P.

PR 27-MAR-2000; 2000US-0192179P.

PR 01-JUN-2000; 2000US-0208538P.

PR 30-OCT-2000; 2000US-0244989P.

XX

PA (UYDE ) UNIV DELAWARE.

XX

PI Kmiec EB, Gamper HB, Rice MC;

XX

DR WPI; 2001-639230/73.

XX

PT Oligonucleotide for targeted alterations of genetic sequences and for

PT treating cystic fibrosis, comprises at least one mismatch and chemical

PT modification.

XX

PS Claim 7; Page 257; 294pp; English.

XX

CC The present invention provides single-stranded oligonucleotides which can

CC be used for the targeted alteration of genomic sequences, where the

CC oligonucleotide has at least one mismatch compared with the genomic

CC sequence to be altered. In particular, these sequences are directed at

CC the following genes: adenosine deaminase, p53, beta-globin,

CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A

CC

CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus

CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,

CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase

CC (UGT1), amyloid precursor protein (APP), presenilin-1 (PSEN1) and

CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases

CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,

CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,

CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and

CC various syndromes. The present sequence is one of the gene correcting

CC oligonucleotides of the invention

XX

SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;

Best Local Similarity 92.3%; Pred. No. 4.7e+02;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1668 CAGCTGGAGCCT 1680

DB 14 CAGCTGGAGCCT 2

RESULT 537

ABA81113

ID ABA81113 standard; DNA; 17 BP.

XX

AC ABA81113;

XX

DT 24-JAN-2002 (first entry)

XX

DE LDLR mutation correcting oligonucleotide SEQ ID NO: 3959.

XX

KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;

KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;

KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;

KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;

KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;

KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;

KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;

KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;

KW Alzheimer's disease; cytostatic; antickling; antianaemic; haemostatic;

KW antilipemic; ss.

XX

OS Homo sapiens.

XX

PN WO200173002-A2.

XX

PD 04-OCT-2001.

XX

PF 27-MAR-2001; 2001WO-US009761.

XX

PR 27-MAR-2000; 2000US-0192176P.

PR 27-MAR-2000; 2000US-0192179P.

PR 01-JUN-2000; 2000US-0208538P.

PR 30-OCT-2000; 2000US-0244989P.

XX

PA (UYDE ) UNIV DELAWARE.

XX

PI Kmiec EB, Gamper HB, Rice MC;

XX

DR WPI; 2001-639230/73.

XX

PT Oligonucleotide for targeted alterations of genetic sequences and for

PT treating cystic fibrosis, comprises at least one mismatch and chemical

PT modification.

XX

PS Claim 7; Page 257; 294pp; English.

XX

CC The present invention provides single-stranded oligonucleotides which can

CC be used for the targeted alteration of genomic sequences, where the

CC oligonucleotide has at least one mismatch compared with the genomic

CC sequence to be altered. In particular, these sequences are directed at

CC the following genes: adenosine deaminase, p53, beta-globin,

CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A

CC

CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A  
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus  
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,  
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase  
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and  
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases  
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,  
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,  
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and  
 CC various syndromes. The present sequence is one of the gene correcting  
 CC oligonucleotides of the invention  
 XX  
 SQ Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1668 CAGCTGGAAACCCCT 1680  
 |||||  
 DB 4 CAGCTGGAGCCT 16

RESULT 538  
 AAQ67730/c  
 ID AAQ67730 standard; cDNA; 17 BP.  
 XX  
 AC AAQ67730;

XX 25-MAR-2003 (revised)  
 DT 22-MAR-1995 (first entry)  
 XX  
 XX Primer for human spasmodic polypeptide.  
 DE  
 XX  
 XX Primer; polymerase chain reaction; spasmodic;  
 KW gastrointestinal disorder; prophylaxis; therapy; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9417102-A1.  
 FN  
 XX 04-AUG-1994.  
 PD  
 XX 20-JAN-1994; 94WO-DK000037.  
 PF  
 XX 21-JAN-1993; 93DK-00000068.  
 PR  
 XX (NOVO) NOVO-NORDISK AS.  
 PA  
 XX Thim L, Norris K, Norris F, Bjorn SE, Christensen M, Nielsen PF;  
 PT WPI; 1994-264034/32.  
 DR  
 XX Human spasmodic polypeptide in glycosylated form - useful for  
 PT prophylaxis or treatment of gastrointestinal disorders.  
 XX  
 PS Disclosure; Page 13; 52pp; English.

CC The primer (based on the human spasmodic protein (HSP) sequence) is  
 CC used to isolate DNA fragments encoding the trefoil domains of HSP by PCR  
 CC from human genomic DNA. The HSP (glycosylated at Asn15) is used in a  
 CC pharmaceutical composition for the prophylaxis and treatment of  
 CC gastrointestinal disorders. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 17 BP; 6 A; 4 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1677 CCCTGGTGTCTCC 1689  
 |||||  
 DB 14 CCCTGGTGTCTCC 2

RESULT 539  
 AAX70103  
 ID AAX70103 standard; RNA; 17 BP.  
 XX  
 AC AAX70103;  
 XX  
 DT 28-JUL-1999 (first entry)  
 XX  
 DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1398.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX  
 OS Homo sapiens.

XX  
 PN WO9715662-A2.  
 XX  
 PD 01-MAY-1997.  
 XX  
 PF 25-OCT-1996; 96WO-US017480.  
 XX  
 PR 26-OCT-1995; 95US-0005974P.  
 PR 11-JAN-1996; 96US-00584040.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR) CHIRON CORP.

XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 PI WPI; 1997-259017/23.  
 XX  
 DR  
 XX  
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.

XX  
 PS Claim 4; Page 89; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 4 A; 1 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 61.5%; Pred. No. 4.7e+02;  
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1725 ATGGAGATGGCT 1737  
 :|||:|:|:|:  
 DB 1 AUGGAUAUUGGU 13

RESULT 540  
 AAX70102  
 ID AAX70102 standard; RNA; 17 BP.  
 XX  
 AC AAX70102;  
 XX  
 DT 28-JUL-1999 (first entry)  
 XX  
 DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1397.

```

XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX OS Homo sapiens.
XX PN WO9715662-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US017480.
XX PR 26-OCT-1995; 95US-0005974P.
XX PR 11-JAN-1996; 96US-00584040.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR) CHIRON CORP.
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WIPI; 1997-259017/23.
XX CC Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX PS Claim 4; Page 89; 218pp; English.
XX CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX SQ Sequence 17 BP; 4 A; 2 C; 5 G; 0 T; 6 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 61.5%; Pred. No. 4.7e+02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1725 ATGGAGATTGGCT 1737
DB 3 AUGGAUAUUGGCU 15

RESULT 541
AAX62178/c
ID AAX62178 standard; RNA; 17 BP.
XX AC AAX62178;
XX 16-JUL-1999 (first entry)
XX DT
XX DE Granule bound starch synthase hammerhead substrate SEQ ID NO:53.
XX KW Maize; corn; Zea mays; delta-9 desaturase; GBS; target; substrate;
KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
KW modulation; gene expression; transgenic plant; cleavage; canola plant;
KW caffeine synthesis; coffee plant; nicotine production; tobacco;
KW fruit ripening; flower pigmentation; lignin production; ss.
XX OS Zea mays.
XX PN WO9710328-A2.

PD 20-MAR-1997.
XX 12-JUL-1996; 96WO-US011689.
XX 13-JUL-1995; 95US-0001135P.
XX (RIBO-) RIBOZYME PHARM INC.
XX (DOWC) DOWELANCO.
XX Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA;
XX Young SA, Folkerts O, Merlo DJ;
XX WIPI; 1997-202224/18.
XX Ribozyne which modulates plant gene expression - preferably modulates
PT expression of DELTA-9 desaturase or granule bound starch synthase in
PT maize or canola.
XX PS Claim 41; Page 73; 155pp; English.
XX CC The present invention describes an enzymatic nucleic acid molecule (I)
CC with RNA cleaving activity, which modulates the expression of a plant
CC gene. Also described is a gene comprising a cDNA sequence encoding maize
CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,
CC preferably Delta-9 desaturase or a granule bound starch synthase (GBS)
CC gene, in a plant (preferably a maize or canola plant). (I) can be used to
CC modulate caffeine synthesis in a coffee plant, nicotine production in a
CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum
CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or
CC marigold plant or lignin production in a tobacco, aspen, poplar or pine
XX plant
XX SQ Sequence 17 BP; 4 A; 7 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1636 GGCGTTGTAGCAG 1648
DB 16 GCAGTTGTAGCAG 4

RESULT 542
AAX97519
ID AAX97519 standard; RNA; 17 BP.
XX AC AAX97519;
XX 17-MAR-1999 (first entry)
XX DT
XX DE Human EGF-R target sequence nucleotide position 2613.
XX KW Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
KW cancer; genetic drift; detection; mutation; ss.
XX OS Homo sapiens.
XX PN WO9833893-A2.
XX PD 06-AUG-1998.
XX PF 14-JAN-1998; 98WO-US000730.
XX PR 31-JAN-1997; 97US-0036476P.
XX PR 04-DEC-1997; 97US-00985162.
XX (RIBO-) RIBOZYME PHARM INC.
XX (UYAS-) UNIV ASTON.
XX PI Akhtar S, Fell P, Mcswiggen JA;
XX

```



DR WPI; 1998-437449/37.  
 XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal  
 PT growth factor receptor, useful for inhibiting cell proliferation and for  
 PT treating cancers.  
 XX  
 PS Claim 5; Page 74; 109pp; English.  
 XX  
 CC The present invention describes enzymatic nucleic acid molecules (NAMs)  
 CC which specifically cleave RNA derived from an epidermal growth factor  
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090  
 CC represent specifically claimed target sequence from human EGF-R. AAV98044  
 CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and  
 CC hairpin ribozymes respectively for human EGF-R. The NAMs are useful for  
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR  
 CC expression levels e.g. to inhibit cell proliferation in the prevention or  
 CC treatment of cancers. The NAMs can also be used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of EGF-R RNA in a cell  
 XX  
 SQ Sequence 17 BP; 5 A; 5 C; 3 G; 0 T; 4 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 69.2%; Pred. No. 4.7e+02;  
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1729 AGATTGGCTCCCA 1741  
 ID AAAA18625/c  
 ID AAA18625 standard; RNA; 17 BP.  
 XX AAA18625;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Human TIE-2 substrate sequence SEQ ID NO:1851.  
 XX  
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;  
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;  
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
 KW age related macular degeneration; inflammation; neovascular glaucoma;  
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;  
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 DN WO9950403-A2.  
 XX  
 XX 07-OCT-1999.  
 XX  
 XX 24-MAR-1999; 99WO-US006507.  
 XX  
 PR 27-MAR-1998; 98US-0079678P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;  
 XX WPI; 1999-591315/50.  
 DR  
 XX Novel ribozymes for modulating the synthesis, expression and/or stability  
 PT of an mRNA encoding an angiogenic factors.  
 XX  
 PS Claim 56; Page 107; 305pp; English.  
 XX  
 CC The present invention describes enzymatic nucleic acid molecules with RNA

CC cleaving activity, which specifically cleave RNA encoded by an aryl  
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their  
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to  
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;  
 CC sequences for integrin alpha 6 subunit, and AAA20361 to AAA21595 represent ribozyme  
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
 CC AAA21596 to AAA21688 represent their corresponding target sequences;  
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence  
 CC for integrin subunit beta 3, and AAA22476 to AAA23362, AAA23343 to  
 CC AAA23422 represent their corresponding target sequences. The ribozymes of  
 CC the invention are used for modulating the synthesis, expression and/or  
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are  
 CC especially used to treat cancer, diabetic retinopathy, age related  
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber  
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,  
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
 CC integrin subunit alpha-6, or integrin subunit beta-3  
 XX  
 SQ Sequence 17 BP; 3 A; 6 C; 3 G; 0 T; 5 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1661 AGGCTCACAGCTG 1673  
 ID AAA18519/c  
 ID AAA18519 standard; RNA; 17 BP.  
 XX AAA18519;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Human TIE-2 substrate sequence SEQ ID NO:1745.  
 XX  
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;  
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;  
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
 KW age related macular degeneration; inflammation; neovascular glaucoma;  
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;  
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 DN WO9950403-A2.  
 XX  
 XX 07-OCT-1999.  
 XX  
 XX 24-MAR-1999; 99WO-US006507.  
 XX  
 PR 27-MAR-1998; 98US-0079678P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;  
 XX WPI; 1999-591315/50.  
 DR  
 XX Novel ribozymes for modulating the synthesis, expression and/or stability

PT of an mRNA encoding an angiogenic factors.  
XX Claim 56; Page 100; 305pp; English.  
PS The present invention describes enzymatic cleave RNA encoded by an aryl  
XX cleaving activity, which specifically cleave RNA encoded by an aryl  
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their  
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to  
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
CC and AAA19155 to AAA19222 represent their corresponding target sequences;  
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme  
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
CC AAA21596 to AAA21688 represent their corresponding target sequences;  
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence  
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to  
CC AAA23422 represent their corresponding target sequences. The ribozymes of  
CC the invention are used for modulating the synthesis, expression and/or  
CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are  
CC especially used to treat cancer, diabetic retinopathy, age related  
CC macular degeneration (AMD), inflammation, and arthritis, as well as  
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
CC angioblastoma of tuberous sclerosis, pot-wine stains, Sturge Weber  
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,  
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
CC integrin subunit alpha-6, or integrin subunit beta-3  
XX Sequence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;  
SQ

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1716 AGTACGAGATGG 1728  
Db 17 AGTACAGAGATGG 5  
|||||  
RESULT 545  
AAV92465/C  
ID AAV92465 standard; RNA; 17 BP.  
XX AAV92465;  
AC  
XX 18-FEB-1999 (first entry)  
DT  
XX Human A-Raf substrate position 747.  
DE  
XX Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
KW screening; identification; synthesis; deprotection; purification; cancer;  
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
KW restenosis; rheumatoid arthritis; ss.  
XX Homo sapiens.  
OS  
XX WO9850530-A2.  
XX 12-NOV-1998.  
PD  
XX 05-MAY-1998; 98WO-US009249.  
PF  
XX 09-MAY-1997; 97US-0046059P.  
XX 09-JUN-1997; 97US-0049002P.  
PR  
XX 03-JUL-1997; 97US-0051718P.  
PR  
XX 02-AUG-1997; 97US-0056808P.  
PR  
XX 02-OCT-1997; 97US-0061321P.  
PR  
XX 02-OCT-1997; 97US-0061324P.  
PR  
XX 05-NOV-1997; 97US-0064866P.  
PR  
XX 19-DEC-1997; 97US-0068212P.  
PR

XX (RIBO-) RIBOZYME PHARM INC.  
PA Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
PI Parry T, Beigelman L, McSwiggen JA, Karpeisky A, Burgin A;  
PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
XX WPI; 1999-009494/01.  
DR  
XX Identifying new catalytic nucleic acid that modulates selected processes  
PT - especially ribozymes that cleave Raf RNA for treating cancer,  
PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
PT used as antiviral agents and synthons.  
XX Claim 177; Page 158; 259pp; English.  
PS  
XX A method has been developed for the identification of a nucleic acid  
CC capable of modulating a process in a biological system. The method  
CC comprises: (a) introducing into the system a random library of nucleic  
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
CC in systems where modulation has occurred and/or determining the sequence  
CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
CC endonuclease activity and catalytic activity, from the present invention,  
CC are used to modulate gene expression in plant and mammalian cells and to  
CC cleave target nucleic acid, particularly for treating systemic diseases  
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
CC ascites and infection. They may also be used to detect genetic drift and  
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs  
CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
CC generally any condition associated with the level of c-raf. Introduction  
CC of sugar/phosphate modifications increases stability against nuclease and  
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the  
CC method, specifically for modulating the expression of a Raf gene  
XX Sequence 17 BP; 2 A; 10 C; 4 G; 0 T; 1 U; 0 Other;  
SQ

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1670 GCTGGAACCTCG 1682  
Db 14 GCTGGGACCTCG 2  
|||||  
RESULT 546  
AAV92632  
ID AAV92632 standard; RNA; 17 BP.  
XX AAV92632;  
AC  
XX 18-FEB-1999 (first entry)  
DT  
XX Human A-Raf substrate position 2216.  
DE  
XX Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
KW screening; identification; synthesis; deprotection; purification; cancer;  
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
KW restenosis; rheumatoid arthritis; ss.  
XX Homo sapiens.  
OS  
XX WO9850530-A2.  
XX 12-NOV-1998.  
PD  
XX 05-MAY-1998; 98WO-US009249.  
PF  
XX 09-MAY-1997; 97US-0046059P.  
XX 09-JUN-1997; 97US-0049002P.  
PR

```

PR 03-JUL-1997; 97US-0051718P.
PR 22-AUG-1997; 97US-0056808P.
PR 02-OCT-1997; 97US-0061321P.
PR 02-OCT-1997; 97US-0061324P.
PR 05-NOV-1997; 97US-0064866P.
PR 19-DEC-1997; 97US-0068212P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
PI Parry T, Beigelman L, Mcswigen JA, Karpeisky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
XX WPI; 1999-009494/01.
XX
XX Identifying new catalytic nucleic acid that modulates selected processes
PT - especially ribozymes that cleave Raf RNA for treating cancer,
PT restenosis, and also new ribozymes and modified nucleoside triphosphates
PT used as antiviral agents and synthons.
XX
XX Claim 177; Page 161; 259pp; English.
XX
XX A method has been developed for the identification of a nucleic acid
CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD) comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC ascites and infection. They may also be used to detect genetic drift and
CC mutations in diseased cells and to determine c-rat RNA. Specifically NACs
CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-rat. Introduction
CC of sugar/phosphate modifications increases stability against nuclease and
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene
XX
XX Sequence 17 BP; 2 A; 9 C; 1 G; 0 T; 5 U; 0 Other;
SQ
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 61.5%; Pred. No. 4.7e+02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1693 TGCTCCCTCCAGC 1695
Db 4 UGUCUCCUCCAU 16
RESULT 547
AAV72307/c
ID AAV72307 standard; DNA; 17 BP.
XX
XX AAV72307;
XX
XX Human blood bacterium intergenic spacer primer 2.
DT 28-JUL-1999 (first entry)
XX
XX
XX 16S rRNA; drug resistant protein; pathophysiology; human blood bacterium;
KW disease; multiple sclerosis; chronic fatigue; treatment; fibromyalgia;
KW lupus erythematosus; rheumatoid arthritis; toxic metabolite; plasma;
KW serum; antibiotic; vaccine; antibiotic; 23S rRNA; primer; ss.
XX
XX Synthetic.
OS Bacteria.
XX
XX W09924613-A1.
XX

```

---

```

PD 20-MAY-1999.
XX
XX 06-NOV-1998; 98WO-US023674.
XX
XX 06-NOV-1997; 97US-0064472P.
XX
XX (PATH-) PATHOBIOTEK INC.
XX
XX Lindner L, Macphee K;
PI WPI; 1999-327419/27.
XX
XX A human blood bacterium, characterization, culturing and diagnostic
PT methods.
XX
XX Claim 10; Page 92; 95pp; English.
XX
XX This invention describes methods for culturing and detecting a human
CC blood bacterium (HBB), implicated in several disease e.g. multiple
CC sclerosis and chronic fatigue. Quantification of levels of HBB in an
CC individual can be used to determine the efficacy of a treatment for a HBB
CC related disease. HBB-related diseases include chronic fatigue syndrome,
CC multiple sclerosis, lupus erythematosus, rheumatoid arthritis and
CC fibromyalgia. HBB vaccines can be used to treat diseased individuals.
CC Engineered HBB is administered to individuals where the disease has the
CC condition of a toxic metabolite being accumulated in plasma or serum of
CC the individual. A range of antibiotics can be used to treat
CC pathophysiological states associated with HBB. The invention describes
CC the isolation of HBB 16S rRNA, 23S rRNA and drug resistant protein
CC encoding nucleic acid. The products of the invention have antibiotic
CC activity
XX
XX Sequence 17 BP; 2 A; 11 C; 1 G; 3 T; 0 U; 0 Other;
SQ
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1698 GGTGGAAGTGTGG 1710
Db 16 GGTGGAAGTGTGG 4
RESULT 548
AAA60267/c
ID AAA60267 standard; DNA; 17 BP.
XX
XX AAA60267;
XX
XX 07-DEC-2000 (first entry)
XX
XX Mouse HPC2 cDNA expression construct PCR primer SEQ ID NO: 88.
DE
XX Human; mouse; prostate cancer predisposing gene; HPC2;
KW human chromosome 17p; gene therapy; peptide therapy; drug design;
KW PCR primer; sequencing primer; ss.
XX
XX Homo sapiens.
OS
XX W0200027864-A1.
XX
XX 18-MAY-2000.
XX
XX 05-NOV-1999; 99WO-US026055.
XX
XX 06-NOV-1998; 98US-0107468P.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Tavtigian SV, Teng DHF, Simard J, Rommens JM;
XX WPI; 2000-376481/32.
XX

```

PT Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies,  
PT useful for treatment and diagnosis of prostate cancer.  
XX  
PS Example 4; Page 58; 157pp; English.  
XX  
CC The present sequence is a primer used in the isolation of the human and  
CC murine prostate cancer predisposing genes HPC2 and Mm.HPC2. The human  
CC version of the gene is found on chromosome 17p. Some alleles cause a  
CC predisposition to cancer, particularly prostate cancer. This gene and its  
CC protein can be used in peptide and gene therapy for cancer patients, as  
CC well as being useful as diagnostic tools (both for cancer sufferers and  
CC those with a predisposition to the disease) and in the production of  
CC cancer drugs  
XX  
SQ Sequence 17 BP; 1 A; 5 C; 6 G; 5 T; 0 U; 0 Other;  
Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1657 CACCAGGCTCACA 1669  
Db 17 CACCAGGCTGACA 5  
RESULT 549  
AAF02259/c  
ID AAF02259 standard; DNA; 17 BP.  
XX  
AC AAF02259;  
XX  
DT 16-FEB-2001 (first entry)  
XX  
DE Hammerhead ribozyme substrate #554.  
XX  
DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;  
KW interferon alpha; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200061729-A2.  
XX  
PD 19-OCT-2000.  
XX  
XX 11-APR-2000; 2000WO-US009721.  
XX  
XX 12-APR-1999; 99US-0129390P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Blatt L, Zwick M, Pavco P, Meswiggen J;  
XX  
XX WPI; 2000-647423/62.  
XX  
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,  
PT useful for producing e.g. granulocyte colony stimulating factor protein,  
PT interferon alpha and erythropoietin.  
XX  
PS Claim 37; Page 68; 164pp; English.  
XX  
CC The present invention relates to enzymatic and antisense nucleic acid  
CC molecules that act as inhibitors of the expression of repressor genes  
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription  
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).  
CC Inhibition of the repressors removes prevents inhibition (and  
CC consequently increases expression of) genes involved in the production of  
CC erythropoietin, granulocyte colony stimulating factor protein and  
CC interferon alpha  
XX  
SQ Sequence 17 BP; 5 A; 5 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1686 CTCCTCCAGCGTG 1698  
Db 17 CTCCTCCAGAGTG 5  
RESULT 550  
ABL46650/c  
ID ABL46650 standard; RNA; 17 BP.  
XX  
AC ABL46650;  
XX  
DT 27-JUN-2003 (first entry)  
XX  
DE Human GRID NCH ribozyme substrate oligonucleotide #104.  
XX  
KW Human; Grb2-related with Insert Domain; GRID; T-cell;  
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;  
KW leukaemia; cytostatic; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200162911-A2.  
XX  
PD 30-AUG-2001.  
XX  
XX 23-FEB-2001; 2001WO-US(05957.  
XX  
XX 24-FEB-2000; 2000US-014594P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PI Jarvis T, Von Carlowitz I, Meswiggen JA, Hamblin PA, Ellis JH;  
XX  
XX WPI; 2001-550088/61.  
XX  
XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain  
PT (GRID) gene comprises using antisense and enzymatic nucleic acid  
PT molecules such as hammerhead ribozymes.  
XX  
XX Claim 4; Page 64; 108pp; English.  
XX  
CC The present invention relates to oligonucleotides that downregulate the  
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is  
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful  
CC for modulating the expression of GRID, to treat conditions such as  
CC tissue/graft rejection and leukaemia. The oligonucleotides can also be  
CC administered in conjunction with other therapies such as radiation,  
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was  
CC used to illustrate the invention  
XX  
SQ Sequence 17 BP; 2 A; 7 C; 1 G; 0 T; 7 U; 0 Other;  
Query Match 3.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1719 ACGAGATGGAGA 1731  
Db 16 ACAGAGATGGAGA 4  
RESULT 551  
ABL46649/c  
ID ABL46649 standard; RNA; 17 BP.  
XX  
AC ABL46649;  
XX  
XX 27-JUN-2003 (first entry)  
XX  
DE Human GRID NCH ribozyme substrate oligonucleotide #103.



XX  
SO Sequence 17 BP; 4 A; 8 C; 5 G; 0 T; 0 U; 0 Other;

expressing the proteins. The hGMDLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGMDLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGMDLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption/ionisation, as therapeutic supplement in patients having specific deficiency in hGMDLP-1 production, and in vaccines or for replacement therapy. The

CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMLP-  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp.wipo.int/pub/published\\_pct\\_sequence](http://ftp.wipo.int/pub/published_pct_sequence)  
CC XX  
CC SQ Sequence 17 BP; 5 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred.No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1661 AGGCTCACAGCTG 1673  
|| |||||  
DB 4 AGCCTCACAGCTG 16

RESULT 557  
AAS99002/c  
ID AAS99002 standard; DNA; 17 BP.  
XX  
XX AAS99002;  
XX  
XX 12-MAR-2002 (first entry)  
XX Mouse prostate cancer predisposing gene (HPC2) PCR primer #5.  
XX  
XX Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; ss;  
XX gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla;  
XX sequencing primer; PCR primer.  
XX  
XX Mus musculus.  
XX  
XX W0200185911-A2.  
XX  
XX 15-NOV-2001.  
XX  
XX 07-MAY-2001; 2001WO-US014602.  
XX  
XX 05-MAY-2000; 2000US-00564805.  
XX  
XX (MYRI-) MYRIAD GENETICS INC.  
XX (HOSP-) HOSPITAL FOR SICK CHILDREN.  
XX  
XX Tavtavian SV, Teng DHP, Simard J, Rommens JM;  
XX  
XX WPI; 2002-066599/09.  
XX  
XX Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker  
XX for prostate cancer, is useful in gene therapy techniques to restore HPC2  
XX normal levels by which neoplastic growth is suppressed in recipient cell.  
XX  
XX Example 6; Page 70; 239pp; English.  
XX  
XX The invention relates to a human prostate cancer predisposing gene coding  
XX for an HPC2 polypeptide. The DNA and protein sequences are useful as  
XX diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in  
XX a suspected mutant HPC2 allele by comparing the sequence of the suspected  
XX mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also

CC useful for detecting an alteration in HPC2, where the alteration is  
 CC associated with cancer in a human. The method involves analysing an HPC2  
 CC gene or an HPC2 gene expression product from a tissue of the human. The  
 CC HPC2 gene is useful as a marker for prostate cancer and can be used in  
 CC gene therapy techniques to suppress neoplastic growth of recipient cells  
 CC which carry the mutant HPC2 allele. The sequences represent primers used  
 CC in the methods of the invention, cDNA encoding human and mouse HPC2 and  
 CC cDNA encoding HPC2 paralogues and orthologues

XX SQ Sequence 17 BP; 1 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1657 CACCAGGCTGACA 1669

Db 17 CACCAGGCTGACA 5

RESULT 558

ABV78964  
 ID ABV78964 standard; DNA; 17 BP.

XX AC ABV78964;

XX DT 03-JAN-2003 (first entry)

XX DE Human HTPL scanning oligonucleotide SEQ ID 210.

XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
 KW human testis expressed Patched like protein; testis; adrenal; liver;  
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX PN EP1229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX WPI; 2002-676582/73.

XX Novel isolated human testis expressed Patched like protein (HTPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPL.

XX Example 2; Page 91; 718pp; English.

XX The present invention relates to human testis expressed Patched like  
 CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was

CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention

XX SQ Sequence 17 BP; 6 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1646 CAGAAGCGCAAGCA 1658

Db 4 CGGAAGCGCAAGCA 16

RESULT 559

ABV79490

ID ABV79490 standard; DNA; 17 BP.

XX AC ABV79490;

XX DT 03-JAN-2003 (first entry)

XX DE Human HTPL scanning oligonucleotide SEQ ID 736.

XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;

KW human testis expressed Patched like protein; testis; adrenal; liver;

KW male germ cell development; bone marrow; brain; kidney; lung; placenta;

KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX PN EP1229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX WPI; 2002-676582/73.

XX Novel isolated human testis expressed Patched like protein (HTPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPL.

XX Example 2; Page 160; 718pp; English.

XX The present invention relates to human testis expressed Patched like  
 CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPL plays a role similar



CC to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was  
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention

SQ Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1684 GTCTCTCCAGCG 1696

Db 5 GTCTCTACAGCG 17

RESULT 560

ABV79494  
 ID ABV79494 standard; DNA; 17 BP.

XX  
 AC ABV79494;

DT 03-JAN-2003 (first entry)

XX Human HTPL scanning oligonucleotide SEQ ID 740.

XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
 KW human testis expressed Patched like protein; testis; adrenal; liver;  
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

OS Homo sapiens.

XX EP1229046-A2.

XX 07-AUG-2002.

XX 28-JAN-2002; 2002EP-00001167.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 23-MAY-2001; 2001US-00864761.

XX 09-OCT-2001; 2001US-0327898P.

XX (AEOM-) ABOMICA INC.

XX Zhan J;

XX WPI; 2002-676582/73.

XX Novel isolated human testis expressed Patched like protein (HTPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPL.

XX Example 2; Page 160; 718pp; English.

XX The present invention relates to human testis expressed Patched like  
 CC protein (HTPL), see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL

CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was  
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention

SQ Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;

Best Local Similarity 92.3%; Pred. No. 4.7e+02;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1684 GTCTCTCCAGCG 1696

Db 1 GTCTCTACAGCG 13

RESULT 561

ABV79491

ID ABV79491 standard; DNA; 17 BP.

XX  
 AC ABV79491;

DT 03-JAN-2003 (first entry)

XX Human HTPL scanning oligonucleotide SEQ ID 737.

XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
 KW human testis expressed Patched like protein; testis; adrenal; liver;  
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

OS Homo sapiens.

XX EP1229046-A2.

XX 07-AUG-2002.

XX 28-JAN-2002; 2002EP-00001167.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 23-MAY-2001; 2001US-00864761.

XX 09-OCT-2001; 2001US-0327898P.

XX (AEOM-) ABOMICA INC.

XX Zhan J;

XX WPI; 2002-676582/73.

XX Novel isolated human testis expressed Patched like protein (HTPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPL.

XX Example 2; Page 160; 718pp; English.

XX The present invention relates to human testis expressed Patched like  
 CC protein (HTPL), see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL  
 CC has two isoforms, with a few single base pair differences between the

CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was  
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention

XX Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1684 GTCTCTCCAGCG 1696  
 Db 4 GTCTCTACAGCG 16  
 ||||| |||||

RESULT 562  
 ABV79492  
 ID ABV79492 standard; DNA; 17 BP.  
 AC ABV79492;  
 XX  
 DT 03-JAN-2003 (first entry)  
 DE Human HTPL scanning oligonucleotide SEQ ID 738.  
 XX  
 KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
 KW human testis expressed Patched like protein; testis; adrenal; liver;  
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1229046-A2.  
 XX  
 PD 07-AUG-2002.  
 XX  
 PF 28-JAN-2002; 2002EP-00001167.  
 XX  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 09-OCT-2001; 2001US-0327898P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Zhan J;  
 XX  
 DR WPI; 2002-676582/73.  
 XX  
 PT Novel isolated human testis expressed Patched like protein (HTPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPL.  
 XX  
 PS Example 2; Page 160; 718pp; English.  
 XX  
 CC The present invention relates to human testis expressed Patched like

CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was  
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention

XX Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1684 GTCTCTCCAGCG 1696  
 Db 3 GTCTCTACAGCG 15  
 ||||| |||||

RESULT 563  
 ABV79493  
 ID ABV79493 standard; DNA; 17 BP.  
 AC ABV79493;  
 XX  
 DT 03-JAN-2003 (first entry)  
 DE Human HTPL scanning oligonucleotide SEQ ID 739.  
 XX  
 KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
 KW human testis expressed Patched like protein; testis; adrenal; liver;  
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1229046-A2.  
 XX  
 PD 07-AUG-2002.  
 XX  
 PF 28-JAN-2002; 2002EP-00001167.  
 XX  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 09-OCT-2001; 2001US-0327898P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Zhan J;  
 XX  
 DR WPI; 2002-676582/73.  
 XX  
 PT Novel isolated human testis expressed Patched like protein (HTPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPL.  
 XX  
 PS Example 2; Page 160; 718pp; English.  
 XX

XX The present invention relates to human testis expressed Patched like  
 CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was  
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention  
 XX  
 SQ Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1684 GTCCTCTCAGCG 1696  
 Db ||||| |||||  
 2 GTCCTCTCAGCG 14  
 RESULT 564  
 ABV78968  
 ID ABV78968 standard; DNA; 17 BP.  
 XX AC ABV78968;  
 XX DT 03-JAN-2003 (first entry)  
 XX DE Human HTPL scanning oligonucleotide SEQ ID 214.  
 KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
 KW human testis expressed Patched like protein; testis; adrenal; liver;  
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.  
 XX OS Homo sapiens.  
 XX PN EP1229046-A2.  
 XX PD 07-AUG-2002.  
 XX PF 28-JAN-2002; 2002EP-00001167.  
 XX PR 30-JAN-2001; 2001WO-US0000663.  
 XX PR 30-JAN-2001; 2001WO-US0000664.  
 XX PR 30-JAN-2001; 2001WO-US0000665.  
 XX PR 30-JAN-2001; 2001WO-US0000667.  
 XX PR 30-JAN-2001; 2001WO-US0000668.  
 XX PR 23-MAY-2001; 2001US-00864761.  
 XX PR 09-OCT-2001; 2001US-0327898P.  
 XX PA (AEOM-) AEOMICA INC.  
 XX PI Zhan J;  
 XX DR WPI; 2002-676582/73.  
 XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPL.

XX Example 2; Page 91; 718pp; English.  
 XX The present invention relates to human testis expressed Patched like  
 CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was  
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention  
 XX  
 SQ Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1648 GAAGGCAAGCACC 1660  
 Db ||||| |||||  
 2 GAAGGCAAGCAGC 14  
 RESULT 565  
 ABV78963  
 ID ABV78963 standard; DNA; 17 BP.  
 XX AC ABV78963;  
 XX DT 03-JAN-2003 (first entry)  
 XX DE Human HTPL scanning oligonucleotide SEQ ID 209.  
 KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
 KW human testis expressed Patched like protein; testis; adrenal; liver;  
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.  
 XX OS Homo sapiens.  
 XX PN EP1229046-A2.  
 XX PD 07-AUG-2002.  
 XX PF 28-JAN-2002; 2002EP-00001167.  
 XX PR 30-JAN-2001; 2001WO-US0000663.  
 XX PR 30-JAN-2001; 2001WO-US0000664.  
 XX PR 30-JAN-2001; 2001WO-US0000665.  
 XX PR 30-JAN-2001; 2001WO-US0000667.  
 XX PR 30-JAN-2001; 2001WO-US0000668.  
 XX PR 23-MAY-2001; 2001US-00864761.  
 XX PR 09-OCT-2001; 2001US-0327898P.  
 XX PA (AEOM-) AEOMICA INC.  
 XX PI Zhan J;  
 XX DR WPI; 2002-676582/73.  
 XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful

PA (AEOM-) AEOMICA INC.

PA (AEOM-) AEOMICA INC.

PI Shannon M;  
 XX WPI; 2002-684061/74.  
 DR  
 XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL  
 PT -1, useful for treating disorders associated with decreased expression or  
 PT activity of human POSHL1.  
 XX  
 XX Example 2; SEQ ID NO 1759; 60pp + Sequence Listing; English.  
 PS  
 CC The invention relates to an isolated SH3 domain (POSH)-like signalling  
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
 CC acids (S1, AB883999), a sequence having 65% sequence identity to (S1),  
 CC (S1) having 95% deviations, especially conservative substitutions or a  
 CC fragment of the sequences comprising at least 8 contiguous amino acids.  
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
 CC adaptor protein that interacts with Rho family small GTPases as well as  
 CC downstream components of the signal transduction pathway. (I) is useful  
 CC for identifying a specific binding partner. (I) and nucleic acids (II)  
 CC encoding (I) are useful for diagnosing, monitoring disease and treating  
 CC caused by altered expression of human POSHL1 including diagnosing and  
 CC treating cancer, they are useful in the development of vaccines and (II) is  
 CC useful in gene therapy. (II) is useful for constructing microarrays which  
 CC are useful for measuring and for surveying gene expression and creating  
 CC transgenic non-human animals capable of producing the proteins. The  
 CC present sequence is that of a scanning oligonucleotide useful in examples  
 CC of the invention. Note: The present sequence did not form part of the  
 CC printed specification, but is based on sequence information supplied to  
 CC Derwent by the European Patent Office  
 XX  
 SQ Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1753 TCCTAAAGGCCCA 1765  
 Db 16 TCCTAAAGTCCCA 4  
 RESULT 568  
 ABV90586/c  
 ID ABV90586 standard; DNA; 17 BP.  
 AC ABV90586;  
 DT 23-DEC-2002 (first entry)  
 XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1299.  
 DE  
 XX Human: POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
 KW gene therapy; transgenic; ss.  
 XX Homo sapiens.  
 OS  
 PN EPI2339051-A2.  
 XX  
 FD 11-SEP-2002.  
 PF  
 XX 28-JAN-2002; 2002EP-00001165.  
 XX  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.  
 XX Shannon M;  
 PI  
 XX WPI; 2002-684061/74.  
 DR  
 XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL  
 PT -1, useful for treating disorders associated with decreased expression or  
 PT activity of human POSHL1.  
 XX  
 XX Example 2; SEQ ID NO 1299; 60pp + Sequence Listing; English.  
 PS  
 CC The invention relates to an isolated SH3 domain (POSH)-like signalling  
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
 CC acids (S1, AB883999), a sequence having 65% sequence identity to (S1),  
 CC (S1) having 95% deviations, especially conservative substitutions or a  
 CC fragment of the sequences comprising at least 8 contiguous amino acids.  
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
 CC adaptor protein that interacts with Rho family small GTPases as well as  
 CC downstream components of the signal transduction pathway. (I) is useful  
 CC for identifying a specific binding partner. (I) and nucleic acids (II)  
 CC encoding (I) are useful for diagnosing, monitoring disease and treating  
 CC caused by altered expression of human POSHL1 including diagnosing and  
 CC treating cancer, they are useful in the development of vaccines and (II) is  
 CC useful in gene therapy. (II) is useful for constructing microarrays which  
 CC are useful for measuring and for surveying gene expression and creating  
 CC transgenic non-human animals capable of producing the proteins. The  
 CC present sequence is that of a scanning oligonucleotide useful in examples  
 CC of the invention. Note: The present sequence did not form part of the  
 CC printed specification, but is based on sequence information supplied to  
 CC Derwent by the European Patent Office  
 XX  
 SQ Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1664 CTCACAGCTGGAA 1676  
 Db 14 CACACAGCTGGAA 2  
 RESULT 569  
 ABV90585/c  
 ID ABV90585 standard; DNA; 17 BP.  
 AC ABV90585;  
 DT 23-DEC-2002 (first entry)  
 XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1298.  
 DE  
 XX Human: POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
 KW gene therapy; transgenic; ss.  
 XX Homo sapiens.  
 OS  
 PN EPI2339051-A2.  
 XX  
 FD 11-SEP-2002.  
 PF  
 XX 28-JAN-2002; 2002EP-00001165.  
 XX  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.

```

PR 30-JAN-2001; 2001WO-US000667.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
PI WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 1298; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (SI, AB883999), a sequence having 65% sequence identity to (SI),
CC (SI) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX Sequence 17 BP; 1 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
SQ Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1664 CTCACAGCTGGAA 1676
DB | | | | | | | | | |
15 CACACAGCTGGAA 3

RESULT 570
ABV91045/C
ID ABV91045 standard; DNA; 17 BP.
XX AC ABV91045;
XX DT 23-DEC-2002 (first entry)
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1758.
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX KW gene therapy; transgenic; ss.
XX OS Homo sapiens.
XX PN EF1239051-A2.
XX PD 11-SEP-2002.
XX PF 28-JAN-2002; 2002EP-00001165.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
PI WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 1758; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (SI, AB883999), a sequence having 65% sequence identity to (SI),
CC (SI) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
SQ Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1753 TCCTAAGGCCCA 1765
DB | | | | | | | | | |
17 TCCTAAGGCCCA 5

RESULT 571
ABV90583/C
ID ABV90583 standard; DNA; 17 BP.
XX AC ABV90583;
XX DT 23-DEC-2002 (first entry)
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1296.
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX KW gene therapy; transgenic; ss.
XX OS Homo sapiens.
XX PN EF1239051-A2.
XX PD 11-SEP-2002.
XX PF 28-JAN-2002; 2002EP-00001165.
XX PR 30-JAN-2001; 2001WO-US000663.

```







XX WPI; 2002-122074/16.  
 XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of  
 PT individuals e.g. by determining immunogenetic differences when  
 PT transplating between them.  
 XX  
 XX Claim 10; Page 293; 345pp; Japanese.  
 XX  
 XX The invention relates to a typing kit for judging human leukocyte antigen  
 CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base  
 CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of  
 CC genes e.g. belonging to HLA class I antigens on human genome and  
 CC containing gene polymorphisms as allantoigens have been immobilised as  
 CC primers for amplification of cleaved nucleic acids relating to gene  
 CC polymorphisms. The method is useful for judging HLA genotypes of  
 CC individuals by determining immunogenetic differences before transplanting  
 CC between them, providing genetic information to decide compatibility of  
 CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,  
 CC pancreas, langerhans islet in pancreas and cornea, susceptibility  
 CC diagnosis of genetic diseases and identifying individuals  
 XX  
 XX Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1661 AGGCTCACAGCTG 1673  
 Db 17 AGGCTCTCAGCTG 5  
 ||||| |||||  
 RESULT 576  
 ABX72073/c  
 ID ABX72073 standard; DNA; 17 BP.  
 AC ABX72073;  
 XX  
 DT 12-MAR-2003 (first entry)  
 XX  
 DE Human tumour endothelial marker TEM 6 DNA long tag.  
 XX  
 KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
 KW Tumour endothelial marker; normal endothelial marker; PEM;  
 KW pan-endothelial marker; polycystic kidney disease; psoriasis;  
 KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
 KW neovascularization; immune response; cytostatic; antidiabetic;  
 KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO20020283874-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US008253.  
 XX  
 XX 11-APR-2001; 2001US-0282850P.  
 PR 06-FEB-2002; 2002US-0354262P.  
 XX  
 XX (UWJO) UNIV JOHNS HOPKINS.  
 XX  
 XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
 PI WPI; 2003-093016/08.  
 XX  
 DR New purified human transmembrane protein, designated as tumor endothelial  
 PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,  
 PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
 PT psoriasis.  
 XX  
 XX Disclosure; Page 359; 374pp; English.

XX The present invention relates to a novel method for the isolation of  
 CC endothelial cells (ECs), and the identification of genes expressed in  
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal  
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
 CC identified in human ECs. The human EC marker proteins and the  
 CC polynucleotide sequences encoding them are useful for detecting,  
 CC diagnosing or treating tumours as well as polycystic kidney disease,  
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
 CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for  
 CC inducing an immune response to tumour endothelial cells in a patient, or  
 CC for identifying candidate drugs for treating tumours. ABX72067-ABX72116  
 CC represent human TEM DNA tags  
 XX  
 SQ Sequence 17 BP; 4 A; 8 C; 5 G; 0 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1678 CCGTGGTCTCTCT 1690  
 Db 14 CCGTGGTCTCTCT 2  
 ||||| |||||  
 RESULT 577  
 ABZ69604  
 ID ABZ69604 standard; DNA; 17 BP.  
 XX  
 AC ABZ69604;  
 XX  
 DT 11-AUG-2003 (first entry)  
 XX  
 DE Human telomerase coding sequence PCR primer #5.  
 XX  
 KW Transient immortalisation; immortalisation protein; transplant; PCR;  
 KW primer; ss; cardiant; osteopathic; hepatotropic; antiparkinsonian;  
 KW organ regeneration; degenerative disease; cardiac infarct;  
 KW bone degeneration; osteoporosis; liver regeneration; Parkinson's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003035984-A2.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 07-OCT-2002; 2002WO-EP011200.  
 XX  
 PR 18-OCT-2001; 2001DE-01052972.  
 XX  
 XX (HEAR-) HEART BIOSYSTEMS GMBH.  
 XX  
 XX Kueper J, Meyer R, Meyer-Ficca M, Kuhn A;  
 XX WPI; 2003-430421/40.  
 XX  
 XX Transient immortalization of cells, useful for preparing transplant  
 PT material and for organ regeneration, by supplying immortalizing proteins  
 PT externally.  
 XX  
 XX Example 5; Page 29; 59pp; German.  
 XX  
 XX The present invention relates to a method for the transient  
 CC immortalisation of cells by introducing immortalisation proteins into  
 CC them from the outside. The method is used to immortalise cells  
 CC transiently to allow their expansion, particularly to produce transplant  
 CC material for regenerating organs, for treating chronic (degenerative)  
 CC diseases, e.g. in cases of cardiac infarct (with simultaneous reduction  
 CC in the risk of congestive heart failure and future infarcts) or chronic  
 CC bone degeneration (osteoporosis), for regeneration of the liver, for  
 CC treating Parkinson's disease (using dopaminergic cells) and for ex vivo  
 CC production of heart and venous valves. The present sequence is a PCR  
 CC primer used in the exemplification of the invention

```
XX SQ Sequence 17 BP; 0 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1679 CTGGTGTCTCCCTC 1691
DB 2 CTGGTGTCTGCTC 14

RESULT 578
ABT35614
ID ABT35614 standard; DNA; 17 BP.
XX AC ABT35614;
XX DT 12-JUN-2003 (first entry)
XX DE Tumour suppression related human fukutin oligo SEQ ID No 1251.
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; protein chip; gene therapy; tumour suppression;
XX KW human fukutin; ds.
XX OS Homo sapiens.
XX PN WO2003025175-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB004208.
XX PR 17-SEP-2001; 2001FR-00011978.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-313353/30.
XX DR New isolated nucleic acid, useful for treating viral diseases associated
XX PT with tumors and cell degeneration, also related polypeptides, antibodies
XX PT and transfected cells.
XX PS Disclosure; Page 179; 720pp; French.
XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX CC given in the specification, a sequence containing at least 15 consecutive
XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal
XX CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX CC hybridizes to them under highly stringent conditions, or the complement
XX CC of any of them, or the corresponding RNA. The novel isolated nucleic
XX CC acids of the invention are useful as probes and primers for detecting,
XX CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX CC component of a gene chip, in vitro as (anti)sense reagents, and for
XX CC production of recombinant polypeptides. Any of the nucleic acids
XX CC polypeptides, vectors containing the nucleic acids, cells containing the
XX CC vector or antibodies directed against the polypeptides are useful for
XX CC preparation of pharmaceuticals for prevention and/or treatment of viral
XX CC diseases that are characterised by development of tumours or cell
XX CC degeneration, specifically cancer but also Alzheimer's disease and
XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX CC patient samples is useful for diagnosis and/or prognosis of these
XX CC diseases. The polypeptides can also be used to generate antibodies, and
XX CC both the polypeptide and antibodies are useful as components of protein
XX CC chips. The nucleic acid sequences of the invention can be used in gene
XX CC therapy. This polynucleotide sequence represents a tumour suppression
XX CC related human fukutin oligonucleotide of the invention
XX SQ Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match      8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1679 TCTCCTCCAGCGT 1697
DB 3 TCTCCTCAAGCGT 15

RESULT 579
ABT36109
ID ABT36109 standard; DNA; 17 BP.
XX AC ABT36109;
XX DT 12-JUN-2003 (first entry)
XX DE Tumour suppression related human fukutin oligo SEQ ID No 1746.
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; protein chip; gene therapy; tumour suppression;
XX KW human fukutin; ds.
XX OS Homo sapiens.
XX PN WO2003025175-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB004208.
XX PR 17-SEP-2001; 2001FR-00011978.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-313353/30.
XX DR New isolated nucleic acid, useful for treating viral diseases associated
XX PT with tumors and cell degeneration, also related polypeptides, antibodies
XX PT and transfected cells.
XX PS Disclosure; Page 237; 720pp; French.
XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX CC given in the specification, a sequence containing at least 15 consecutive
XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal
XX CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX CC hybridizes to them under highly stringent conditions, or the complement
XX CC of any of them, or the corresponding RNA. The novel isolated nucleic
XX CC acids of the invention are useful as probes and primers for detecting,
XX CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX CC component of a gene chip, in vitro as (anti)sense reagents, and for
XX CC production of recombinant polypeptides. Any of the nucleic acids
XX CC polypeptides, vectors containing the nucleic acids, cells containing the
XX CC vector or antibodies directed against the polypeptides are useful for
XX CC preparation of pharmaceuticals for prevention and/or treatment of viral
XX CC diseases that are characterised by development of tumours or cell
XX CC degeneration, specifically cancer but also Alzheimer's disease and
XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX CC patient samples is useful for diagnosis and/or prognosis of these
XX CC diseases. The polypeptides can also be used to generate antibodies, and
XX CC both the polypeptide and antibodies are useful as components of protein
XX CC chips. The nucleic acid sequences of the invention can be used in gene
XX CC therapy. This polynucleotide sequence represents a tumour suppression
XX CC related human fukutin oligonucleotide of the invention
XX SQ Sequence 17 BP; 1 A; 5 C; 3 G; 8 T; 0 U; 0 Other;
```

Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1679 CTGGTGTCTCCTC 1691  
Db 4 CTTGTGTCTCCTC 16

RESULT 580  
ABT38378/C  
ID ABT38378 standard; DNA; 17 BP.  
XX  
AC ABT38378;

Tumour suppression related human fukutin oligo SEQ ID No 4015.

DE XX  
KW KW  
XX KW  
KW KW  
KW KW

Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
schizophrenia; protein chip; gene therapy; tumour suppression;  
human fukutin; ds.  
KW

The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppressor related human fukutin oligonucleotide of the invention

QY 1714 GGAGTACGGAGAT 1726  
|||||  
Db 14 GGAGTAAGGAGAT 2

RESULT 581  
ACA06206/C  
ID ACA06206 standard; RNA; 17 BP.  
XX  
XX  
ACA06206;  
XX  
XX 03-JUN-2003 (first entry)  
DD  
DE NFkB sub-unit modulating inozyme substrate #25.

Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinyzyme; G-cleaver; amberyzyme; cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate; gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes; rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammation; inflammatory bowel disease; infection; ss

OS Homo sapiens.

PN US2002177568-A1.

PD 28-NOV-2002.

PF 23-MAY-2001; 2001US-00864785.

PR 07-DEC-1992; 92US-00987132.

PR 15-AUG-1994; 94US-00291932.

XX  
1000

PA (MCSW/) MCSWIGGEN J.

XX  
XX

XX

XX

PT a sequence encoding a subunit of nuclear

XX

XXXX

CC regulates expression of a sequence

configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially  $Mg^{2+}$ . The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic

acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents the substrate of a novel enzymatic nucleic acid molecule

Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1639 CTTGTAGCAGAG 1651  
Db 17 CTTGTAGCGGAG 5  
|||||||

RESULT 582  
ACA06207/C  
ID ACA06207 standard; RNA; 17 BP.  
XX ACA06207;  
XX  
XX  
DT 03-JUN-2003 (first entry)  
XX  
DE NFKB sub-unit modulating inozyme substrate #26.  
XX  
KW Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;  
KW G-cleaver; amberyne; cancer; REL-A activity; breast cancer; human;  
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;  
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.  
XX  
OS Homo sapiens.  
XX  
XX US2002177568-A1.  
XX  
XX 28-NOV-2002.  
XX  
XX 23-MAY-2001; 2001US-00864785.  
XX  
XX 07-DEC-1992; 92US-00987132.  
XX  
XX 18-MAY-1994; 94US-00245466.  
XX  
XX 15-AUG-1994; 94US-00291932.  
XX  
XX 23-DEC-1996; 96US-00777916.  
XX  
XX (STIN/) STINCHOMB D T.  
PA PA (MCSW/) MCSWIGGEN J.  
PA PA (DRAP/) DRAPER K G.  
XX  
XX Stinchcomb DT, Mcswiggen J, Draper KG;  
XX  
XX WPI; 2003-340953/32.  
XX  
XX Novel enzymatic nucleic acid molecules which down regulates expression of  
XX a sequence encoding a subunit of nuclear factor kappa B useful for  
XX treating cancer, inflammatory disorders and autoimmune diseases.  
XX  
XX Claim 3; Page 27; 72pp; English.  
XX  
XX The invention describes an enzymatic nucleic acid molecule (I) which down  
XX regulates expression of a sequence encoding a subunit of nuclear factor

kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberyne configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents the substrate of a novel enzymatic nucleic acid molecule

Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1639 CTTGTAGCAGAG 1651  
Db 14 CTTGTAGCGGAG 2  
|||||||

RESULT 583  
ACA07619/C  
ID ACA07619 standard; RNA; 17 BP.  
XX ACA07619;  
XX  
XX  
DT 03-JUN-2003 (first entry)  
XX  
DE NFKB sub-unit modulating zinzyme substrate #18.  
XX  
KW Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;  
KW G-cleaver; amberyne; cancer; REL-A activity; breast cancer; human;  
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;  
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.  
XX  
XX Homo sapiens.  
OS  
XX US2002177568-A1.  
XX  
XX 28-NOV-2002.  
XX  
XX 23-MAY-2001; 2001US-00864785.  
XX  
XX 07-DEC-1992; 92US-00987132.  
XX  
XX 18-MAY-1994; 94US-00245466.  
XX  
XX 15-AUG-1994; 94US-00291932.  
XX  
XX 23-DEC-1996; 96US-00777916.  
XX  
XX (STIN/) STINCHOMB D T.  
PA PA (MCSW/) MCSWIGGEN J.  
PA PA (MCSW/) MCSWIGGEN J.

PA (DRAP/) DRAPER K G.  
 XX Stinchcomb DT, Mcswiggen J, Draper KG;  
 XX WPI; 2003-340953/32.  
 XX  
 XX Novel enzymatic nucleic acid molecules which down regulates expression of  
 PT a sequence encoding a subunit of nuclear factor kappa B useful for  
 PT treating cancer, inflammatory disorders and autoimmune diseases.  
 XX  
 XX Claim 3; Page 38; 72pp; English.  
 XX  
 XX The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,  
 CC gencitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule  
 XX  
 XX Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;  
 SQ  
 Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1639 CTTGTAGCGAAG 1651  
 Db ||||| |||||  
 16 CTTGTAGCGAAG 4  
 RESULT 584  
 ACA08196/C  
 ID ACA08196 standard; RNA; 17 BP.  
 XX  
 XX ACA08196;  
 XX  
 XX  
 XX 03-JUN-2003 (first entry)  
 DT  
 XX NFkB sub-unit modulating DNazyme substrate #3.  
 DE  
 XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;  
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;  
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;  
 KW gencitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.  
 XX  
 XX Homo sapiens.

XX US2002177568-A1.  
 PN  
 XX 28-NOV-2002.  
 PD  
 XX  
 XX 23-MAY-2001; 2001US-00864785.  
 PF  
 XX 07-DEC-1992; 92US-00987132.  
 PR 18-MAY-1994; 94US-00245466.  
 PR 15-AUG-1994; 94US-00291932.  
 PR 23-DEC-1996; 96US-00777916.  
 PS  
 XX (STIN/) STINCHOMB D T.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (DRAP/) DRAPER K G.  
 XX  
 XX Stinchcomb DT, Mcswiggen J, Draper KG;  
 PI WPI; 2003-340953/32.  
 DR  
 XX Novel enzymatic nucleic acid molecules which down regulates expression of  
 CC a sequence encoding a subunit of nuclear factor kappa B useful for  
 CC treating cancer, inflammatory disorders and autoimmune diseases.  
 CC  
 CC Claim 3; Page 42; 72pp; English.  
 XX  
 XX The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,  
 CC gencitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule  
 XX  
 XX Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;  
 SQ  
 Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1639 CTTGTAGCGAAG 1651  
 Db ||||| |||||  
 13 CTTGTAGCGAAG 1  
 RESULT 585  
 ADB03602  
 ID ADB03602 standard; DNA; 17 BP.  
 XX  
 XX ADB03602;  
 AC  
 XX 20-NOV-2003 (first entry)  
 DT  
 XX Human MDZ7 scanning oligonucleotide SEQ ID 4588.  
 DE  
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW

KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.

XX Homo sapiens.

PN EP1281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 4588; 103pp; English.

XX The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 7 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 GTAGCAGAGGCA 1654

DB 2 GTAGCAGAGGAA 14

RESULT 586  
ADA99413  
ID ADA99413 standard; DNA; 17 BP.

AC ADA99413;

XX 20-NOV-2003 (first entry)

XX Human MDZ3 scanning oligonucleotide SEQ ID 402.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.

XX Homo sapiens.

XX EP1281758-A2.

XX 05-FEB-2003.

PD 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 402; 103pp; English.

XX The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 2 A; 8 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1744 TCCTCCTATCCT 1756

DB 2 TCCTCCTATCCT 14

RESULT 587  
ADA99414  
ID ADA99414 standard; DNA; 17 BP.

AC ADA99414;

XX 20-NOV-2003 (first entry)

XX Human MDZ3 scanning oligonucleotide SEQ ID 403.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.

XX Homo sapiens.

XX EP1281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX

```
PI Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 403; 103pp; English.
PS
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 2 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
SQ Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1744 TCCTCCCTATCCT 1756
Db 1 TCCTCACTATCCT 13
RESULT 588
ADA99411
ID ADA99411 standard; DNA; 17 BP.
XX
XX ADA99411;
AC
XX 20-NOV-2003 (first entry)
DT
XX Human MDZ3 scanning oligonucleotide SEQ ID 400.
DE
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI281758-A2.
PN
XX 05-FEB-2003.
PD
XX 30-JUL-2002; 2002EP-00016874.
PF
XX 02-AUG-2001; 2001US-00922181.
PR
XX (AEOM-) AEOMICA INC.
PA
XX Shannon M, Gu Y, Nguyen C;
PI
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
```

```
XX Example 8; SEQ ID NO 400; 103pp; English.
PS
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
SQ Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1744 TCCTCCCTATCCT 1756
Db 4 TCCTCACTATCCT 16
RESULT 589
ADB03600
ID ADB03600 standard; DNA; 17 BP.
XX
XX ADB03600;
AC
XX 20-NOV-2003 (first entry)
DT
XX Human MDZ7 scanning oligonucleotide SEQ ID 4586.
DE
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI281758-A2.
PN
XX 05-FEB-2003.
PD
XX 30-JUL-2002; 2002EP-00016874.
PF
XX 02-AUG-2001; 2001US-00922181.
PR
XX (AEOM-) AEOMICA INC.
PA
XX Shannon M, Gu Y, Nguyen C;
PI
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
```

CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 17 BP; 7 A; 2 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1642 GTAGCAGAAGGCA 1654  
Db 4 GTAGCAGAAGGAA 16  
|||||  
  
RESULT 590  
ADB03601  
ID ADB03601 standard; DNA; 17 BP.  
XX  
AC ADB03601;  
XX  
DT 20-NOV-2003 (first entry)  
DE Human MDZ7 scanning oligonucleotide SEQ ID 4587.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1281758-A2.  
XX  
PD 05-FEB-2003.  
XX  
PF 30-JUL-2002; 2002EP-00016874.  
XX  
PR 02-AUG-2001; 2001US-00922181.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M, Gu Y, Nguyen C;  
XX  
DR WPI; 2003-423107/40.  
XX  
PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 4587; 103pp; English.  
XX  
CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences; MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The

CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 17 BP; 7 A; 2 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1642 GTAGCAGAAGGCA 1654  
Db 3 GTAGCAGAAGGAA 15  
|||||  
  
RESULT 591  
ADB03603  
ID ADB03603 standard; DNA; 17 BP.  
XX  
AC ADB03603;  
XX  
DT 20-NOV-2003 (first entry)  
DE Human MDZ7 scanning oligonucleotide SEQ ID 4589.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1281758-A2.  
XX  
PD 05-FEB-2003.  
XX  
PF 30-JUL-2002; 2002EP-00016874.  
XX  
PR 02-AUG-2001; 2001US-00922181.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M, Gu Y, Nguyen C;  
XX  
DR WPI; 2003-423107/40.  
XX  
PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 4589; 103pp; English.  
XX  
CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences; MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 17 BP; 6 A; 2 C; 7 G; 2 T; 0 U; 0 Other;  
  
Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;





KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
KW anti-rheumatic; cancer; AIDS; ss.  
XX  
OS Homo sapiens.  
PN WO200297114-A2.  
XX  
XX 05-DEC-2002.  
PD  
XX  
PF 29-MAY-2002; 2002WO-US016840.  
XX  
XX 29-MAY-2001; 2001US-0294140P.  
PR 06-JUN-2001; 2001US-0296249P.  
PR 10-SEP-2001; 2001US-0318471P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
XX Mcswiggen J;  
PI  
XX WPI; 2003-140484/13.  
DR  
XX Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
XX  
XX Claim 4; Page 147; 185pp; English.  
PS  
XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
CC rheumatic activity. The nucleic acid molecules are useful for reducing  
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ5531, ABZ6520 - ABZ6524,  
CC ABZ6530 - ABZ6595 represent substrate/target sequences for the human  
CC ribozymes of the invention  
XX  
SQ Sequence 17 BP; 3 A; 5 C; 6 G; 0 T; 3 U; 0 Other;  
  
Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 76.9%; Pred. No. 4.7e+02;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1663 GCTCAGCTGGA 1675  
DB 2 GCUCACUGGUGA 14  
||:|||||  
||:|||||  
  
RESULT 595  
ABZ65290  
ID ABZ65290 standard; RNA; 17 BP.  
XX  
AC ABZ65290;  
XX  
DT 21-MAR-2003 (first entry)  
XX  
DE Human HER2 DNzyme substrate #747.  
XX  
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
KW anti-rheumatic; cancer; AIDS; ss.  
XX  
OS Homo sapiens.  
PN WO200297114-A2.  
XX  
XX 05-DEC-2002.  
PD  
XX  
XX 29-MAY-2002; 2002WO-US016840.  
PF

XX 29-MAY-2001; 2001US-0294140P.  
PR 06-JUN-2001; 2001US-0296249P.  
PR 10-SEP-2001; 2001US-0318471P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
XX Mcswiggen J;  
PI  
XX WPI; 2003-140484/13.  
DR  
XX Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
XX  
XX Claim 4; Page 147; 185pp; English.  
PS  
XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
CC rheumatic activity. The nucleic acid molecules are useful for reducing  
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ5531, ABZ6520 - ABZ6524,  
CC ABZ6530 - ABZ6595 represent substrate/target sequences for the human  
CC ribozymes of the invention  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;  
  
Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 76.9%; Pred. No. 4.7e+02;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1663 GCTCAGCTGGA 1675  
DB 5 GCUCACUGGUGA 17  
||:|||||  
||:|||||  
  
RESULT 596  
ACD63408  
ID ACD63408 standard; RNA; 17 BP.  
XX  
AC ACD63408;  
XX  
DT 30-SEP-2003 (first entry)  
XX  
DE HCV minus strand DNzyme substrate sequence #1047.  
XX  
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; zinzyme;  
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX  
OS Hepatitis C virus.  
XX  
XX WO200281494-A1.  
PN  
XX 17-OCT-2002.  
PD  
XX  
XX 26-MAR-2002; 2002WO-US009187.  
PF  
XX  
XX 26-MAR-2001; 2001US-00817879.  
PR 08-JUN-2001; 2001US-00677478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
PF

XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX WPI; 2003-229207/22.  
 XX  
 PT Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 PS Claim 1; Page 293; 387pp; English.  
 XX  
 CC The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberyms, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNazyme or minus strand DNazyme sequences disclosed in the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 4 A; 4 C; 3 G; 0 T; 6 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 63.5%; Pred. No. 4.7e+02;  
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1675 AACCTGGTGCT 1687  
 |||||:|:|:|:  
 Db 2 AACCCUGGUGUAU 14  
 RESULT 597  
 ACDS5657/C  
 ID ACDS5657 standard; RNA; 17 BP.  
 XX  
 AC ACDS5657;  
 XX  
 DT 23-SEP-2003 (first entry)  
 XX  
 DE HBV amberyms substrate sequence #167.  
 XX  
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberyms; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis B virus.  
 XX

PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX WPI; 2003-229207/22.  
 XX  
 PT Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 PS Example 1; Page 206; 387pp; English.  
 XX  
 CC The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberyms, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HBV  
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberyms sequences  
 CC disclosed in the present invention  
 XX  
 SQ Sequence 17 BP; 4 A; 0 C; 11 G; 0 T; 2 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1736 CTCGCCAATCTCTC 1748  
 |||||:|:|:|:  
 Db 13 CCCCCCACTCTCTC 1  
 RESULT 598  
 ACDS59262/C  
 ID ACDS59262 standard; RNA; 17 BP.  
 XX  
 AC ACDS59262;  
 XX  
 DT 24-SEP-2003 (first entry)  
 XX  
 DE HCV DNazyme substrate sequence #1232.  
 XX

KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;  
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEF/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX  
 DR WPI; 2003-229207/22.  
 XX  
 PT Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 XX Claim 1; Page 256; 387pp; English.  
 CC The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,  
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNzyme or minus strand DNzyme sequences disclosed in the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. NO. 4.7e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1673 GGAACCTGGTGT 1685  
 DB 13 GCAACCTGGTGT 1

RESULT 599  
 ACD59261/C  
 ID ACD59261 standard; RNA; 17 BP.  
 XX  
 AC ACD59261;  
 XX  
 DT 24-SEP-2003 (first entry)  
 XX  
 DE HCV DNzyme substrate sequence #1231.  
 XX  
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;  
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEF/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX  
 DR WPI; 2003-229207/22.  
 XX  
 PT Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 XX Claim 1; Page 256; 387pp; English.  
 CC The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,  
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNzyme or minus strand DNzyme sequences disclosed in the present  
 CC invention



```

XX 21-NOV-2002.
PD
XX
PF 13-MAY-2002; 2002WO-US014877.
XX
XX 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
XX
XX Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;
PI WPI; 2003-129214/12.
XX
XX New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
PT diagnosing a HBM-like phenotype in a subject and for preparing a
PT composition for modulating bone mass and/or lipid levels in a subject
PT suffering from e.g. osteoporosis.
XX
XX Disclosure; Page 53; 629pp; English.
XX
XX The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a
CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid
CC level modulation. The invention is useful for diagnosing a HBM-like
CC phenotype in a subject and for preparing a composition for modulating
CC bone mass and/or lipid levels in a subject suffering from e.g.
CC osteoporosis. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 2 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
SQ
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1722 GAGATGGAGATTG 1734
DB 14 GAGAGGGAGATTG 2
RESULT 603
ADB42129
ID ADB42129 standard; DNA; 17 BP.
XX
XX ADB42129;
XX
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
XX Tumour suppression/reversion associated nucleotide #2452.
DE
XX cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
OS
XX WO2003040369-A2.
XX
XX 15-MAY-2003.
XX
XX 17-SEP-2002; 2002WO-IB004219.
XX
XX 17-SEP-2001; 2001FR-00011981.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT

```

---

```

DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX Disclosure; Page 318; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
XX Sequence 17 BP; 1 A; 5 C; 3 G; 8 T; 0 U; 0 Other;
SQ
Query Match 8.2%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1679 CTGGTGTCCTCCTC 1691
DB 4 CTGGTGTCCTCCTC 16
RESULT 604
ADB39940/C
ID ADB39940 standard; DNA; 17 BP.
XX
XX ADB39940;
XX
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
XX Tumour suppression/reversion associated nucleotide #263.
DE
XX
XX cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
OS
XX WO2003040369-A2.
XX
XX 15-MAY-2003.
XX
XX 17-SEP-2002; 2002WO-IB004219.
XX
XX 17-SEP-2001; 2001FR-00011981.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT

```

PT useful e.g. for treatment of tumors and viral infection, also related  
PT polypeptide and antibodies.  
PS Disclosure; Page 62; 77lpp; French.  
XX  
CC The invention relates to the isolation of 6327 nucleotide sequences,  
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
CC sequence having at least 80% identity, after optimal alignment, with the  
CC nucleotides, a sequence that hybridizes under stringent conditions with  
CC the nucleotides, or the complement, or corresponding RNA, of the  
CC nucleotides. The nucleotides are used as probes or primers for detecting,  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
CC sense and antisense sequences, of nucleotides involved in tumour  
CC suppression or reversion, apoptosis and or viral resistance, to produce  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC cells containing the vectors), the encoded polypeptides and antibodies  
CC (Ab) against the polypeptide are useful for prevention and/or treatment  
CC of viral infections or diseases characterized by development of tumours  
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
CC Analysis of the expression of the nucleotides can be used for diagnosis  
CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
CC also be used to screen for their specific interactive molecules,  
CC potentially useful for treating diseases associated with abnormal  
CC expression of the nucleotides.  
XX  
SQ Sequence 17 BP; 7 A; 5 C; 2 G; 3 T; 0 U; 0 Other;  
Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1637 GGCTTGTAGCAGA 1649  
Db |||||  
15 GGTTGTAGCAGA 3  
RESULT 605  
ADB39941/C  
ID ADB39941 standard; DNA; 17 BP.  
XX  
AC ADB39941;  
XX  
DT 18-DEC-2003 (revised)  
DT 04-DEC-2003 (first entry)  
XX  
DE Tumour suppression/reversion associated nucleotide #264.  
XX  
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
KW diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN WO2003040369-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 17-SEP-2002; 2002WO-IB004219.  
XX  
PR 17-SEP-2001; 2001FR-00011981.  
XX  
FA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
XX Tellerman A, Amson R, Tuijnder M;  
XX  
XX WPI; 2003-441574/41.  
XX  
XX New nucleic acid encoding human prostate membrane-specific antigen,  
PT useful e.g. for treatment of tumors and viral infection, also related  
PT polypeptide and antibodies.  
XX

PS Disclosure; Page 63; 77lpp; French.  
XX  
CC The invention relates to the isolation of 6327 nucleotide sequences,  
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
CC sequence having at least 80% identity, after optimal alignment, with the  
CC nucleotides, a sequence that hybridizes under stringent conditions with  
CC the nucleotides, or the complement, or corresponding RNA, of the  
CC nucleotides. The nucleotides are used as probes or primers for detecting,  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
CC sense and antisense sequences, of nucleotides involved in tumour  
CC suppression or reversion, apoptosis and or viral resistance, to produce  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC cells containing the vectors), the encoded polypeptides and antibodies  
CC (Ab) against the polypeptide are useful for prevention and/or treatment  
CC of viral infections or diseases characterized by development of tumours  
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
CC Analysis of the expression of the nucleotides can be used for diagnosis  
CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
CC also be used to screen for their specific interactive molecules,  
CC potentially useful for treating diseases associated with abnormal  
CC expression of the nucleotides.  
XX  
SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1637 GGCTTGTAGCAGA 1649  
Db |||||  
15 GGTTGTAGCAGA 3  
RESULT 606  
ADC37717  
ID ADC37717 standard; DNA; 17 BP.  
XX  
AC ADC37717;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Human AMLP1a scanning 17-mer oligonucleotide SEQ ID NO:66.  
XX  
KW human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;  
KW AMLP1a; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO2003037931-A2.  
XX  
PD 08-MAY-2003.  
XX  
PF 01-NOV-2002; 2002WO-US035129.  
XX  
PR 01-NOV-2001; 2001US-0334773P.  
XX  
FA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.  
XX  
XX Shannon M, Phan T;  
XX  
XX WPI; 2003-430501/40.  
XX  
XX New isolated nucleic acid molecule encoding a human angiominotin-like  
PT protein, useful for treating or preventing a disorder associated with  
PT decreased or increased expression or activity of AMLP1.  
XX  
XX Example 2; SEQ ID NO 66; 172pp; English.  
PS  
XX The present invention describes the human angiominotin-like protein 1  
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene  
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and

CC compositions of the present invention can be used for treating or  
CC preventing a disorder associated with decreased or increased expression  
CC or activity of AMLP1. The present sequence represents a scanning  
CC oligonucleotide for human AMLP1a, which is used in an example from the  
CC present invention.  
XX Sequence 17 BP; 7 A; 2 C; 6 G; 2 T; 0 U; 0 Other;  
SQ

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1719 ACGGAGATGGAGA 1731  
Db 1 ACGGTGATGGAGA 13

RESULT 607  
ADB44320/c  
ID ADB44320 standard; DNA; 17 BP.  
XX  
AC ADB44320;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Tumour suppression/reversion associated nucleotide #4643.  
XX  
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
KW diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN WO2003040369-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 17-SEP-2002; 2002WO-IB004219.  
XX  
PR 17-SEP-2001; 2001PR-00011981.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
PI Telerman A, Amson R, Tuijnder M;  
XX  
DR WPI; 2003-441574/41.  
XX  
PT New nucleic acid encoding human prostate membrane-specific antigen,  
PT useful e.g. for treatment of tumors and viral infection, also related  
PT polypeptide and antibodies.  
XX  
PS Disclosure; Page 574; 771pp; French.  
XX  
CC The invention relates to the isolation of 6327 nucleotide sequences,  
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
CC sequence having at least 80% identity, after optimal alignment, with the  
CC nucleotides, a sequence that hybridizes under stringent conditions with  
CC the nucleotides, or the complement, or corresponding RNA, of the  
CC nucleotides. The nucleotides are used as probes or primers for detecting,  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
CC sense and antisense sequences, of nucleotides involved in tumour  
CC suppression or reversion, apoptosis and or viral resistance, to produce  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC cells containing the vectors), the encoded polypeptides and antibodies  
CC (Ab) against the polypeptide are useful for prevention and/or treatment  
CC of viral infections or diseases characterized by development of tumours  
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
CC Analysis of the expression of the nucleotides can be used for diagnosis  
CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
CC also be used to screen for their specific interactive molecules,  
CC potentially useful for treating diseases associated with abnormal

CC expression of the nucleotides.  
XX Sequence 17 BP; 5 A; 3 C; 5 G; 4 T; 0 U; 0 Other;  
SQ

Query Match 8.2%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1665 TCACAGCTGGAAAC 1677  
Db 13 TCACAGCTGGATC 1

RESULT 608  
AAT66085/c  
ID AAT66085 standard; DNA; 20 BP.  
XX  
AC AAT66085;  
XX  
DT 25-MAR-2003 (revised)  
DT 18-JUN-1997 (first entry)  
XX  
DE Plasminogen activator/urokinase gene repeat sequence primer #1.  
XX  
KW Polymorphism; repeat sequence; genetic marker; primer; amplification;  
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;  
KW linkage analysis; genetic disease; animal; plant; breeding; locus;  
KW hybridisation; chromosome; ds.  
OS Synthetic.  
XX  
PN US5582979-A.  
XX  
PD 10-DEC-1996.  
XX  
PF 04-APR-1994; 94US-00222177.  
XX  
PR 21-APR-1989; 89US-00341562.  
PR 05-SEP-1991; 91US-00754351.  
XX  
PA (MARS-) MARSHFIELD CLINIC.  
XX  
PI Weber JL;  
XX  
DR WPI; 1997-042299/04.  
XX  
PT Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -  
PT using novel nucleic acid moles. as primers.  
XX  
PS Example 9; Col 59-60; 186pp; English.  
XX  
CC The invention relates to the isolation of polymorphic repeat sequences  
CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic  
CC markers. Primers based on these sequences can be used to detect these  
CC repeats, especially for use in e.g paternity or maternity testing, human  
CC genetic analysis such as linkage analysis of genetic disease, commercial  
CC animal or plant breeding or pedigree analysis. The sequences AAT66084-  
CC 166107 represent repeat sequences of low informativeness found in  
CC specific human genes. The primers AAT66085-6 were used to amplify a 111  
CC bp fragment of the plasminogen activator/urokinase gene which contains  
CC the repeat sequence of AAT66084. (Updated on 25-MAR-2003 to correct PF  
CC field.)  
XX  
SQ Sequence 20 BP; 5 A; 1 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 8.2%; Score 11.4; DB 1; Length 20;  
Best Local Similarity 92.3%; Pred. No. 5.8e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 GCTCCCAACTCCT 1747  
Db 13 GCTCCTAACTCCT 1





```

PR 14-MAY-1992; 92US-00832888.
PR 14-MAY-1992; 92US-00882889.
PR 14-MAY-1992; 92US-00882921.
PR 14-MAY-1992; 92US-00882922.
PR 14-MAY-1992; 92US-00883823.
PR 14-MAY-1992; 92US-00883849.
PR 14-MAY-1992; 92US-00884073.
PR 14-MAY-1992; 92US-00884074.
PR 14-MAY-1992; 92US-00884333.
PR 14-MAY-1992; 92US-00884422.
PR 14-MAY-1992; 92US-00884431.
PR 14-MAY-1992; 92US-00884436.
PR 14-MAY-1992; 92US-00884521.
PR 31-JUL-1992; 92US-00923738.
PR 26-AUG-1992; 92US-00935854.
PR 26-AUG-1992; 92US-00936086.
PR 18-SEP-1992; 92US-00948359.
PR 15-OCT-1992; 92US-00963322.
PR 07-DEC-1992; 92US-00987129.
PR 07-DEC-1992; 92US-00987130.
PR 07-DEC-1992; 92US-00987133.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Draper KG, Dudycz LW, Mcswiggen JA, Macejak DG, Holeczek JJ;
PI Mamone JA;
XX
XX WPI; 1993-386599/48.
XX
PT Enzymatic RNA molecules - used to inhibit viral replication, infection
PT and gene expression.
XX
PS Claim 5; Fig 13; 287pp; English.
XX
CC The sequences (AAQ52824-Q52890) are pref. Cytomegalovirus target
CC sequences for enzymatic RNA molecules. The RNA molecules are
CC complementary to a substrate binding region in the specified gene target.
CC They also have enzymatic activity, in that they specifically cleave RNA
CC in the target. The ERMs interfere with viral replication and therefore
CC have anti-viral properties. They can be used to attenuate viruses to be
CC used in vaccines. (Updated on 25-MAR-2003 to correct FN field.) (Updated
CC on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
CC PI field.)
XX
SQ Sequence 16 BP; 2 A; 6 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 4.8e+02;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1679 CTGGTGCTCTCCACG 1694
DB 1 CUGGUGUGACCCCCAG 16

RESULT 612
AAA74719/c
ID AAA/4719 standard; DNA; 16 BP.
XX
XX AAA74719;
XX
XX AC
XX
XX 12-JAN-2001 (first entry)
XX
XX Mycobacterium BCG transposition mutant cloned insertion site MYC7.
XX
XX Mycobacterium bovis; Mycobacterium tuberculosis; SacB; levane saccharase;
XX BCG transposition mutant; insertion site; transposon mutagenesis; ds.
XX
XX Mycobacterium sp.
XX
XX US6096549-A.
XX
XX 01-AUG-2000.
XX
XX

XX 11-JUN-1997; 97US-00872917.
XX
XX 11-JUN-1996; 96US-00661658.
XX
XX (INSP ) INST PASTEUR.
XX
XX Gicquel B, Guilhot C, Jackson M, Pellicic V, Reyrat J;
XX
XX WPI; 2000-542306/49.
XX
XX Transforming Mycobacterium strains for positive selection of allelic
XX exchange mutants, involves transfecting cells with vector comprising
XX marker gene and transposon and selecting in medium containing sucrose.
XX
XX Disclosure; Fig 15; 29pp; English.
XX
XX The present sequence is one of a number of cloned insertion sites for
XX Mycobacterium tuberculosis and Mycobacterium bovis BCG transposition
XX mutants. BCG transposition mutants were made as part of a process for
XX replacing a nucleotide sequence in the genome of a slow growing
XX Mycobacterium strain. The process comprises transfecting Mycobacterium
XX with a vector containing SacB gene coding for levane saccharase enzyme
XX and selecting clones of transformed Mycobacteria by propagating the
XX clones in a culture medium supplemented with sucrose. The method is
XX useful for inserting a transposon in the genome of a Mycobacterium
XX strain. Protective antigens, e.g. for use in BCG vaccine strains, may be
XX cloned into the Mycobacterium genome. The process is also useful for
XX random inactivation of genes coding for a protein involved in the
XX virulence of a pathogenic mycobacterium strain. The method facilitates an
XX increase of the proportion of allelic exchange mutants, making the
XX screening of transformants easier
XX
XX Sequence 16 BP; 4 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1754 CCTAAGGCCCTCTGG 1769
DB 16 CCTAATGGCCTAATGG 1

RESULT 613
AAS56873
ID AAS56873 standard; DNA; 16 BP.
XX
XX AC AAS56873;
XX
XX 16-JAN-2002 (first entry)
XX
XX Validation ribozyme DNA sequence #47.
XX
XX Human; BRCA-1 regulator; ribozyme; BR1; RNA target recognition; probe;
XX cytosolic; RNA cleavage; tumour suppressor; PCR primer; CHLR2; AF6; BR2;
XX inhibitor dominant negative 4; breast basic conserved protein 1; BBC1;
XX BR3; ID4; cancer; proliferative disorder; tumour proliferation; ss.
XX
XX Homo sapiens.
XX
XX WO200170982-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09559.
XX
XX 23-MAR-2000; 2000US-00536058.
XX
XX (IMMU-) IMMUSOL INC.
XX
XX (BEGE/) BEGER C.
XX
XX Beger C, Barber J, Wong-Staal F;

```

XX WPI; 2001-611503/70.  
 XX Novel polypeptides that are the regulators of BRCA-1, useful for treating  
 PT cancer and diagnosing the presence of neoplastic cells in biological  
 PT sample.  
 XX  
 XX Disclosure; Fig 8; 97pp; English.  
 XX  
 XX Sequences AAS56729-AAS5698 represent DNA encoding BRCA-1 regulators,  
 CC ribozyme target recognition RNA sequences, DNA fragments encoding the RNA  
 CC and primers used in the methods of the invention. Hybridisation of  
 CC ribozymes to their targets results in cleavage of the RNA target. The  
 CC ribozymes can be used to cleave regulators of the tumour suppressor BRCA-  
 CC 1, resulting in upregulation or downregulation of BRCA-1 in a cell. The  
 CC mRNA targets include those encoding the BRCA-1 regulator BR1, inhibitor  
 CC dominant negative 4 (ID4), breast basic conserved protein 1 (BBC1),  
 CC CHIR2, AFE, BR2 and BR3. Regulation of BRCA-1 is useful for treating and  
 CC diagnosing cancer and other proliferative disorders. The severity of an  
 CC incidence of cancer can be lessened by regulating tumour proliferation  
 CC through modulation of BRCA-1 expression. The sequences of the invention  
 CC are useful in the development of anti-cancer drugs  
 XX  
 XX Sequence 16 BP; 3 A; 5 C; 3 G; 5 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 16;  
 Best Local Similarity 81.2%; Pred. No. 4.8e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1679 CTGGTGTCTCCTCCAG 1694  
 Db 1 CTGCTGTCTACTACAG 16  
 RESULT 614  
 AA168609/c  
 ID AA168609 standard; DNA; 16 BP.  
 XX  
 XX AC AA168609;  
 XX  
 XX 14-JAN-2002 (first entry)  
 DT  
 XX ICAM-1 triple helix associated oligonucleotide SEQ ID 11.  
 DE  
 XX ICAM-1; triple helix; transcription inhibition; antipsoriatic;  
 KW intracellular adhesion molecule; dermatological; antiasthmatic;  
 KW antiinflammatory; immunosuppressive; gastrointestinal; psoriasis;  
 KW neurodermatitis; allergic asthma; Crohn's disease; autoimmune disease;  
 KW transplant rejection; psoralen; photo-ultra-violet therapy; ds.  
 XX  
 XX Unidentified.  
 OS  
 XX WO200179487-A2.  
 PN  
 XX 25-OCT-2001.  
 PD  
 XX 18-APR-2001; 2001WO-DE0001509.  
 PF  
 XX 18-APR-2000; 2000DE-01019252.  
 PR  
 XX (DEGI/) DEGITZ K K.  
 PA (BESC/) BESCH R.  
 PA  
 XX Degitz KK, Besch R;  
 PI  
 XX WPI; 2002-017614/02.  
 DR  
 XX Triple-helix forming polydeoxyribonucleotides, useful for treating  
 PT intracellular adhesion molecule-1 related diseases, e.g. psoriasis, are  
 PT directed against transcribed or promoter regions of the ICAM-1 gene.  
 XX  
 XX Claim 5; Page 4; 61pp; German.  
 PS  
 XX

CC This invention describes novel polydeoxyribonucleotides (A), for use as  
 CC triple-helix forming oligonucleotides, having at least 3 sequential  
 CC purine and/or pyrimidine bases, capable of inhibiting transcription of  
 CC ICAM-1. (A) has a sequence specific for the transcribed or promoter  
 CC regions of the ICAM-1 (intracellular adhesion molecule) gene. The  
 CC products of the invention have antipsoriatic, dermatological,  
 CC antiasthmatic, antiinflammatory, immunosuppressive and gastrointestinal  
 CC activity. (A) are used for treatment or prevention of ICAM-1-associated  
 CC diseases, specifically psoriasis, neurodermatitis, allergic asthma,  
 CC Crohn's disease, autoimmune diseases and transplant rejection. Compared  
 CC with antisense oligonucleotides, (A) provide a longer-lasting effect  
 CC (they bind directly to the gene, so a compensatory increase in  
 CC transcription is not possible). (A) may be coupled to psoralen to provide  
 CC light-regulatable, sequence-specific downregulation of genes; this should  
 CC make photo-ultra-violet therapy more specific, with reduced side effects.  
 CC AA168599-AA168673 represent oligonucleotides used to illustrate the  
 CC method of the invention  
 XX  
 SQ Sequence 16 BP; 4 A; 0 C; 11 G; 1 T; 0 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 16;  
 Best Local Similarity 81.2%; Pred. No. 4.8e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1736 CTCCCACTCTCCTCT 1751  
 Db 16 CCCCCACCTTCTCCT 1  
 RESULT 615  
 ABZ34019/c  
 ID ABZ34019 standard; DNA; 16 BP.  
 XX  
 XX AC ABZ34019;  
 XX  
 XX 31-JAN-2003 (first entry)  
 DT  
 XX HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:261.  
 DE  
 XX Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;  
 KW detection; mutation; anti-HIV drug resistance; polymorphism; resistance;  
 KW probe; ss.  
 XX  
 XX Human immunodeficiency virus 1.  
 OS  
 XX Synthetic.  
 XX  
 XX WO200255741-A2.  
 PN  
 XX 18-JUN-2002.  
 PD  
 XX 09-JAN-2002; 2002WO-EP000153.  
 PF  
 XX 11-JAN-2001; 2001EP-00870005.  
 PR  
 XX 20-APR-2001; 2001EP-00870085.  
 PR  
 XX 24-APR-2001; 2001US-0286102P.  
 XX  
 XX (INNO-) INNOGENETICS NV.  
 PA  
 XX De Smet K, Stuyver L;  
 PI  
 XX WPI; 2002-590680/63.  
 DR  
 XX  
 XX Detecting mutations associated with anti-HIV drug resistance comprises  
 PT detecting at least one of the mutations in the HIV reverse transcriptase  
 PT gene by using probes optimized to function together in a reverse-  
 PT hybridization assay.  
 XX  
 XX Claim 2; Page 19; 117pp; English.  
 PS  
 XX The present invention describes a method for detecting mutations  
 CC associated with anti-HIV drug resistance in a patient by detecting at  
 CC least one of the mutations K103N/R, V106N/I/L, Y181C/I, M184V/I, Y188L,  
 CC G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)  
 CC

of HIV strains in a biological sample using a specific set of probes optimised to function together in a reverse-hybridisation assay. The method and the nucleic acid sequences used in the method are useful for determining viral mutations and/or polymorphisms in the HIV RT gene associated with resistance. The probes are useful for the genetic detection, preferably in vitro detection of the mutations K103N/R, V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the mutation is associated with anti-HIV drug resistance. The method provides a rapid, reliable and precise assay or determination and monitoring of antiviral drug resistance or mutations associated with drug resistance of viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT sequences and probes which are used in the exemplification of the present invention

XX Sequence 16 BP; 5 A; 4 C; 4 G; 3 T; 0 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 16;  
 Best Local Similarity 81.2%; Pred. No. 4.8e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1690 TCCAGCGTGGTGAAG 1705  
 |||||  
 Db 16 TCCATCCTTGTGAAG 1

RESULT 616  
 ADE14208/c  
 ID ADE14208 standard; DNA; 16 BP.  
 AC ADE14208;  
 XX  
 XX 29-JAN-2004 (first entry)  
 DT  
 DE Optineurin promoter motif, repeat element or regulatory region #317.  
 XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;  
 KW SNP; glaucoma; progressive ocular hypertensive disorder;  
 KW glaucoma related disorder; motif; repeat element; regulatory region.  
 XX  
 XX Homo sapiens.  
 XX US2003190617-A1.  
 PN  
 XX 09-OCT-2003.  
 PD  
 XX 06-MAR-2002; 2002US-00091281.  
 PF  
 XX 06-MAR-2002; 2002US-00091281.  
 PR  
 XX (SIEB/) SI E.  
 PA (RAYM/) RAYMOND V.  
 PA (MORI/) MORISSETTE J.  
 XX  
 XX Raymond V, Morissette J, Si E;  
 PI WPI; 2003-864168/80.  
 XX  
 XX New nucleic acid sequences of the optineurin gene are useful to detect  
 PT polymorphisms particularly single nucleotide polymorphisms in the  
 PT optineurin promoter to diagnose, prognose and treat glaucoma and related  
 PT disorders.  
 XX  
 PS Claim 11; SEQ ID NO 319; 159pp; English.  
 XX  
 XX The invention relates to an isolated nucleic acid (N1) comprising at  
 CC least 20 but not more than 1500 consecutive nucleotides of the optineurin  
 CC promoter appearing as ADE13890. Also included are the optineurin promoter  
 CC operably linked to a heterologous nucleic acid, a nucleic acid capable of  
 CC detecting a single nucleotide polymorphism (SNP) in the optineurin  
 CC promoter, a host cell comprising the promoter operably linked to a  
 CC heterologous sequence, diagnosing or prognosing glaucoma in a sample  
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism

CC in a promoter region of the optineurin gene, associated with a glaucoma  
 CC phenotype), detecting a SNP sequence variation in a sample containing  
 CC DNA, detecting the presence of an optineurin promoter sequence variation  
 CC in a sample containing DNA, determining the presence or increased  
 CC susceptibility to glaucoma or to a progressive ocular hypertensive  
 CC disorder resulting in loss of visual field in a patient for the severity  
 CC or progression of glaucoma in a patient, comprising providing  
 CC amplification reaction primers that direct amplification of a selected  
 CC nucleic acid region containing the variation within the optineurin  
 CC promoter and amplifying the DNA) and detecting a polymorphism (comprising  
 CC obtaining a sample containing human genomic DNA, providing a nucleic acid  
 CC capable of detecting a SNP located within an optineurin promoter, and  
 CC detecting the polymorphism). The invention is used to diagnose and  
 CC prognose glaucoma and also to treat glaucoma related disorders. The  
 CC present sequence is an optineurin promoter motif, repeat element or  
 CC putative regulatory region.  
 XX  
 XX Sequence 16 BP; 4 A; 2 C; 6 G; 4 T; 0 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 16;  
 Best Local Similarity 81.2%; Pred. No. 4.8e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1663 GCTCACGCTGAACC 1678  
 |||||  
 Db 16 GCTCACGCTGAATC 1

RESULT 617  
 ADA99593  
 ID ADA99593 standard; DNA; 17 BP.  
 AC ADA99593;  
 XX  
 XX 20-NOV-2003 (first entry)  
 DT  
 DE Human MDZ3 scanning oligonucleotide SEQ ID 582.  
 XX  
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 PN EP1281758-A2.  
 XX  
 XX 05-FEB-2003.  
 PD  
 XX 30-JUL-2002; 2002EP-00C16874.  
 PF  
 XX 02-AUG-2001; 2001US-00522181.  
 PR  
 XX (AEOM-) AEOMICA INC.  
 PA  
 XX Shannon M, Gu Y, Nguyen C;  
 PI WPI; 2003-423107/40.  
 XX  
 XX New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MDZ3,  
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
 XX  
 XX Example 8; SEQ ID NO 582; 103pp; English.  
 PS  
 XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences; MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder,  
 CC associated with decreased or increased expression or activity of MDZ3,  
 CC associated with decreased or increased expression or activity of MDZ4,

CC MD24, MD27, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MD24, MD27, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MD24, MD27, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1659 CCAGGCTCACAGCTGG 1674  
Db 1 CCAGGCATCCAGCTGG 16

## RESULT 618

ABZ65014/C

ID ABZ65014 standard; RNA; 17 BP.

XX AC ABZ65014;

XX AC 21-MAR-2003 (first entry)

XX DE Human HER2 DNzyme substrate #471.

XX DE

KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
KW anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX XX WO200297114-A2.

XX XX 05-DEC-2002.

XX XX 29-MAY-2002; 2002WO-US016840.

XX XX 29-MAY-2001; 2001US-0294140P.

XX PR 06-JUN-2001; 2001US-0296249P.

XX PR 10-SEP-2001; 2001US-0318471P.

XX XX (RIBO-) RIBOZYME PHARM INC.

XX XX Mcswiggen J;

XX XX WPI; 2003-140484/13.

XX PT Novel short interfering RNA and enzymatic nucleic acid useful for  
XX PT treating cancer, modulates the expression of a nucleic acid encoding  
XX PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX PS Claim 4; Page 142; 185pp; English.

XX XX

CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
CC rheumatic activity. The nucleic acid molecules are useful for reducing  
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ6531, ABZ6520 - ABZ6524,  
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
CC ribozymes of the invention

SQ Sequence 17 BP; 3 A; 9 C; 1 G; 0 T; 4 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1636 GGGCTTGATGACAGAG 1651  
Db 16 GGGCATGTAGAGAGG 1

## RESULT 619

ADA99592

ID ADA99592 standard; DNA; 17 BP.

XX AC ADA99592;

XX XX 20-NOV-2003 (first entry)

XX XX Human MDZ3 scanning oligonucleotide SEQ ID 581.

XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
XX KW zinc finger protein; MDZ3; MD24; MDZ7; MDZ12; chromosome 7q22.1;  
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
XX KW developmental disorder; ss.

XX OS Homo sapiens.

XX XX EP1281758-A2.

XX XX 05-FEB-2003.

XX XX 30-JUL-2002; 2002EP-00016874.

XX XX 02-AUG-2001; 2001US-00922181.

XX XX (AECOM-) AECOMICA INC.

XX XX Shannon M, Gu Y, Nguyen C;

XX XX WPI; 2003-423107/40.

XX XX New zinc finger-containing proteins and nucleic acids, useful in  
XX PT manufacturing a medicament for treating or preventing a disorder  
XX PT associated with decreased or increased expression or activity of MDZ3,  
XX PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX PS Example 8; SEQ ID NO 581; 103pp; English.

XX CC The present invention relates to novel human zinc finger-containing  
XX CC proteins and their coding sequences: MDZ3, MD24, MDZ7, MDZ12. MDZ3 is  
XX CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
XX CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
XX CC 15q26.1. The MDZ3, MD24, MDZ7, and MDZ12 sequences are useful in therapy,  
XX CC or in manufacturing a medicament for treating or preventing a disorder  
XX CC associated with decreased or increased expression or activity of MDZ3,  
XX CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
XX CC acids and proteins are also useful for diagnosing or monitoring a disease  
XX CC caused by altered expression of MDZ3, MD24, MDZ7, or MDZ12. The nucleic  
XX CC acids can also be used as probes to detect and characterize gross  
XX CC alterations in MDZ3, MD24, MDZ7, or MDZ12 genetic locus. The probes are  
XX CC useful in constructing microarrays for measuring gene expression. The  
XX CC proteins are useful as therapeutic agents for gene therapy or as  
XX CC vaccines. The present sequence was used to illustrate the invention.

SQ Sequence 17 BP; 3 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1659 CCAGGCTCACAGCTGG 1674  
Db 2 CCAGGCATCCAGCTGG 17



PS Disclosure; Page 19; 29pp; English.

XX The sequences given in AAQ29787-816 are probes which were used within the  
CC method of the invention for detecting the presence of a variant sequence  
CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be  
CC distinguished from one another by the polymorphic sequence corresponding  
CC to the HindIII site of the A allele. The sequences of the three alleles  
CC are given in AAQ29842-44. The methods for determining an individual's  
CC genotype at the GGG locus with respect to a set of alleles improves the  
CC discriminatory power of GGG typing methodology compared to previous  
CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 17 BP; 2 A; 1 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1672 TGGAAACCTGGTGCT 1687

Db 2 TGGAAATCTGGTGCT 17

RESULT 623

AAQ29789/c

ID AAQ29789 standard; DNA; 17 BP.

XX AC AAQ29789;

XX 25-MAR-2003 (revised)

DT 19-MAR-1993 (first entry)

DE A allele probe VP11.

XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;

XX paternity; forensic; ss.

XX Synthetic.

XX EP512342-A2.

XX 11-NOV-1992.

XX 25-APR-1992; 92EP-00107084.

XX 07-MAY-1991; 91US-00696793.

XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.

XX Saiki RK, Nasarabadi SL;

XX WPI; 1992-374679/46.

XX Determn. of an individuals genotype at the gamma-globin locus - using

XX sequence-specific oligo-nucleotide probes corresp. to 3 alleles.

XX Disclosure; Page 13; 29pp; English.

XX The sequences given in AAQ29787-816 are probes which were used within the

XX method of the invention for detecting the presence of a variant sequence

XX in the G-gamma globulin (GGG) locus. The A, B and C alleles can be

XX distinguished from one another by the polymorphic sequence corresponding

XX to the HindIII site of the A allele. The sequences of the three alleles

XX are given in AAQ29842-44. The methods for determining an individual's

XX genotype at the GGG locus with respect to a set of alleles improves the

XX discriminatory power of GGG typing methodology compared to previous

XX methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 17 BP; 6 A; 7 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1672 TGGAAACCTGGTGCT 1687

Db 17 TGGAAAGCTGGTGCT 2

RESULT 624

AAQ29812/c

ID AAQ29812 standard; DNA; 17 BP.

XX AC AAQ29812;

XX 25-MAR-2003 (revised)

DT 19-MAR-1993 (first entry)

DE C allele probe VP24.

XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;

XX paternity; forensic; ss.

XX Synthetic.

XX EP512342-A2.

XX 11-NOV-1992.

XX 25-APR-1992; 92EP-00107084.

XX 07-MAY-1991; 91US-00696793.

XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.

XX Saiki RK, Nasarabadi SL;

XX WPI; 1992-374679/46.

XX Determn. of an individuals genotype at the gamma-globin locus - using

XX sequence-specific oligo-nucleotide probes corresp. to 3 alleles.

XX Disclosure; Page 19; 29pp; English.

XX The sequences given in AAQ29787-816 are probes which were used within the

XX method of the invention for detecting the presence of a variant sequence

XX in the G-gamma globulin (GGG) locus. The A, B and C alleles can be

XX distinguished from one another by the polymorphic sequence corresponding

XX to the HindIII site of the A allele. The sequences of the three alleles

XX are given in AAQ29842-44. The methods for determining an individual's

XX genotype at the GGG locus with respect to a set of alleles improves the

XX discriminatory power of GGG typing methodology compared to previous

XX methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 17 BP; 8 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1672 TGGAAACCTGGTGCT 1687

Db 17 TGGAAATCTGGTGCT 2

RESULT 625

AAQ29788/c

ID AAQ29788 standard; DNA; 17 BP.

XX AC AAQ29788;

XX 25-MAR-2003 (revised)

DT 19-MAR-1993 (first entry)

DE A allele probe VP10.

XX

KW G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;  
 XX paternity; forensic; ss.  
 OS Synthetic.  
 XX  
 PN EP512342-A2.  
 XX  
 PD 11-NOV-1992.  
 XX  
 XX 25-APR-1992; 92EP-00107084.  
 XX  
 XX 07-MAY-1991; 91US-00696793.  
 PR  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 XX  
 PI Saiiki RK, Nasarabadi SL;  
 XX  
 DR WPI; 1992-374679/46.  
 XX  
 PT Determn. of an individuals genotype at the gamma-globin locus - using  
 sequence-specific oligo-nucleotide probes corresp. to 3 alleles.  
 XX  
 PS Disclosure; Page 13; 29pp; English.  
 XX  
 CC The sequences given in AAQ29787-816 are probes which were used within the  
 method of the invention for detecting the presence of a variant sequence  
 in the G-gamma globulin (GGG) locus. The A, B and C alleles can be  
 distinguished from one another by the polymorphic sequence corresponding  
 to the HindIII site of the A allele. The sequences of the three alleles  
 are given in AAQ29842-44. The methods for determining an individuals  
 genotype at the GGG locus with respect to a set of alleles improves the  
 discriminatory power of GGG typing methodology compared to previous  
 methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 17 BP; 5 A; 9 C; 1 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 CC The sequences given in AAQ29787-816 are probes which were used within the  
 method of the invention for detecting the presence of a variant sequence  
 in the G-gamma globulin (GGG) locus. The A, B and C alleles can be  
 distinguished from one another by the polymorphic sequence corresponding  
 to the HindIII site of the A allele. The sequences of the three alleles  
 are given in AAQ29842-44. The methods for determining an individuals  
 genotype at the GGG locus with respect to a set of alleles improves the  
 discriminatory power of GGG typing methodology compared to previous  
 methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 17 BP; 5 A; 9 C; 1 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 QY 1670 GCTGGAACCCCTGGTGT 1685  
 DB 17 GGTGGAAGCTTGGTGT 2  
 XX  
 RESULT 626  
 AAQ29811/C  
 ID AAQ29811 standard; DNA; 17 BP.  
 XX  
 AC AAQ29811;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 19-MAR-1993 (first entry)  
 XX  
 DE C allele probe VP17.  
 XX  
 XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;  
 KW paternity; forensic; ss.  
 XX Synthetic.  
 OS  
 XX  
 PN EP512342-A2.  
 XX  
 PD 11-NOV-1992.  
 XX  
 XX 25-APR-1992; 92EP-00107084.  
 PF  
 XX  
 XX 07-MAY-1991; 91US-00696793.  
 PR  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 XX  
 PI Saiiki RK, Nasarabadi SL;  
 XX

DR WPI; 1992-374679/46.  
 XX  
 PT Determn. of an individuals genotype at the gamma-globin locus - using  
 sequence-specific oligo-nucleotide probes corresp. to 3 alleles.  
 XX  
 PS Disclosure; Page 19; 29pp; English.  
 XX  
 CC The sequences given in AAQ29787-816 are probes which were used within the  
 method of the invention for detecting the presence of a variant sequence  
 in the G-gamma globulin (GGG) locus. The A, B and C alleles can be  
 distinguished from one another by the polymorphic sequence corresponding  
 to the HindIII site of the A allele. The sequences of the three alleles  
 are given in AAQ29842-44. The methods for determining an individuals  
 genotype at the GGG locus with respect to a set of alleles improves the  
 discriminatory power of GGG typing methodology compared to previous  
 methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 17 BP; 7 A; 6 C; 1 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 QY 1672 TCGAACCCTGGTGTCT 1687  
 DB 17 TGGATCTTGGTGTCT 2  
 XX  
 RESULT 627  
 AAQ66711/C  
 ID AAQ66711 standard; DNA; 17 BP.  
 XX  
 AC AAQ66711;  
 XX  
 DT 22-DEC-1994 (first entry)  
 XX  
 DE Primer to amplify HHV6 derived sequences.  
 XX  
 KW HHV6; Human Herpes Virus 6; Primers; Probes; PCR; amplify;  
 KW polymerase chain reaction; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06133799-A.  
 XX  
 PD 17-MAY-1994.  
 XX  
 XX 27-OCT-1992; 92JP-00311416.  
 PF  
 XX 27-OCT-1992; 92JP-00311416.  
 PR  
 XX (KOKU-) KOKUSAI SHIYAKU KK.  
 PA  
 XX WPI; 1994-196175/24.  
 DR  
 XX HHV-6 derived nucleotide(s) - useful for identification of HHV-6 DNA.  
 PT  
 XX Claim 4; Page 2; 13pp; Japanese.  
 PS  
 XX The inventors provide human Herpes virus 6 derived nucleotide sequences  
 useful for identification of HHV-6 DNA. AAQ66705-12 are primer set 1 (I),  
 CC are used in the invention  
 CC  
 XX Sequence 17 BP; 3 A; 4 C; 3 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 QY 1665 TCACAGCTGGACCT 1680  
 DB 16 TCACAGATGAAGACT 1



RESULT 628  
AAT53734/c  
ID AAT53734 standard; RNA; 17 BP.  
XX AC  
XX AAT53734;  
XX  
XX 25-MAR-2003 (revised)  
DT 03-APR-1997 (first entry)  
DT  
DE  
DE Rat ICAM hammerhead ribozyme target sequence (nt. position 2847).  
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
KW translocation; chronic myelogenous leukaemia; CML; cancer;  
KW Philadelphia chromosome; inflammation; autoimmune disease;  
KW atherosclerosis; myocardial infarction; stroke; restenosis;  
KW transplant rejection; rheumatoid arthritis; psoriasis;  
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
KW ss.  
XX  
XX Rattus rattus.  
XX  
XX W09523225-A2.  
XX  
XX 31-AUG-1995.  
XX  
XX 23-FEB-1995; 95WO-IB000156.  
XX  
XX 23-FEB-1994; 94US-00201109.  
XX 29-MAR-1994; 94US-00218934.  
XX 04-APR-1994; 94US-00222795.  
XX 07-APR-1994; 94US-00224483.  
XX 15-APR-1994; 94US-00227958.  
XX 15-APR-1994; 94US-00228041.  
XX 18-MAY-1994; 94US-00245736.  
XX 06-JUL-1994; 94US-00271280.  
XX 15-AUG-1994; 94US-00291433.  
XX 16-AUG-1994; 94US-00292620.  
XX 17-AUG-1994; 94US-00291433.  
XX 19-AUG-1994; 94US-00292620.  
XX 19-AUG-1994; 94US-00292620.  
XX 02-SEP-1994; 94US-00293520.  
XX 02-SEP-1994; 94US-00300000.  
XX 08-SEP-1994; 94US-00303039.  
XX 23-SEP-1994; 94US-00311486.  
XX 28-SEP-1994; 94US-00311749.  
XX 30-JAN-1995; 95US-00380734.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Stinchcomb DT, Chowira B, Dizenzo A, Draper KG, Dudycz LW;  
PI Grimm S, Karpeisky A, Kislich K, Matulic-Adamic J, Mcswiggen JA;  
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
PI Tracz D, Usman N, Wincott FE, Woolf T;  
XX  
XX WPI; 1995-351090/45.  
XX  
XX Ribozymes having modified bases and methods for producing them - for use  
PT in inhibiting disease related genes.  
XX  
XX Claim 2; Page 204; 407pp; English.

CC The present sequence represents a preferred target sequence for an  
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the  
CC nucleotide base position indicated in the DE line. Regions of the mRNA  
CC that do not form secondary folding structures and that contain potential  
CC hammerhead and hairpin ribozyme cleavage sites were identified by  
CC computer analysis. Ribozymes directed against these mRNA sequences were  
CC designed and synthesised with modifications that improve their nuclease  
CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby  
CC inhibit ICAM-1 expression, making them useful for reducing transplant  
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,  
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to  
CC correct PI field.)  
XX  
XX Sequence 17 BP; 3 A; 10 C; 0 G; 0 T; 4 U; 0 Other;  
SQ  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1704 AGTTGGGTAGGACTA 1719  
DB 17 AGGTGGGTAGGGGTA 2  
RESULT 629  
AAT53501/c  
ID AAT53501 standard; RNA; 17 BP.  
XX AC  
XX AAT53501;  
XX  
XX 25-MAR-2003 (revised)  
DT 27-MAR-1997 (first entry)  
DT  
XX  
XX Rat ICAM hammerhead ribozyme target sequence (nt. position 374).  
XX  
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
KW translocation; chronic myelogenous leukaemia; CML; cancer;  
KW Philadelphia chromosome; inflammation; autoimmune disease;  
KW atherosclerosis; myocardial infarction; stroke; restenosis;  
KW transplant rejection; rheumatoid arthritis; psoriasis;  
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
KW ss.  
XX  
XX Rattus rattus.  
XX  
XX W09523225-A2.  
XX  
XX 31-AUG-1995.  
XX  
XX 23-FEB-1995; 95WO-IB000156.  
XX  
XX 23-FEB-1994; 94US-00201109.  
XX 29-MAR-1994; 94US-00218934.  
XX 04-APR-1994; 94US-00222795.  
XX 07-APR-1994; 94US-00224483.  
XX 15-APR-1994; 94US-00227958.  
XX 15-APR-1994; 94US-00228041.  
XX 18-MAY-1994; 94US-00245736.  
XX 06-JUL-1994; 94US-00271280.  
XX 15-AUG-1994; 94US-00291433.  
XX 16-AUG-1994; 94US-00292620.  
XX 17-AUG-1994; 94US-00291433.  
XX 19-AUG-1994; 94US-00293520.  
XX 02-SEP-1994; 94US-00300000.  
XX 08-SEP-1994; 94US-00303039.  
XX 23-SEP-1994; 94US-00311486.  
XX 28-SEP-1994; 94US-00311749.  
XX 30-OCT-1994; 94US-00316771.



```

XX Fildes NJ, Reynolds RL;
XX WPI; 1997-350231/32.
XX Detection of glycophorin A allele(s) - by hybridisation assay using
XX sequence-specific oligo:nucleotide probes.
XX Example 3; Col 15-16; 16pp; English.
XX Glycophorin A is a major sialoglycoprotein of the human erythrocyte
XX membrane. Glycophorin A carries the M or N blood group antigen, which is
XX determined by the amino acid at residues 1 and 5. Allele A encodes the
XX protein carrying the M blood group antigen and allele B encodes the
XX protein carrying the N blood group antigen. Three additional alleles have
XX been discovered, designated A', A'', and B'. Detecting an A', A'', or B'
XX allele of the Glycophorin A locus in a human nucleic acid sample
XX comprises mixing the sample under stringent hybridisation conditions with
XX a sequence-specific oligonucleotide probe that distinguishes the A', A'',
XX or B' allele from A and B alleles, and detecting any hybridisation. The
XX method and probes are used for determining an individual's Glycophorin A
XX genotype, especially useful for determining individual identity for
XX forensic purposes. AAT70558-67 (and also AAT70582-83) are primers from
XX the AmpliType (R) PM kit used in a Glycophorin A typing system developed
XX by Hoffmann-La Roche. The primers direct the simultaneous amplification
XX of specific regions of the following six genetic loci: Glycophorin A, HLA
XX DQA1, Low density lipoprotein receptor, Haemoglobin G gamma-globin, D7S8
XX and group specific component. Probe strips are also provided in the kit
XX (AAT70568-81)
XX Sequence 17 BP; 2 A; 1 C; 8 G; 6 T; 0 U; 0 Other;

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1670 GCTGGAACCCCTGGTGT 1685
Db 1 GGTGGAATCTGGTGT 16

RESULT 632
AAX68727/c
ID AAX68727 standard; RNA; 17 BP.
XX AAX68727;
XX 28-JUL-1999 (first entry)
XX Human flt1 VEGF receptor hammerhead ribozyme substrate #22.
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX Homo sapiens.
XX WO9715662-A2.
XX 01-MAY-1997.
XX 25-OCT-1996; 96WO-US017480.
XX 26-OCT-1995; 95US-0005974P.
XX 11-JAN-1996; 96US-00584040.
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR ) CHIRON CORP.
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX Claim 4; Page 134; 218pp; English.
XX The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
XX treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention.
XX Sequence 17 BP; 1 A; 5 C; 7 G; 0 T; 4 U; 0 Other;

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAAACCCCTG 1681
Db 17 CACAGCAGGACCCCGG 2

RESULT 633
AAX72948/c
ID AAX72948 standard; RNA; 17 BP.
XX AAX72948;
XX 28-JUL-1999 (first entry)
XX Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #381.
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX Mus sp.
XX WO9715662-A2.
XX 01-MAY-1997.
XX 25-OCT-1996; 96WO-US017480.
XX 26-OCT-1995; 95US-0005974P.
XX 11-JAN-1996; 96US-00584040.
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR ) CHIRON CORP.
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX Claim 4; Page 134; 218pp; English.
XX The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient

```

CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention

XX SQ Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1642 GTAGCAGAGGCAAGC 1657  
 Db 16 GCATCATAGGCAAGC 1

RESULT 634  
 AAX73306/C  
 ID AAX73306 standard; RNA; 17 BP.

XX AC AAX73306;

DT 28-JUL-1999 (first entry)

DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #739.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.

XX Mus sp.

XX WO9715662-A2.

XX 01-MAY-1997.

XX 25-OCT-1996; 96WO-US017480.

XX 26-OCT-1995; 95US-0005974P.

XX 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.  
 XX (CHIR ) CHIRON CORP.

XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 146; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention

XX SQ Sequence 17 BP; 1 A; 3 C; 7 G; 0 T; 6 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAACCCCTG 1681

Db 16 CCCAGCAGAAACCCCTG 1

RESULT 635

AAX73324

ID AAX73324 standard; RNA; 17 BP.

XX AC AAX73324;

DT 28-JUL-1999 (first entry)

DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #757.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.

XX Mus sp.

XX WO9715662-A2.

XX 01-MAY-1997.

XX 25-OCT-1996; 96WO-US017480.

XX 26-OCT-1995; 95US-0005974P.

XX 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.  
 XX (CHIR ) CHIRON CORP.

XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 147; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention

XX SQ Sequence 17 BP; 4 A; 7 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 56.2%; Pred. No. 5.2e+02;

Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1738 CCCAACTCTCCCTAT 1753

Db 2 CCCAAGUCCUAGU 17

RESULT 636

AAX69487/C

ID AAX69487 standard; RNA; 17 BP.

XX AAX69487;  
 AC  
 XX 28-JUL-1999 (first entry)  
 DT  
 XX  
 XX Human flt1 VEGF receptor hammerhead ribozyme substrate #782.  
 DE  
 XX  
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO9715662-A2.  
 FN  
 XX 01-MAY-1997.  
 PD  
 XX 25-OCT-1996; 96WO-US017480.  
 XX  
 XX 26-OCT-1995; 95US-0005974P.  
 PF  
 XX 11-JAN-1996; 96US-00584040.  
 ER  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX (CHIR ) CHIRON CORP.  
 PA  
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 PI WPI; 1997-259017/23.  
 XX  
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 ET  
 XX Claim 4; Page 70; 218pp; English.  
 PS  
 XX The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 XX Sequence 17 BP; 2 A; 8 C; 2 G; 0 T; 5 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1661 AGGCTCAGCTGGAA 1676  
 DB |||||  
 16 AGGCTCAGCTGGGA 1  
 RESULT 637  
 AAX73305/c  
 ID AAX73305 standard; RNA; 17 BP.  
 XX  
 XX AC AAX73305;  
 AC  
 XX 28-JUL-1999 (first entry)  
 DT  
 XX Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #738.  
 DE  
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.

XX foetal liver kinase 1; ss.  
 XX  
 XX Mus sp.  
 OS  
 XX WO9715662-A2.  
 PN  
 XX 01-MAY-1997.  
 PD  
 XX 25-OCT-1996; 96WO-US017480.  
 XX  
 XX 26-OCT-1995; 95US-0005974P.  
 PR  
 XX 11-JAN-1996; 96US-00584040.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR ) CHIRON CORP.  
 XX  
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 PI WPI; 1997-259017/23.  
 XX  
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 ET  
 XX Claim 4; Page 146; 218pp; English.  
 PS  
 XX The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 XX Sequence 17 BP; 1 A; 3 C; 7 G; 0 T; 6 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1666 CACAGCTGGAAACCCCTG 1681  
 DB |||||  
 17 CCCAGCAGAAACCCCTG 2  
 RESULT 638  
 AAT95345  
 ID AAT95345 standard; DNA; 17 BP.  
 XX  
 XX AC AAT95345;  
 AC  
 XX 20-APR-1998 (first entry)  
 DT  
 XX Treatment of human melanoma using c-myc oligonucleotide 12.  
 DE  
 XX  
 XX Melanoma; c-myc oligonucleotide; c-myc mRNA; cis-platin; inhibition;  
 KW metastasis; treatment; proliferation; human; tumour; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX Homo sapiens.  
 OS  
 XX WO9736005-A1.  
 FN  
 XX 02-OCT-1997.  
 PD  
 XX 24-MAR-1997; 97WO-US004703.  
 XX  
 XX 26-MAR-1996; 96US-0014089P.  
 PR  
 XX (LYNX-) LYNX THERAPEUTICS INC.  
 XX PA

XX Zupi G;  
 XX WPI; 1997-489662/45.  
 XX Inhibiting proliferation of human melanoma cells with anti-c-myc  
 PT oligo:nucleotide(s) - particularly used together with cis-platin.  
 PT inhibits metastasis, induces regression or prevents further growth.  
 XX  
 PS Claim 1; Page 22; 68pp; English.  
 XX This c-myc oligonucleotide is complementary to a sequence of human c-myc  
 CC mRNA and is used for inhibiting the proliferation of human melanoma cells  
 CC (HMC). The c-myc oligonucleotide is at least 10 bases long and inhibits  
 CC proliferation of HMC by at least 10 percent at 10 mM M, when the cells  
 CC are cultured at 37 degree. C in presence of serum. The method is  
 CC particularly used to treat human melanoma, and inhibits metastasis,  
 CC promotes regression or prevents any increase in tumour mass. The c-myc  
 CC oligonucleotide can be used together with cis-platin and which then  
 CC reduces resistance of tumour cells to cis-platin. The oncogene c-myc is  
 CC found to be essential for growth and metastasis of melanoma, and the c-  
 CC myc oligonucleotides are designed to target double-stranded DNA or single  
 CC -stranded RNA. A combination of c-myc oligonucleotide and cis-platin is  
 CC more effective than either component used alone  
 XX  
 SQ Sequence 17 BP; 3 A; 6 C; 1 G; 7 T; 0 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1731 ATTGGCTCCCACTCC 1746  
 DB 2 ATGTGTTTCCCACTCC 17  
 RESULT 639  
 AAU14126/C  
 ID AAV14126 standard; DNA; 17 BP.  
 XX  
 AC AAV14126;  
 XX  
 XX 27-AUG-2003 (revised)  
 DT 19-MAY-1998 (first entry)  
 XX  
 DE Probe HBP42 for preCore region of HBV.  
 XX  
 KW Probe; hepatitis b virus; HBV detection; RT pol region; genetic analysis;  
 KW preCore region; HBsAg region; genotype specific target;  
 KW mutation detection; ss.  
 XX  
 OS Synthetic.  
 OS Hepatitis B virus.  
 XX  
 PN WO9740193-A2.  
 XX  
 PD 30-OCT-1997.  
 XX  
 PF 21-APR-1997; 97WO-EP002002.  
 XX  
 PR 19-APR-1996; 96EP-00870053.  
 XX  
 XX (INNO-) INNOGENETICS NV.  
 PA  
 XX Stuyver L, Rossau R, Maertens G;  
 PI  
 XX WPI; 1997-535867/49.  
 DR  
 XX Detection and/or genetic analysis of hepatitis B virus - specifically  
 PT genotype, preCore mutations, vaccine escape mutations and RT gene  
 PT mutations selected by treatment with drugs.  
 XX  
 XX Claim 5; Page 27; 80pp; English.

XX This sequence represents a probe for the preCore region of hepatitis b  
 CC virus (HBV). This sequence can be used in the method of the invention for  
 CC detection and/or genetic analysis of hepatitis B virus (HBV) in a sample.  
 CC The method comprises: (a) optionally releasing, isolating or  
 CC concentrating polynucleic acids (I) in the sample, and amplifying the  
 CC relevant part of a suitable HBV gene in the sample with at least 1  
 CC suitable primer pair; (b) hybridising (I) with a combination of at least  
 CC 2 nucleotide probes, which are applied to known locations on a solid  
 CC support and hybridise specifically to mutant target sequences chosen from  
 CC the HBV RT pol gene region, HBV preCore region, HBsAg region and/or HBV  
 CC genotype specific target sequences, or their complements or U for T  
 CC homologues; (c) detecting the hybrids formed in step (b), and inferring  
 CC the HBV genotype and/or mutants present in the sample from the  
 CC differential hybridisation signal(s). The composition can be used to  
 CC diagnose and/or monitor HBV mutants and/or genotypes in a sample,  
 CC specifically genotype, preCore mutations, vaccine escape mutations and RT  
 CC gene mutations selected by treatment with drugs, e.g. lamivudine and  
 CC penciclovir. (Updated on 27-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 17 BP; 4 A; 2 C; 6 G; 5 T; 0 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1747 TCCCTATCCTAAAGCC 1762  
 DB 17 TCCATGTCCTAAAGCC 2  
 RESULT 640  
 AAX62812/C  
 ID AAX62812 standard; RNA; 17 BP.  
 XX  
 AC AAX62812;  
 XX  
 DT 16-JUL-1999 (first entry)  
 XX  
 DE Delta-9 desaturase hamerhead ribozyme target SEQ ID NO:687.  
 XX  
 KW Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;  
 KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;  
 KW modulation; gene expression; transgenic plant; cleavage; canola plant;  
 KW caffeine synthesis; coffee plant; nicotine production; tobacco;  
 KW fruit ripening; flower pigmentation; lignin production; ss.  
 XX  
 XX Zea mays.  
 OS  
 XX WO9710328-A2.  
 PN  
 XX 20-MAR-1997.  
 PD  
 XX 12-JUL-1996; 96WO-US(11689.  
 PF  
 XX 13-JUL-1995; 95US-00(1135P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (DOWC) DOWELANCO.  
 XX  
 XX Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA;  
 PI Young SA, Folkerts O, Merlo DJ;  
 XX WPI; 1997-202224/18.  
 DR  
 XX Ribozyme which modulates plant gene expression - preferably modulates  
 PT expression of DELTA-9 desaturase or granule bound starch synthase in  
 PT maize or canola.  
 XX  
 XX Claim 38; Page 85; 155pp; English.  
 PS  
 XX The present invention describes an enzymatic nucleic acid molecule (I)  
 CC with RNA cleaving activity, which modulates the expression of a plant

CC gene. Also described is a gene comprising a cDNA sequence encoding maize  
 CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,  
 CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)  
 CC gene, in a plant (preferably a maize or canola plant). (I) can be used to  
 CC modulate caffeine synthesis in a coffee plant, nicotine production in a  
 CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum  
 CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or  
 CC marigold plant or lignin production in a tobacco, aspen, poplar or pine  
 CC plant

XX  
 SQ Sequence 17 BP; 5 A; 3 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1733 TGGTCCCAACTCTTC 1748  
 Db 17 TGGTGTCCCAACACTTC 2

RESULT 641  
 AAV44920/c  
 ID AAV44920 standard; DNA; 17 BP.

XX  
 AC AAV44920;

DT 28-OCT-1998 (first entry)

XX Promoter molecule.

XX Promoter molecule; activator sequence; E2F protein; CDF-1 protein;  
 KW tumour; leukaemia; cardiovascular disease; autoimmune disease; allergy;  
 KW arthritis; psoriatic disease; CNS damage; infectious disease;  
 KW blood clotting disorder; therapy; ss.

XX Synthetic.

XX EP860445-A1.

PD 26-AUG-1998.

PF 18-FEB-1997; 97EP-00102547.

PR 18-FEB-1997; 97EP-00102547.

XX (FARH) HOECHST AG.

XX Mueller R, Liu N, Zwicker J, Sedlacek H;

XX WPI; 1998-439301/38.

XX DNA construct comprising activator, chimeric promoter and structural gene  
 PT - where promoter has E2F and CDF-1 protein binding sequences.

XX Disclosure; Page 16; 34pp; English.

XX This sequence represents a promoter molecule that can be used in the  
 CC nucleic acid construct of the invention. The nucleic acid construct  
 CC comprises: (a) at least one activator sequence; (b) at least one promoter  
 CC module comprising a nucleotide sequence which binds a protein of the E2F  
 CC family and a protein of the CDF-1 family; and (c) at least one structural  
 CC gene. The construct, or a vector containing it can be used for local  
 CC application or injection for treating or preventing disease, i.e.  
 CC tumours, leukaemia, cardiovascular disease, autoimmune disease, allergy,  
 CC arthritis, psoriatic disease, impending rejection of a transplanted  
 CC organ, CNS damage, infectious disease or a blood clotting disorder

XX Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GGCTCCCAACTCTTCC 1749  
 Db 17 GCCTCCCAACACCTGC 2

RESULT 642

AAV97520  
 ID AAV97520 standard; RNA; 17 BP.

XX  
 AC AAV97520;

XX 17-MAR-1999 (first entry)

XX Human EGF-R target sequence nucleotide position 2618.

XX Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;  
 KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;  
 KW cancer; genetic drift; detection; mutation; ss.

XX Homo sapiens.

XX WO9833893-A2.

XX 06-AUG-1998.

XX 14-JAN-1998; 98WO-US000730.

XX 31-JAN-1997; 97US-0036476P.

XX 04-DEC-1997; 97US-00985162.

XX (RIBO-) RIBOZYME PHARM INC.

XX (UYAS-) UNIV ASTON.

XX Akhtar S, Fell P, Mcswiggen JA;

XX WPI; 1998-437449/37.

XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal  
 PT growth factor receptor, useful for inhibiting cell proliferation and for  
 PT treating cancers.

XX Claim 5; Page 74; 109pp; English.

XX The present invention describes enzymatic nucleic acid molecules (NAMS)  
 CC which specifically cleave RNA derived from an epidermal growth factor  
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090  
 CC represent specifically claimed target sequence from human EGF-R. AAV98044  
 CC to AAV98866 and AAV98867 to 9878 represent hammerhead ribozymes and  
 CC hairpin ribozymes respectively for human EGF-R. The NAMS are useful for  
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR  
 CC expression levels e.g. to inhibit cell proliferation in the prevention or  
 CC treatment of cancers. The NAMS can also be used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of EGF-R RNA in a cell

XX Sequence 17 BP; 3 A; 6 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 5.2e+02;  
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1731 ATTGGCTCCCAACTTCC 1746

Db 2 AATGGCUCCAGUACC 17

RESULT 643

AAV97591/c  
 ID AAV97591 standard; RNA; 17 BP.

XX  
 AC AAV97591;

DT 17-MAR-1999 (first entry)  
 XX Human EGF-R target sequence nucleotide position 3177.  
 DE  
 XX  
 KW Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;  
 KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;  
 KW cancer; genetic drift; detection; mutation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9833893-A2.  
 XX  
 XX 06-AUG-1998.  
 PD  
 XX  
 PF 14-JAN-1998; 98WO-US000730.  
 XX  
 XX 31-JAN-1997; 97US-0036476P.  
 PR 04-DEC-1997; 97US-00985162.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (UYAS-) UNIV ASTON.  
 XX  
 XX Akhtar S, Fell P, Mcswiggen JA;  
 XX WPI; 1998-437449/37.  
 DR  
 XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal  
 PT growth factor receptor, useful for inhibiting cell proliferation and for  
 PT treating cancers.  
 XX  
 PS Claim 5; Page 75; 109pp; English.  
 XX  
 CC The present invention describes enzymatic nucleic acid molecules (NAMs)  
 CC which specifically cleave RNA derived from an epidermal growth factor  
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090  
 CC represent specifically claimed target sequence from human EGF-R. AAV98044  
 CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and  
 CC hairpin ribozymes respectively for human EGF-R. The NAMs are useful for  
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR  
 CC expression levels e.g. to inhibit cell proliferation in the prevention or  
 CC treatment of cancers. The NAMs can also be used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of EGF-R RNA in a cell  
 XX  
 XX Sequence 17 BP; 3 A; 7 C; 2 G; 0 T; 5 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1694 GCGTGGTGAAGTTGG 1709  
 DB || ||| |||||  
 17 GCACGGTAGAAGTTGG 2  
 RESULT 644  
 AAV49878/c  
 ID AAV49878 standard; DNA; 17 BP.  
 XX  
 AC AAV49878;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 02-NOV-1998 (first entry)  
 XX  
 DE Myo-D E-box muscle-specific helix-loop-helix binding site.  
 XX cdc25B promoter; murine; medicament; treatment; tumour; disease; CNS;  
 KW leukaemia; autoimmune disease; allergy; arthritis; inflammation;  
 KW organ rejection; graft-versus-host reaction; blood clot; infection;  
 KW circulation; anaemia; hormonal disorders; central nervous system; ss.  
 XX  
 OS unidentified.  
 XX

PN EP864651-A2.  
 XX  
 PD 16-SEP-1998.  
 XX  
 PF 13-MAR-1998; 98EP-00104597.  
 XX  
 PR 14-MAR-1997; 97DE-01010643.  
 XX  
 PA (FARH ) HOECHST AG.  
 XX  
 XX Koerner K, Mueller R, Sedlacek H;  
 PI WPI; 1998-469235/41.  
 DR  
 XX New cdc25B gene promoter used to produce medicaments to treat - e.g.  
 PT tumours, leukaemia, autoimmune diseases, allergies, arthritis,  
 PT inflammation, organ rejection, blood clotting and circulatory disorders,  
 PT anaemia and hormonal disorders.  
 XX  
 PS Disclosure; Page 9; 30pp; German.  
 XX  
 CC This sequence is a muscle-specific binding site for the Myo-D E-box helix  
 CC -loop-helix protein. This sequence is used to describe a method resulting  
 CC in the isolation of a cdc25B gene promoter. Identification of cdc25B  
 CC promoters comprising labelling the promoter (preferably radioactively)  
 CC and using it to screen genomic DNA libraries (preferably of mammalian  
 CC cells) by hybridisation under stringent conditions. Isolation of the  
 CC murine cdc25B promoter comprises screening a murine genomic phage library  
 CC obtained from mouse strain 129FVJ with a probe comprising part of the  
 CC promoter. Constructs containing this promoter can be used to produce a  
 CC medicament for treating tumour diseases, leukaemia, autoimmune diseases,  
 CC allergies, arthritis, inflammations, organ rejection, graft-versus-host  
 CC reactions, blood clotting disorders, circulatory disorders, anaemia,  
 CC infections, hormonal disorders and/or CNS damage. (Updated on 17-OCT-2003  
 CC to standardise OS field)  
 XX  
 XX Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1734 GGCTCCCAACTCTCTCC 1749  
 DB ||||| |||||  
 17 GCCTCCCAACTCTGC 2  
 RESULT 645  
 AAV43831/c  
 ID AAV43831 standard; DNA; 17 BP.  
 XX  
 AC AAV43831;  
 XX  
 DT 22-OCT-1998 (first entry)  
 DT  
 XX Artificial promoter sequence 1 to be used as an activator sequence.  
 DE  
 XX E2F; CDF-1; chimeric promoter module; B-myb promoter; cdc25C promoter;  
 KW tumour; leukaemia; cardiovascular disease; psoriatic disease; allergy;  
 KW arthritis; inflammatory reaction; auto-immune disease; CNS damage;  
 KW transplanted organ rejection; infectious disease; CDE-CHR motif;  
 KW blood clotting disorder; chronic viral infection; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN EP859008-A2.  
 XX  
 PD 19-AUG-1998.  
 PD  
 PF 18-FEB-1998; 98EP-00102812.  
 XX  
 XX 18-FEB-1997; 97EP-00102547.  
 PR  
 XX



PA (FARH ) HOECHST AG.  
 XX  
 PI Mueller R, Liu N, Zwicker J, Sedlacek H;  
 XX  
 DR WPI; 1998-429649/37.  
 XX  
 XX New nucleic acid construct comprises activator, chimeric promoter which  
 PT binds to E2F and CDF-1 proteins and structural gene - used to treat e.g.  
 PT tumours, leukaemia, cardiovascular diseases, inflammatory reactions and  
 PT auto-immune disorders.  
 XX  
 XX Disclosure; Page 11; 21pp; English.  
 PS  
 XX This represents an artificial promoter sequence that can be used as an  
 CC activator sequence in the nucleic acid construct of the invention. The  
 CC construct comprises at least one activator sequence, at least one  
 CC chimeric promoter module comprising a nucleotide sequence which binds a  
 CC protein of the E2F family and a protein of the CDF-1 family and at least  
 CC one structural gene, where the chimeric promoter module causes an up-  
 CC regulation of gene expression in the cell cycle later than the B-myb  
 CC promoter but earlier than the cdc25C promoter. The nucleic acid construct  
 CC or a vector comprising such a nucleic acid construct can be used for the  
 CC treatment of tumours, leukaemia, cardiovascular diseases, inflammatory  
 CC reactions, auto-immune diseases, allergies, arthritis, psoriatic  
 CC diseases, impending rejection of a transplanted organ, CNS damage,  
 CC infectious disease, blood clotting disorders and chronic viral  
 CC infections. A CDF-1 protein obtained by preparing a nuclear extract from  
 CC HeLa cells and purifying by affinity chromatography in the presence of an  
 CC oligonucleotide containing a CDE-CHR sequence motif can be used to  
 CC identify inhibitors or stimulators of CDF-1  
 XX  
 XX Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1734 GGCTCCCACTCTCC 1749  
 DB 17 GCCTCCCACTCTCC 2  
 RESULT 646  
 AAV44681/C  
 ID AAV44681 standard; DNA; 17 BP.  
 XX  
 AC AAV44681;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 21-OCT-1998 (first entry)  
 XX  
 DE Bromocontryphan-specific probe.  
 XX  
 XX bromo-tryptophan; conopeptide; antihelminthic; hypnotic; anticonvulsant;  
 KW neuroprotective; anaesthesia; epilepsy; N-methyl-D-aspartate receptor;  
 KW 5HT3 serotonin receptor; bromocontryphan; probe; primer; PCR; ss.  
 XX  
 XX Synthetic.  
 OS  
 OS Conus radiatus.  
 XX  
 XX WO9831705-A1.  
 FN  
 XX 23-JUL-1998.  
 PD  
 XX 16-JAN-1998; 98WO-US000851.  
 PF  
 XX 17-JAN-1997; 97US-00785534.  
 PR  
 XX (UTAH ) UNIV UTAH RES FOUND.  
 PA (SALK ) SALK INST.  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 XX Cruz LJ, Olivera BM, McIntosh JM, Jimenez E, Craig AG, Rivier JA;

PI Julius D, England L;  
 XX  
 DR WPI; 1998-414034/35.  
 XX  
 PT New conopeptide(s) containing bromo-tryptophan residue - useful as  
 PT antihelminthic, anti-emetic, hypnotic, anticonvulsant and neuro:protective  
 PT agents, and as adjuncts to anaesthesia.  
 XX  
 PS Example 1; Page 18; 64pp; English.  
 XX  
 XX The invention relates to bromo-tryptophan conopeptides which are useful  
 CC as anti-helminthics, anti-emetics, hypnotics, anticonvulsants, neuro-  
 CC protective agents and adjuncts for anaesthesia, especially for treating  
 CC epilepsy; for reducing neurotoxic injury caused by hypoxia, anoxia or  
 CC ischaemia (of any origin); for treating Alzheimer's, Huntington's or  
 CC Parkinson's diseases, Down's syndrome, amyotrophic lateral sclerosis,  
 CC AIDS-related dementia, chemical toxicity etc.; also for control of pain  
 CC and for treatment or prevention of migraine. Some of these peptides act  
 CC by antagonising the N-methyl-D-aspartate receptor, others bind to the  
 CC 5HT3 serotonin receptor. The present sequence represents a bromo-  
 CC contryphan-specific probe. (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 17 BP; 3 A; 8 C; 2 G; 1 T; 0 U; 3 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 76.9%; Pred. No. 5.2e+02;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1673 GGACCCCTGGTGT 1685  
 DB 15 GGARCCNTGGTGY 3  
 RESULT 647  
 AAV42344/C  
 ID AAV42344 standard; DNA; 17 BP.  
 XX  
 AC AAV42344;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 25-SEP-1998 (first entry)  
 XX  
 DE E box nucleotide sequence.  
 XX  
 XX Activation sequence; structural gene; transcription factor protein;  
 KW prevention; ameliorate; disease; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX EP848061-A2.  
 PN  
 XX 17-JUN-1998.  
 PD  
 XX 10-DEC-1997; 97EP-00121752.  
 PF  
 XX 11-DEC-1996; 96DE-01051443.  
 ER  
 XX (FARH ) HOECHST AG.  
 PA  
 XX Mueller R, Sedlacek H;  
 PI  
 XX WPI; 1998-314476/28.  
 DR  
 XX Self-enhancing nucleic acid construct - containing transcription factor  
 PT coding sequence and binding site.  
 PT  
 XX Disclosure; Page 15; 56pp; English.  
 PS  
 XX The present sequence represents an E box sequence. The sequence is used  
 CC to exemplify the invention. The specification describes a nucleic acid  
 CC construct which comprises at least one structural gene that encodes an  
 CC active compound, at least one structural gene that encodes a  
 CC transcription factor protein and at least one activation sequence that

CC contains a sequence that binds the transcription factor protein and one  
 CC promoter sequence. Each activation sequence activates the expression of a  
 CC structural gene and the expression of the transcription factor protein.  
 CC The construct is used to prevent or ameliorate disease. (Updated on 25-  
 CC MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI  
 CC field.)

XX Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GGCTCCGCACTCTCTCC 1749  
 DB 17 GGCTCCGCACTCTCTCC 2

RESULT 648  
 AAV80328  
 ID AAV80328 standard; DNA; 17 BP.

XX AAV80328;

XX 29-MAR-1999 (first entry)

XX Phage lambda PCR primer OMS178.

XX RCE1; hrCE1; hrCE1p; CAAX processing enzyme; human; tumour; cancer;  
 KW therapy; diagnosis; Ras protein; endoproteinase; PCR; primer; ss.

XX Synthetic.

OS Bacteriophage lambda.

XX WO9854333-A2.

PN 03-DEC-1998.

XX 02-JUN-1998; 98WO-US011415.

XX 02-JUN-1997; 97US-00047369.

PR 14-JUL-1997; 97US-0052389P.

XX (ACAC-) ACACIA BIOSCIENCES INC.

XX Ashby MN, Dimster-Denk DG, Philips JW;

PI WPI; 1999-059843/05.

XX New DNA encoding mammalian CAAX-processing enzymes - used e.g. to treat  
 PT CAAX-protein mediated diseases such as cancers and tumours associated  
 PT with mutant Ras.

XX Example 1; Page 54; 98pp; English.

XX This is the nucleotide sequence of lambda phage primer OMS178. It was  
 CC used with primers (see AAV80326-28) specific for human hrCE1 cDNA (see  
 CC AAV80322) in the PCR amplification of hrCE1 lambda clones. The invention  
 CC relates to new mammalian CAAX-processing enzymes, including hrCE1 protein  
 CC (see AAV86009), a human functional homologue of yeast Rce1 protein, and  
 CC nucleic acids encoding them. The new mammalian DNA and CAAX processing  
 CC proteins represent potential targets for blocking the oncogenic action of  
 CC mutant Ras protein in tumours or for modulating the activity of  
 CC prenylated peripheral membrane proteins

XX Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1634 TGGGCGTAGCAGA 1649  
 ||| ||| ||| ||| |||

Db 1 TGGCGCAGGTAGCAGA 16

RESULT 649  
 AAA20626/c

ID AAA20626 standard; RNA; 17 BP.

XX AC AAA20626;

XX 19-JUN-2000 (first entry)

DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:3852.

XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
 KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;  
 KW ophthalmologic; antiinflammatory; antiarthritis; antiporiatic; ARMD;  
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
 KW age related macular degeneration; inflammation; neovascular glaucoma;  
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;  
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

OS WO9950403-A2.

PN 07-OCT-1999.

XX 24-MAR-1999; 99WO-US006507.

PR 27-MAR-1998; 98US-0079678P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;

PI WPI; 1999-591315/50.

XX Novel ribozymes for modulating the synthesis, expression and/or stability  
 PT of an mRNA encoding an angiogenic factors.

XX Claim 55; Page 157; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA  
 CC cleaving activity, which specifically cleave RNA encoded by an aryl  
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their  
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to  
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;  
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme  
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
 CC AAA21596 to AAA21688 represent their corresponding target sequences;  
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence  
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to  
 CC AAA24222 represent their corresponding target sequences. The ribozymes of  
 CC the invention are used for modulating the synthesis, expression and/or  
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are  
 CC especially used to treat cancer, diabetic retinopathy, age related  
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber  
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,  
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
 CC integrin subunit alpha-6, or integrin subunit beta-3

XX Sequence 17 BP; 4 A; 7 C; 2 G; 0 T; 4 U; 0 Other;

SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;

```
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1704 AGTTGGTTAGGAGTA 1719
   || ||||| |||||
DB 17 AGCGGGTTAGCAGTA 2

RESULT 650
AA18708
ID AAA18708 standard; RNA; 17 BP.
XX
AC AA18708;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human TIE-2 substrate sequence SEQ ID NO:1934.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
PS Claim 56; Page 112; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to
CC AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT,
CC and AA17168 to AA17560 and AA17623 to AA17684 represent their
CC corresponding target sequences; AA17685 to AA18385 and AA19087 to
CC AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
CC and AA19155 to AA19222 represent their corresponding target sequences;
CC AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
CC AA21596 to AA21688 represent their corresponding target sequences;
CC AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
CC AA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC
```

```
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 2 A; 6 C; 3 G; 0 T; 6 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 5.2e+02;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1665 TCACAGCTGGAACCT 1680
   ||| ||| |||
DB 1 UCACUGCUGGACCCU 16

RESULT 651
AA18921/C
ID AAA18921 standard; RNA; 17 BP.
XX
AC AA18921;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human TIE-2 substrate sequence SEQ ID NO:2147.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
PS Claim 56; Page 125; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to
CC AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT,
CC and AA17168 to AA17560 and AA17623 to AA17684 represent their
CC corresponding target sequences; AA17685 to AA18385 and AA19087 to
CC AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
CC and AA19155 to AA19222 represent their corresponding target sequences;
CC AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
CC AA21596 to AA21688 represent their corresponding target sequences;
CC AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
CC AA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
```

CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber  
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,  
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
 CC integrin subunit alpha-6, or integrin subunit beta-3  
 XX  
 SQ Sequence 17 BP; 6 A; 4 C; 3 G; 0 T; 4 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1685 TCTCCTCCAGCGTGGT 1700  
 Db 16 TCTCATAAAGCGTGGT 1  
 RESULT 652  
 AAV91363/C  
 ID AAV91363 standard; RNA; 17 BP.  
 XX  
 AC AAV91363;  
 DT 18-FEB-1999 (first entry)  
 DE Human C-raf target site nucleotide position 2735.  
 XX  
 KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
 KW screening; identification; synthesis; deprotection; purification; cancer;  
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
 KW restenosis; rheumatoid arthritis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9850530-A2.  
 PD 12-NOV-1998.  
 XX  
 PF 05-MAY-1998; 98WO-US009249.  
 XX  
 PR 09-MAY-1997; 97US-0046059P.  
 PR 09-JUN-1997; 97US-0049002P.  
 PR 03-JUL-1997; 97US-0051718P.  
 PR 22-AUG-1997; 97US-0056608P.  
 PR 02-OCT-1997; 97US-0061321P.  
 PR 02-OCT-1997; 97US-0061324P.  
 PR 05-NOV-1997; 97US-0064866P.  
 PR 19-DEC-1997; 97US-0068212P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;  
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
 XX  
 DR WPI; 1999-009494/01.  
 XX  
 XX Identifying new catalytic nucleic acid that modulates selected processes  
 PT - especially ribozymes that cleave Raf RNA for treating cancer,  
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
 PT used as antiviral agents and synthons.  
 XX  
 PS Claim 177; Page 153; 259pp; English.  
 XX  
 CC A method has been developed for the identification of a nucleic acid  
 CC capable of modulating a process in a biological system. The method  
 CC comprises: (a) introducing into the system a random library of nucleic  
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
 CC in systems where modulation has occurred and/or determining the sequence  
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with

CC endonuclease activity and catalytic activity, from the present invention,  
 CC are used to modulate gene expression in plant and mammalian cells and to  
 CC cleave target nucleic acid, particularly for treating systemic diseases  
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
 CC ascites and infection. They may also be used to detect genetic drift and  
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs  
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
 CC generally any condition associated with the level of c-raf. Introduction  
 CC of sugar/phosphate modifications increases stability against nuclease and  
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the  
 CC method, specifically for modulating the expression of a Raf gene  
 XX  
 SQ Sequence 17 BP; 4 A; 5 C; 2 G; 0 T; 6 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1690 TCCAGCGTGGTGAAG 1705  
 Db 17 TTCAGCATGATGAAG 2  
 RESULT 653  
 AAV92631  
 ID AAV92631 standard; RNA; 17 BP.  
 XX  
 AC AAV92631;  
 XX  
 DT 18-FEB-1999 (first entry)  
 XX  
 DE Human A-Raf substrate position 2214.  
 XX  
 KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
 KW screening; identification; synthesis; deprotection; purification; cancer;  
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
 KW restenosis; rheumatoid arthritis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9850530-A2.  
 PD 12-NOV-1998.  
 XX  
 PF 05-MAY-1998; 98WO-US009249.  
 XX  
 PR 09-MAY-1997; 97US-0046059P.  
 PR 09-JUN-1997; 97US-0049002P.  
 PR 03-JUL-1997; 97US-0051718P.  
 PR 22-AUG-1997; 97US-0056608P.  
 PR 02-OCT-1997; 97US-0061321P.  
 PR 02-OCT-1997; 97US-0061324P.  
 PR 05-NOV-1997; 97US-0064866P.  
 PR 19-DEC-1997; 97US-0068212P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;  
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
 XX  
 DR WPI; 1999-009494/01.  
 XX  
 XX Identifying new catalytic nucleic acid that modulates selected processes  
 PT - especially ribozymes that cleave Raf RNA for treating cancer,  
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
 PT used as antiviral agents and synthons.  
 XX  
 PS Claim 177; Page 161; 259pp; English.  
 XX  
 CC A method has been developed for the identification of a nucleic acid

capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with endonuclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic ascites and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine c-rat RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-rat. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. AAV90922 to AAV93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene

Sequence 17 BP; 1 A; 10 C; 1 G; 0 T; 5 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 56.2%; Pred. No. 5.2e+02;  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1678 CCTGGTGTCTCTCCA 1693  
|| :||:||||  
Db 1 CCCCUGUCUCCUCCA 16

RESULT 654  
AAV91075  
ID AAV91075 standard; RNA; 17 BP.  
XX  
AC AAV91075;  
XX  
DT 18-FEB-1999 (first entry)  
XX  
DE Human C-rat target site nucleotide position 884.  
XX  
KW Human; C-rat; A-rat; hammerhead ribozyme; hairpin ribozyme;  
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
KW screening; identification; synthesis; deprotection; purification; cancer;  
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
KW restenosis; rheumatoid arthritis; ss.  
XX  
OS Homo sapiens.  
XX  
PN W03850530-A2.  
XX  
PD 12-NOV-1998.  
XX  
PF 05-MAY-1998; 98WO-US009249.  
XX  
PR 09-MAY-1997; 97US-0046059P.  
PR 09-JUN-1997; 97US-0049002P.  
PR 03-JUL-1997; 97US-0051718P.  
PR 22-AUG-1997; 97US-0056808P.  
PR 02-OCT-1997; 97US-0061321P.  
PR 02-OCT-1997; 97US-0061324P.  
PR 05-NOV-1997; 97US-0064866P.  
PR 19-DEC-1997; 97US-0068212P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
PI Parry T, Beigelman L, Mcswigen JA, Karpeisky A, Burgin A;  
PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
XX  
DR WPI; 1999-009494/01.  
XX  
PT Identifying new catalytic nucleic acid that modulates selected processes  
PT - especially ribozymes that cleave Raf RNA for treating cancer,

restenosis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons.

Claim 177; Page 148; 259pp; English.

A method has been developed for the identification of a nucleic acid capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with endonuclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic ascites and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine c-rat RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-rat. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. AAV90922 to AAV93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene

Sequence 17 BP; 2 A; 8 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 62.5%; Pred. No. 5.2e+02;  
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1747 TCCCTATCCTAAAGGC 1762  
:||||:||||  
Db 2 UCCCUUCCUCCAGGC 17

RESULT 655  
AAV88523/c  
ID AAV88523 standard; DNA; 17 BP.  
XX  
AC AAV88523;  
XX  
DT 13-SEP-1999 (first entry)  
XX  
DE Conus radiatus contryphan PCR primer DHOG 550.  
XX  
KW Contryphan; leu-tryphan; anticonvulsant; neuroprotective; venom;  
KW cone snail; neurodegenerative disorder; epilepsay; neurotoxic injury;  
KW hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident;  
KW brain trauma; spinal cord trauma; myocardial infarct; physical trauma;  
KW drowning; suffocation; perinatal asphyxia; hypoglycaemia; migraine;  
KW senile dementia; Alzheimer's disease; amyotrophic lateral sclerosis;  
KW Parkinson's disease; Huntington's disease; Down's syndrome; PCR primer;  
KW Korsakoff's disease; schizophrenia; neuronal damage; seizure; ss.  
XX  
OS Synthetic.  
OS Conus radiatus.  
XX  
PN W09933865-A1.  
XX  
PD 08-JUL-1999.  
XX  
PF 16-DEC-1998; 98WO-US026789.  
XX  
PR 24-DEC-1997; 97US-0068737P.  
PR 16-APR-1998; 98US-00061026.  
XX  
PA (UTAH) UNIV UTAH RES FOUND.  
XX  
PI Jacobsen R, Jimenez E, Cruz LJ, Olivera BM, Gray WR, Grilley M;  
PI Watkins M, Hillyard DR;  
XX  
DR WPI; 1999-419087/35.

XX PT New pure contryphan peptides.  
 XX PS Example 4; Page 22; 48pp; English.  
 XX CC The present sequence represents a PCR primer for a contryphan  
 CC peptide sequence. Contryphan peptides are found in the venom of cone  
 CC snails. The contryphan peptides are useful as anticonvulsant agents, as  
 CC neuroprotective agents, for managing pain, and for treating  
 CC neurodegenerative disorders, especially those resulting from an  
 CC overstimulation of excitatory amino acid receptors. The contryphan are  
 CC useful for the treatment and alleviation of epilepsy and as a general  
 CC anticonvulsant agent. The contryphan are also useful to reduce  
 CC neurotoxic injury associated with conditions of hypoxia, anoxia, or  
 CC ischaemia which typically follows stroke, cerebrovascular accident, brain  
 CC or spinal chord trauma, myocardial infarct, physical trauma, drownings,  
 CC suffocation, perinatal asphyxia, or hypoglycaemic events. The contryphan  
 CC are further useful for the treatment of Alzheimer's disease, senile  
 CC dementia, amyotrophic lateral sclerosis, Parkinson's disease,  
 CC Huntington's disease, Down's syndrome, Korsakoff's disease,  
 CC schizophrenia, AIDS dementia, multi-infarct dementia, and neuronal damage  
 CC associated with uncontrolled seizures. The contryphan are further useful  
 CC in controlling pain and are effective in the treatment of migraine. They  
 CC can be used prophylactically or to relieve the symptoms associated with a  
 CC migraine episode  
 XX CC  
 SQ Sequence 17 BP; 3 A; 8 C; 2 G; 1 T; 0 U; 3 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 76.9%; Pred. No. 5.2e+02;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1673 GGAACCTCGTGT 1685  
 DB |||:|||||:  
 15 GGARCCNTGGTGY 3  
 RESULT 656  
 AAX32865/C  
 ID AAX32865 standard; DNA; 17 BP.  
 XX AC AAX32865;  
 XX DT 27-AUG-2003 (revised)  
 XX DT 20-MAR-2003 (revised)  
 XX DT 28-JUN-1999 (first entry)  
 XX DE HBV pre-S gene promoter fragment binding TFO B4.  
 XX KW Triplex-forming oligonucleotide; TFO; promoter region; pre-S gene;  
 XX KW inhibition; hepatitis B virus; HBV adr subtype; DR region; ss.  
 XX OS Synthetic.  
 XX OS Hepatitis B virus.  
 XX FH Key Location/Qualifiers  
 XX FT misc\_feature 17  
 XX FT /tag= a  
 XX FT /note= "optional monophosphorylation (claim 2)"  
 XX PN W09920641-A1.  
 XX PD 29-APR-1999.  
 XX PF 19-OCT-1998; 98WO-CN000248.  
 XX PF 21-OCT-1997; 97CN-00106667.  
 XX PR (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.  
 XX PA Lu C;  
 XX PI WPI; 1999-288270/27.  
 XX DR

XX PT Triplex-forming oligonucleotides, useful for, e.g. inhibition of  
 XX PT hepatitis B virus (HBV).  
 XX PS Claim 1, 2; Page 22; 39pp; Chinese.  
 XX CC The invention provides triplex-forming oligonucleotides (TFO) and their  
 CC modified derivatives. TFO B1-B5 (AAX32862-866) can bind with the promoter  
 CC region of pre-S gene in inhibition of hepatitis B virus (HBV) adr subtype  
 CC and TFO B11, B12 and B15 (AAX32868-870) can bind with DR region of HBV.  
 CC The oligonucleotides are useful for inhibition of HBV and as drug in  
 CC treatment of hepatitis B. Since the length of the oligonucleotides can be  
 CC suitably increased, the stability and specificity of the formed triplex  
 CC DNA with 2 similar homopoly purine/homopoly pyrimidine fragments are  
 CC higher. Triplex formation is specifically targeting on the HBV gene  
 CC expression, DNA replication and reproduction, or to produce (DNA)2:RNA  
 CC hybrid triplex with target sequence of RNA in stopping RNA reverse  
 CC transcription, so there is little effect on the human cells. Such  
 CC oligonucleotides are chemically modified by 3'-terminal  
 CC monophosphorylation, leading to more significant inhibition due to their  
 CC higher stability, and the degradation products of the modified  
 CC oligonucleotides are not toxic to the body. (Updated on 20-MAR-2003 to  
 CC correct DR field.) (Updated on 27-AUG-2003 to correct OS field.)  
 XX CC  
 SQ Sequence 17 BP; 6 A; 0 C; 11 G; 0 T; 0 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1736 CTCCTCCCTCTCCCT 1751  
 DB ||||| ||||| |||||  
 16 CTCCTCTCTCTCTCTCT 1  
 RESULT 657  
 AAX76849/C  
 ID AAX76849 standard; DNA; 17 BP.  
 XX AC AAX76849;  
 XX DT 05-AUG-1999 (first entry)  
 XX DE PCR primer for T66Bk gene.  
 XX DE Transcription unit; MARK2 kinase; rsk3 kinase; regulatory region; T66Bk;  
 XX KW contraceptive; Responder/Distorter signalling cascade; t-Responder;  
 XX KW PCR primer; ss.  
 XX OS Synthetic.  
 XX OS Mus sp.  
 XX PN W09925815-A2.  
 XX PD 27-MAY-1999.  
 XX PF 18-NOV-1998; 98WO-BPC07395.  
 XX PF 18-NOV-1997; 97EP-00120190.  
 XX PR 02-MAR-1998; 98EP-00103596.  
 XX PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX PI Herrmann B, Koschorz E, Kispert A;  
 XX DR WPI; 1999-347466/29.  
 XX PT Nucleic acids involved in the responder phenotype in mice.  
 XX PS Example 7; Page 58; 117pp; English.  
 XX CC This sequence is a PCR primer for the T66Bk gene. The invention related  
 XX CC to a nucleic acid molecule (I) comprising a transcription unit encoding

CC in its 5' portion a kinase having a homology to MARK2 kinase and the 3'  
 CC portion of the nucleotide sequence has a high homology to rsk3 kinase.  
 CC Sperm produced by transgenic creatures containing (I) are useful for  
 CC production of offspring. T66BK, its regulatory region, recombinant DNA,  
 CC vectors, host cells, antibodies, etc., are useful for the isolation of  
 CC receptors on the surface of sperm recognising attractants of the egg cell  
 CC for the development and/or production of contraceptives. They can also be  
 CC used to identify chemicals or biological compounds able to trigger the  
 CC (premature) activation or inhibition of the Responder/Distorter  
 CC signalling cascade, or to identify and isolate receptors and other  
 CC members of the cascade that bind the expression products. The methods for  
 CC detecting the sperm of the transgenic animal, and selecting against (I)  
 CC also provide a means for distorting the transmission ratio of genetic  
 CC traits by altering genes of the Responder/Distorter signal cascade other  
 CC than the t-Responder. They also allow distortion, to a non-Mendelian  
 CC ratio, of the transmission of a genetic trait, i.e. determination of sex,  
 CC from male mammals to their offspring by expressing during  
 CC spermatogenesis/spermiogenesis a gene involved in sperm motility and/or  
 CC fertilisation. The genes and proteins involved in the responder phenotype  
 CC and Responder/Distorter signalling cascade, as well as the inventive  
 CC methods are advantageous in breeding strategies by allowing for specific  
 CC selection of genetic traits and in particular, of sex  
 XX  
 SQ Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. NO. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1690 TCCAGCGTGTGGGAAG 1705  
 ||||| |||||  
 Db 16 TCCAGCCAGGGGAAG 1

RESULT 658  
 AAX77880/c  
 ID AAX77880 standard; DNA; 17 BP.  
 AC AAX77880;  
 XX  
 DT 13-AUG-1999 (first entry)  
 XX  
 DE HLH protein DNA binding motif.  
 XX  
 KW Activation sequence; transcription factor; murine; p163; p27; treatment;  
 KW binding protein; DNA binding domain; effector gene; disease; infection;  
 KW tumour; leukaemia; autoimmune disease; allergy; arthritis; inflammation;  
 KW transplant rejection; graft-versus-host disease; circulatory disorder;  
 KW blood clot; anaemia; hormonal disorder; CNS injury; HLH protein; ss.  
 XX  
 OS Unidentified.  
 XX  
 XX EP926237-A2.  
 XX  
 PD 30-JUN-1999.  
 XX  
 PF 12-DEC-1998; 98EP-00123709.  
 XX  
 PR 20-DEC-1997; 97DE-01056975.  
 XX  
 XX (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.  
 PA  
 PI Eilers M, Buerigin A, Sedlacek H;  
 XX  
 XX WPI; 1999-349238/30.  
 DR  
 XX  
 XX New nucleic acid construct comprising promoter, transcription factor  
 PT gene, activation sequence and effector gene - useful for gene therapy  
 PT treatment of allergies, inflammation, transplant disorders and leukaemia..  
 PT  
 XX  
 XX Disclosure; Page 15; 90pp; German.  
 PS  
 XX  
 CC This invention describes a novel nucleic acid construct comprising the

CC following components (a) an activation sequence for the transcription of  
 CC component b, (b) component b which is constructed from component b1 (a  
 CC transcription factor activating domain), component b2 (murine p163 or p27  
 CC binding protein) and component b3 (a transcription factor DNA binding  
 CC domain), (c) an activation sequence which is activated by binding of the  
 CC expression product of component (b) and which induces transcription of  
 CC component (d) and (d) an effector gene. The construct, preferably in a  
 CC plasmid or viral vector, or cell can be used to treat a disease selected  
 CC from infections, tumours, leukaemia, autoimmune diseases, allergies,  
 CC arthritis, inflammations, transplant rejection, graft-versus-host  
 CC disease, blood clotting disorders, circulatory disorders, anaemia,  
 CC hormonal disorders and CNS injuries. This sequence represents the DNA  
 CC binding motif of the HLH protein which is used to describe the method of  
 CC the invention  
 XX

SQ Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. NO. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GGCTCCCAACTCCTCC 1749  
 ||||| |||||  
 Db 17 GCCTCCCAACACTGC 2

RESULT 659  
 AAZ23521/c  
 ID AAZ23521 standard; DNA; 17 BP.  
 AC AAZ23521;  
 XX  
 DT 20-DEC-1999 (first entry)  
 XX  
 DE MyoD E box DNA motif.  
 XX  
 KW Antigen binding; single chain; variable domain; VH domain; light chain;  
 KW heavy immunoglobulin chain; VL domain; anticancer; antiviral; tumor;  
 KW antibacterial; antimalarial; antiinflammatory; treatment; prevention;  
 KW diagnosis; vaccine; autoimmune disease; inflammation; blood disorder;  
 KW transplant rejection; arthritis; nervous system disorder; infection;  
 KW Myo D box; ss.  
 XX  
 OS Unidentified.  
 XX  
 XX DE19816141-A1.  
 XX  
 PD 14-OCT-1999.  
 XX  
 PF 09-APR-1998; 98DE-01016141.  
 XX  
 PR 09-APR-1998; 98DE-01016141.  
 XX  
 XX (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.  
 PA  
 PI Kontermann R, Sedlacek H, Mueller R;  
 XX  
 XX WPI; 1999-581511/50.  
 DR  
 XX  
 PT New polypeptide binding agents containing variable heavy and light  
 PT constructs connected via peptide linker, used for treatment, prevention  
 PT or diagnosis of e.g. cancer.  
 XX  
 XX Disclosure; Page 13; 20pp; German.  
 PS  
 XX  
 CC This sequence represents a novel single-chain molecule (I) that binds  
 CC multiple antigens and comprises two variable domains of heavy  
 CC immunoglobulin chains (VH), having specificities A and B and two variable  
 CC domains of light chains (VL), also with specificities A and B. The  
 CC domains are provided as two VH-VL constructs which are attached via a  
 CC peptide (P). Any VH and VL may be replaced by their functional fragments.  
 CC The products of the invention have anticancer, antiviral, antibacterial,  
 CC antimalarial and antiinflammatory activity. (I) are used to treat,

CC prevent or diagnose tumors (e.g. as tumor vaccines), autoimmune diseases  
 CC and inflammation (e.g. transplant rejection and arthritis), blood  
 CC disorders (e.g. of the coagulation and/or circulatory systems, such as  
 CC anemia, leucopenia, thrombocytopenia and hypertension), nervous system  
 CC disorders and/or infections (by viruses or bacteria, or malaria),  
 CC including, when (I) include a fusogenic peptide, use for gene transfer.  
 CC (I) are produced simply and in predominantly homogeneous form, in a wide  
 CC variety of hosts, either in secreted or membrane-bound forms. This  
 CC sequence represents a MyoD E box DNA motif which is used to illustrate  
 CC the method of the invention

XX Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GGCTCCCACTCTCC 1749  
 DB 17 GGCTCCCACTCTGC 2

RESULT 660  
 AAZ24146/c  
 ID AAZ24146 standard; DNA; 17 BP.  
 XX AC AAZ24146;  
 XX 20-MAR-2003 (revised)  
 DT 08-FEB-2000 (first entry)  
 XX HLH protein E box (Myo D) DNA motif.  
 XX Immunoglobulin; light chain; VL region; heavy chain; VH region;  
 KW single-chain; antigen binding; variable domain; anticancer; treatment;  
 KW antiviral; antibacterial; antimalarial; antiinflammatory; diagnosis;  
 KW tumor vaccine; autoimmune disease; inflammation; blood disorder;  
 KW nervous system; infection; HLH protein; Myo D; E box; ss.  
 XX Unidentified.  
 OS  
 XX DE19827239-A1.  
 PN 23-DEC-1999.  
 PD 18-JUN-1998; 98DE-01027239.  
 XX 09-APR-1998; 98DE-01016141.  
 PR 18-JUN-1998; 98DE-01027239.  
 XX (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.  
 PA Kontermann R, Sedlacek H, Mueller R;  
 PI WPI; 1999-591691/51.  
 DR New polyspecific binding agents useful for treatment, prevention and  
 PT diagnosis of cancer and autoimmune diseases comprises variable domains of  
 PT heavy and light chains of immunoglobulins bound by a peptide.  
 XX Disclosure; Page 15; 26pp; German.  
 PS This invention describes a novel single-chain molecule (I) that binds  
 CC multiple antigens and comprises two variable domains of heavy  
 CC immunoglobulin chains (VH) and two variable domains of light chains (VL).  
 CC The domains are provided as two VH-VL constructs which are attached via a  
 CC peptide (P). Any VH and VL may be replaced by their functional fragments.  
 CC The products of the invention have anticancer, antiviral, antibacterial,  
 CC antimalarial, and antiinflammatory activity. (I) are used to treat,  
 CC prevent or diagnose tumors (e.g. as tumor vaccines), autoimmune diseases  
 CC and inflammation (e.g. transplant rejection and arthritis), blood  
 CC disorders (e.g. of the coagulation and/or circulatory systems, such as  
 CC anemia, leucopenia, thrombocytopenia and hypertension), nervous system

CC disorders and/or infections (by viruses or bacteria, or malaria),  
 CC including, when (I) include a fusogenic peptide, use for gene transfer.  
 CC This sequence represents an HLH protein E box (Myo D) DNA motif which is  
 CC used to illustrate the method of the invention. NOTE: This specification  
 CC is a treat as basic for CZ-9901215 in Derwent week 9951. (Updated on 20-  
 CC MAR-2003 to correct DR field.)

XX Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 GGCTCCCACTCTCC 1749  
 DB 17 GGCTCCCACTCTGC 2

RESULT 661  
 AAZ29110  
 ID AAZ29110 standard; DNA; 17 BP.  
 XX AC AAZ29110;  
 XX 07-FEB-2000 (first entry)  
 DT Antisense primer sequence, used for localisation of GFR alpha 3.  
 DE Human Glial cell line-derived neurotrophic factor receptor; GFR alpha 3;  
 KW antisense primer; hybridisation probe; mouse; localisation; product;  
 KW adult tissue; foetal tissue; detection; peripheral nervous system;  
 KW diagnosis; autonomic nervous system; disease; ss.  
 XX Synthetic.  
 OS Mus musculus.  
 XX WO9949039-A2.  
 PN 30-SEP-1999.  
 PD 19-MAR-1999; 99WO-US006098.  
 XX 23-MAR-1998; 98US-0079124P.  
 PR 13-APR-1998; 98US-0081569P.  
 XX (GETH ) GENENTECH INC.  
 PA De Sauvage FJ, Klein RD, Phillips HS, Rosenthal A;  
 PI WPI; 2000-038358/03.  
 DR New isolated GFR-alpha3 nucleic acid, used to develop products for  
 PT treating diseases or conditions involving peripheral nervous system or  
 PT autonomic nervous system.  
 XX Example 5; Page 51; 112pp; English.  
 PS The present DNA sequence is an antisense primer, that is used to generate  
 CC a 378 bp hybridisation probe, from mouse GFR alpha 3. It is used as a  
 CC probe, for the localisation of GFR alpha 3 in various foetal and adult  
 CC human tissues. The GFR alpha 3 is used to develop products, that can be  
 CC used for detection and diagnosis of diseases, involving peripheral or  
 CC autonomic nervous system  
 XX Sequence 17 BP; 3 A; 1 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1739 CCACTCTCTCTCTATC 1754  
 DB 2 CCAGTCCTCTCTTACC 17



```

RESULT 662
AAZ88531/C
ID AAZ88531 standard; DNA; 17 BP.
XX
XX AC AAZ88531;
XX
XX DT 27-APR-2000 (first entry)
XX
XX DE MyoD E-box muscle-specific HLH protein DNA binding site.
XX
XX KW Promoter; antiinflammatory; cytostatic; antiarthritic; hormone;
XX KW antianemic; neuroprotective; antimicrobial; immunosuppressive; tumor;
XX KW anticoagulant; treatment; infection; leukemia; autoimmune disease;
XX KW allergy; arthritis; inflammation; organ rejection; transplant; anemia;
XX KW blood clotting disease; circulatory disease; MyoD E-box; HLH protein; ss.
XX
XX OS Unidentified.
XX
XX PN DE19831420-A1.
XX
XX ED 20-JAN-2000.
XX
XX PF 14-JUL-1998; 98DE-01031420.
XX
XX PR 14-JUL-1998; 98DE-01031420.
XX
XX PA (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.
XX
XX PI Mueller R, Nettelbeck D, Sedlacek H;
XX
XX DR WPT; 2000-137953/13.
XX
XX PT Chimeric promoter constructs with binding sites for recombinant
XX PT transcription factors useful for producing agents to treat cancer,
XX PT inflammation, allergy and autoimmune diseases.
XX
XX PS Disclosure; Page 27; 52pp; German.
XX
XX CC This invention describes a novel nucleic acid construct (I) which
XX CC comprises: (1) a minimal promoter (II); (2) a DNA (III) encoding for a
XX CC minimal recombinant transactivator, comprising DNA coding for a DNA
XX CC binding domain and a transactivation domain; (3) a minimal DNA sequence
XX CC (IV) to bind the expression product of (III); (4) a minimal promoter (V)
XX CC which contains a CDE-CHR element or an E2F-BS-CHR element; and (5) a
XX CC minimal effector gene (VI). The products of the invention have
XX CC antimicrobial; immunosuppressive and anticoagulant activity. (I) and
XX CC (VII) are useful for the production of remedies for the prevention or
XX CC treatment of infections, tumors, leukemia, autoimmune disease, allergy,
XX CC arthritis, inflammation, organ rejection, transplants against host
XX CC reaction, blood clotting diseases, circulatory diseases, anemia, hormone
XX CC disease and central nervous system injury. This sequence represents the
XX CC MyoD E-box/muscle-specific HLH protein DNA binding site which is used in
XX CC the method of the invention
XX
XX SQ Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1734 GGCTCCCAACTCTCC 1749
XX | ||||| |||
XX Db 17 GCCTCCCAACACCTGC 2
XX
XX RESULT 663
XX AAZ47108
XX ID AAZ47108 standard; DNA; 17 BP.
XX
XX AC AAZ47108;
XX

```

```

XX DT 15-MAR-2000 (first entry)
XX
XX DE Rat AGRP mRNA PCR primer #294.
XX
XX KW Rat; agouti-related protein; neuropeptide; regulation; antibody; ss;
XX KW feeding behaviour; energy metabolism; melanocortin pathway; recombinant;
XX KW primer; PCR; amplification; probe; hybridisation.
XX
XX OS Synthetic.
XX OS Rattus norvegicus.
XX
XX PN WO9955832-A2.
XX
XX PD 04-NOV-1999.
XX
XX PF 26-APR-1999; 99WO-US008983.
XX
XX PR 29-APR-1998; 98US-0083549P.
XX
XX PA (MERI ) MERCK & CO INC.
XX
XX PI Van Der Ploeg LHT, Guan X, Yu H, Trivedi PG;
XX
XX DR WPI; 2000-062018/05.
XX
XX PT Novel rat agouti-related protein used to regulate feeding behavior and
XX PT energy metabolism via melanocortin pathway interactions.
XX
XX PS Example 2; Page 9; 18pp; English.
XX
XX CC Primers AAZ47107-247108 were used to PCR amplify a 200 bp fragment of a
XX CC novel gene encoding a rat agouti-related protein (AGRP). The amplified
XX CC product was used as a probe to screen a rat hypothalamus cDNA library to
XX CC obtain a cDNA clone of AGRP gene (AAZ47104). The agouti-related protein
XX CC is a neuropeptide which may play a role in the central regulation of
XX CC feeding behaviour and energy metabolism via interactions with the
XX CC melanocortin pathways, in manner similar to the agouti protein. The
XX CC polynucleotide is used to produce the protein recombinantly. The protein
XX CC is used to produce antibodies
XX
XX SQ Sequence 17 BP; 5 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1656 GCACGAGGCTCACAGC 1671
XX ||||| ||||| |||||
XX Db 1 GCACATGGGTCACAGC 16
XX
XX RESULT 664
XX AAZ4961
XX ID AAZ4961 standard; DNA; 17 BP.
XX
XX AC AAZ4961;
XX
XX DT 19-JUL-2000 (first entry)
XX
XX DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1459.
XX
XX KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
XX KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX KW gene expression modification; cancer; phosphorothioate; endonuclease;
XX KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9954459-A2.
XX
XX PD 28-OCT-1999.
XX

```

```

PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PT
XX
XX Claim 77; Page 64; 148pp; English.
XX
XX The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodithioate
XX link, having endonuclease activity. (A), and more generally any catalytic
XX nucleic acid (A') that modulates expression of the oestrogen receptor
XX gene, are used to treat cancer (particularly of breast or endometrium),
XX in vivo or by transforming cells ex vivo and implanting treated cells, or
XX for other conditions associated with levels of oestrogen receptor.
XX Because of the high selectivity for targeted RNA, (A) can also be used to
XX correlate inhibition of gene expression with alterations in phenotype,
XX particularly for identification of therapeutic targets, and as research
XX reagents (for RNA, in the same way that restriction endonucleases are
XX used with DNA). The combination of modifications in (A) improves
XX resistance to nucleases, binding affinity and/or activity. AAA23503 to
XX AAA24748 to AAA25992 represent their corresponding target sequences.
XX AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
XX sequences, and AAA26107 to AAA26218 represent their corresponding target
XX sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
XX antisense oligonucleotides used in the exemplification of the present
XX invention
XX
XX Sequence 17 BP; 2 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1738 CCCAAGCTCTCCCTAT 1753
DB 2 CCCAGCTCTCTCTCAT 17
RESULT 665
AAF02991/C
ID AAF02991 standard; DNA; 17 BP.
XX
XX AAF02991;
XX
XX 16-FEB-2001 (first entry)
DT
XX
XX Hammerhead ribozyme substrate #1286.
DE
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200061729-A2.
PN
XX
XX 19-OCT-2000.
PD
XX
XX 11-APR-2000; 2000WO-US009721.
PF
XX
XX 12-APR-1999; 99US-0129390P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
PI
XX
XX WPI; 2000-647423/62.
DR
XX
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor protein,
XX interferon alpha and erythropoietin.
PT
XX
XX Claim 37; Page 85; 164pp; English.
PS
XX
XX The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
XX factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
XX Inhibition of the repressors removes prevents inhibition (and
XX consequently increases expression of) genes involved in the production of
XX erythropoietin, granulocyte colony stimulating factor protein and
XX interferon alpha
XX
XX Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1647 AGAGGCGACGACCAG 1662
DB 16 AGCAGCGAAGGCCAG 1
RESULT 666
AAF01814/C
ID AAF01814 standard; DNA; 17 BP.
XX
XX AAF01814;
XX
XX 16-FEB-2001 (first entry)
DT
XX
XX Hammerhead ribozyme substrate #109.
DE
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200061729-A2.
PN
XX
XX 19-OCT-2000.
PD
XX
XX 11-APR-2000; 2000WO-US009721.
PF
XX
XX 12-APR-1999; 99US-0129390P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
PI
XX
XX WPI; 2000-647423/62.
DR
XX
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor protein,
XX interferon alpha and erythropoietin.
PT
XX
XX Claim 37; Page 58; 164pp; English.
PS
XX
XX The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
XX factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
XX Inhibition of the repressors removes prevents inhibition (and
XX consequently increases expression of) genes involved in the production of
XX

```

CC erythropoietin, granulocyte colony stimulating factor protein and  
 CC interferon alpha  
 XX  
 SQ Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1638 GCTGTAGCAGAGGC 1653  
 |||||  
 Db 17 GCTGTAGTAGAGGCC 2  
 RESULT 667  
 ABK00575  
 ID ABK00575 standard; RNA; 17 BP.  
 XX  
 AC ABK00575;  
 XX  
 DT 12-MAR-2002 (first entry)  
 DE Human NOGO Hammerhead Ribozyme #575.  
 XX  
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FN WO200159103-A2.  
 PD 16-AUG-2001.  
 XX  
 PF 09-FEB-2001; 2001WO-US004273.  
 XX  
 PR 11-FEB-2000; 2000US-0181797P.  
 PR 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX  
 PI Blatt L, Mcswiggen J, Chowrira BM;  
 XX WPI; 2001-607195/69.  
 DR  
 XX  
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX  
 PS Claim 88; Page 75; 200pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN motif) or  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targetting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-  
 CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targetting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is a hammerhead ribozyme of the invention  
 XX  
 SQ Sequence 17 BP; 5 A; 1 C; 6 G; 0 T; 5 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 56.2%; Pred. No. 5.2e+02;  
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1704 AGTGGGTTAGGAGTA 1719  
 ||::||:|  
 Db 2 AGUUGGUUCAGAGUA 17  
 RESULT 668  
 ABK03212/C  
 ID ABK03212 standard; RNA; 17 BP.  
 XX  
 AC ABK03212;  
 XX  
 DT 12-MAR-2002 (first entry)  
 DE Human CD20 Inozyme #163.  
 XX  
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FN WO200159103-A2.  
 PD 16-AUG-2001.  
 XX  
 PF 09-FEB-2001; 2001WO-US004273.  
 XX  
 PR 11-FEB-2000; 2000US-0181797P.  
 PR 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX  
 PI Blatt L, Mcswiggen J, Chowrira BM;  
 XX WPI; 2001-607195/69.  
 DR  
 XX  
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX  
 PS Claim 88; Page 75; 200pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN motif) or  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA



```
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1706 TTGGTTAGGAGTACG 1721
DB 16 TTGGGCTCGGAGCAG 1
RESULT 670
ABK02836/c
ID ABK02836 standard; RNA; 17 BP.
XX AC ABK02836;
XX DT 12-MAR-2002 (first entry)
XX DE Human CD20 Hammerhead ribozyme #135.
XX KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX OS Homo sapiens.
XX OS Synthetic.
XX FN WO200159103-A2.
XX PD 16-AUG-2001.
XX PF 09-FEB-2001; 2001WO-US004273.
XX PR 11-FEB-2000; 2000US-0181797P.
XX PR 28-FEB-2000; 2000US-0185516P.
XX PR 06-MAR-2000; 2000US-0187128P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J.
XX PA (CHOW/) CHOWRIRA B M.
XX PI Blatt L, Mcswiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
XX DR
CC CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN motif) or
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a VGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg2+.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
```

```
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg2+. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is a hammerhead ribozyme of the invention
SQ Sequence 17 BP; 1 A; 5 C; 3 G; 0 T; 8 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1647 AGAAGGCAAGCACCAG 1662
DB 17 AGAAGGCAAGATCAG 2
RESULT 671
ABK01446
ID ABK01446 standard; RNA; 17 BP.
XX AC ABK01446;
XX DT 12-MAR-2002 (first entry)
XX DE Human NOGO Inozyme #716.
XX KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX OS Homo sapiens.
XX OS Synthetic.
XX FN WO200159103-A2.
XX PD 16-AUG-2001.
XX PF 09-FEB-2001; 2001WO-US004273.
XX PR 11-FEB-2000; 2000US-0181797P.
XX PR 28-FEB-2000; 2000US-0185516P.
XX PR 06-MAR-2000; 2000US-0187128P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J.
XX PA (CHOW/) CHOWRIRA B M.
XX PI Blatt L, Mcswiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
XX DR
CC CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN motif) or
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a VGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg2+.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
```

```
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 88; Page 89; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
CC an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA
CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg2+.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targetting nucleic acid may be used to
CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg2+. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is an inozyme of the invention
XX
SQ Sequence 17 BP; 5 A; 2 C; 5 G; 0 T; 5 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 5.2e+02;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1705 GTTGCGTTAGAGTAC 1720
DB |::|:|::|::|
1 GUUGGUUCAGAGUAC 16
RESULT 672
ABK02837/C
ID ABK02837 standard; RNA; 17 BP.
XX
AC ABK02837;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human CD20 Hammerhead ribozyme #136.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNzyme; inozyme; G-cleaver; amberzyme; zynzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
```

```
XX Homo sapiens.
OS Synthetic.
XX WO200159103-A2.
PN 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-USC04273.
XX
PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
DR
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 30; Page 142; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
CC an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA
CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg2+.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targetting nucleic acid may be used to
CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg2+. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is a hammerhead ribozyme of the invention
XX
SQ Sequence 17 BP; 1 A; 5 C; 2 G; 0 T; 9 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1647 AGAAGCGACAGCCAG 1662
DB |||||
16 AGAAGCGAAAGATCAG 1
```

```
RESULT 673
ABA78857/c
ID ABA78857 standard; DNA; 17 BP.
XX
AC ABA78857;
XX
DT 24-JAN-2002 (first entry)
XX
DE APC mutation correcting oligonucleotide SEQ ID NO: 1703.
XX
DE Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW Alzheimer's disease; cytosolic; antitickling; antianaemic; haemostatic;
KW antilipemic; ss.
XX
OS Homo sapiens.
XX
PN WO200173002-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US009761.
XX
PR 27-MAR-2000; 2000US-0192176P.
PR 27-MAR-2000; 2000US-0192179P.
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
XX
PA (UYDE ) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC;
XX
WPI; 2001-639230/73.
XX
DR Oligonucleotide for targeted alterations of genetic sequences and for
PT treating cystic fibrosis, comprises at least one mismatch and chemical
PT modification.
XX
PS Claim 7; Page 145; 294pp; English.
XX
CC The present invention provides single-stranded oligonucleotides which can
CC be used for the targeted alteration of genomic sequences, where the
CC oligonucleotide has at least one mismatch compared with the genomic
CC sequence to be altered. In particular, these sequences are directed at
CC the following genes: adenosine deaminase, p53, beta-globin,
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC various syndromes. The present sequence is one of the gene correcting
CC oligonucleotides of the invention
XX
SQ Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1674 GAACCCCTGGTCTCC 1689
Db 16 GAACCCCTGCAGTCTGC 1
```

```
RESULT 674
ABA78858
ID ABA78858 standard; DNA; 17 BP.
XX
AC ABA78858;
XX
DT 24-JAN-2002 (first entry)
XX
DE APC mutation correcting oligonucleotide SEQ ID NO: 1704.
XX
DE Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW Alzheimer's disease; cytosolic; antitickling; antianaemic; haemostatic;
KW antilipemic; ss.
XX
OS Homo sapiens.
XX
PN WO200173002-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US009761.
XX
PR 27-MAR-2000; 2000US-0192176P.
PR 27-MAR-2000; 2000US-0192179P.
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
XX
PA (UYDE ) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC;
XX
WPI; 2001-639230/73.
XX
DR Oligonucleotide for targeted alterations of genetic sequences and for
PT treating cystic fibrosis, comprises at least one mismatch and chemical
PT modification.
XX
PS Claim 7; Page 145; 294pp; English.
XX
CC The present invention provides single-stranded oligonucleotides which can
CC be used for the targeted alteration of genomic sequences, where the
CC oligonucleotide has at least one mismatch compared with the genomic
CC sequence to be altered. In particular, these sequences are directed at
CC the following genes: adenosine deaminase, p53, beta-globin,
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC various syndromes. The present sequence is one of the gene correcting
CC oligonucleotides of the invention
XX
SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1674 GAACCCCTGGTCTCC 1689
Db 2 GAACCCCTGCAGTCTGC 17
```

AAFI6612/c  
ID AAFI6612 standard; DNA; 17 BP.  
XX  
AC AAFI6612;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 99.  
XX  
KW Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;  
KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;  
KW DNA-RNA hybrid; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200071164-A1.  
XX  
PD 30-NOV-2000.  
XX  
PF 24-MAY-2000; 2000WO-AU000498.  
XX  
PR 24-MAY-1999; 99AU-00000510.  
XX  
PA (TACH/) TACHAS G.  
XX  
PI Tachas G;  
XX  
XX WPI; 2001-025093/03.  
XX  
PT Treating gastric acid disturbance by administering an oligonucleotide  
PT which modulates the activity of a polypeptide involved in gastric acid  
XX production or secretion..  
PS Example 3; Page 149; 164pp; English.  
XX  
CC The present invention provides oligonucleotides, and methods for their  
CC use, which are useful in modulating the action of proteins involved in  
CC gastric acid production. The target protein is preferably the histamine  
CC H2 receptor or one of the proteins which form part of the gastric proton  
CC pump. The sequences and methods of the invention are useful in the  
CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,  
CC duodenal ulcers and other gastric acid disturbances, most of which are  
CC caused by Helicobacter pylori  
XX  
SQ Sequence 17 BP; 5 A; 0 C; 11 G; 1 T; 0 U; 0 Other;  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1736 CTCCCAACTCTCCT 1751  
Db 17 CTCCCTCTCACTCT 2  
RESULT 677  
ABL46487/c  
ID ABL46487 standard; RNA; 17 BP.  
XX  
AC ABL46487;  
XX  
DT 27-JUN-2003 (first entry)  
XX  
DE Human GRID hammerhead ribozyme substrate oligonucleotide #120.  
XX  
KW Human; Grb2-related with Insert Domain; GRID; T-cell;  
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;  
KW leukaemia; cytostatic; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200162911-A2.  
XX

RESULT 675  
AAH24608  
ID AAH24608 standard; DNA; 17 BP.  
XX  
AC AAH24608;  
XX  
DT 07-AUG-2001 (first entry)  
XX  
DE Human endometrium cDNA clone 18-4-SP6 PCR primer #2.  
XX  
KW Human; endometrium; gynaecological; cytostatic; gene therapy;  
KW peptide therapy; endometriosis; gene expression; drug screening;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200132920-A2.  
XX  
PD 10-MAY-2001.  
XX  
PF 03-NOV-2000; 2000WO-GB004228.  
XX  
PR 03-NOV-1999; 99GB-00026074.  
PR 03-NOV-1999; 99GB-00026076.  
PR 03-NOV-1999; 99GB-00026079.  
PR 03-NOV-1999; 99GB-00026081.  
XX  
PA (MEIR-) METRIS THERAPEUTICS LTD.  
XX  
PI Pappa H, Lnenicek M;  
XX  
DR WPI; 2001-328804/34.  
XX  
XX Screening for a gene or gene product associated with endometriosis, for  
XX diagnosing or treating endometriosis, comprises selecting a gene whose  
XX level of expression differs between healthy and diseased endometrium  
XX tissues.  
XX Example; Fig 3; 106pp; English.  
XX  
CC The invention relates to a method for screening for a gene or gene  
CC product associated with endometriosis. The method comprises comparing the  
CC pattern of gene expression in a diseased endometrium tissue from a  
CC patient suffering from endometriosis to the pattern of gene expression in  
CC healthy endometrium tissue from the same patient, and selecting a gene  
CC whose level of expression differs between healthy and diseased tissues.  
CC The gene, gene product and their antagonists and agonists are useful in  
CC the manufacture of a medicament for diagnosing or treating endometriosis.  
CC The method is useful for screening genes or gene products that are  
CC implicated in endometriosis. It is particularly useful in diagnosing  
CC endometriosis, as well as for screening for agents for treating  
CC endometriosis. Prior methods of diagnosing endometriosis are more  
CC difficult to perform and are more expensive, normally involving surgery.  
CC The present method allows the disease to be diagnosed and treated at  
CC earlier stage. The present sequence is a primer used in a reverse  
CC transcription polymerase chain reaction (RT-PCR) procedure to validate  
CC the results of differential gene expression studies. It was used to  
CC amplify human endometrium cDNA encoding stromelysin  
XX  
SQ Sequence 17 BP; 6 A; 3 C; 7 G; 1 T; 0 U; 0 Other;  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1647 AGAAGGCAAGCACAG 1662  
Db 2 AGAAGGCATGGCCAG 17  
RESULT 676



PD 30-AUG-2001.  
 XX  
 PF 23-FEB-2001; 2001WO-US005957.  
 XX  
 CC 24-FEB-2000; 2000US-0184594P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (GLAX ) GLAXO GROUP LTD.  
 PA  
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;  
 PI WPI; 2001-550088/61.  
 XX  
 DR New nucleic acid(s) for regulating the Grb2-related with Insert Domain  
 XX (GRID) gene comprises using antisense and enzymatic nucleic acid  
 PT molecules such as hammerhead ribozymes.  
 PT  
 XX Claim 4; Page 61; 108pp; English.  
 PS  
 XX The present invention relates to oligonucleotides that downregulate the  
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is  
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful  
 CC for modulating the expression of GRID, to treat conditions such as  
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be  
 CC administered in conjunction with other therapies such as radiation,  
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was  
 CC used to illustrate the invention  
 CC  
 XX Sequence 17 BP; 6 A; 6 C; 1 G; 0 T; 4 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1721 GGAGATGGAGATTGTC 1736  
 DB 16 GGAGATGGAGATTGTC 1  
 RESULT 678  
 ABL46970/C  
 ID ABL46970 standard; RNA; 17 BP.  
 XX  
 AC ABL46970;  
 XX  
 CC 27-JUN-2003 (first entry)  
 DT  
 XX Human GRID zinzyme substrate oligonucleotide #54.  
 DE  
 KW Human; Grb2-related with Insert Domain; GRID; T-cell;  
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;  
 KW leukaemia; cytostatic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200162911-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 23-FEB-2001; 2001WO-US005957.  
 XX  
 CC 24-FEB-2000; 2000US-0184594P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (GLAX ) GLAXO GROUP LTD.  
 PA  
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;  
 PI WPI; 2001-550088/61.  
 XX  
 DR New nucleic acid(s) for regulating the Grb2-related with Insert Domain  
 XX (GRID) gene comprises using antisense and enzymatic nucleic acid  
 PT molecules such as hammerhead ribozymes.  
 PT

XX Claim 4; Page 72; 108pp; English.  
 PS  
 XX The present invention relates to oligonucleotides that downregulate the  
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is  
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful  
 CC for modulating the expression of GRID, to treat conditions such as  
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be  
 CC administered in conjunction with other therapies such as radiation,  
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was  
 CC used to illustrate the invention  
 CC  
 XX Sequence 17 BP; 2 A; 2 C; 9 G; 0 T; 4 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1753 TCCTAAGGCCCACTG 1768  
 DB 17 TCCTAAGGCCCACTG 2  
 RESULT 679  
 ABL46776  
 ID ABL46776 standard; RNA; 17 BP.  
 XX  
 AC ABL46776;  
 XX  
 CC 27-JUN-2003 (first entry)  
 DT  
 XX Human GRID NCH ribozyme substrate oligonucleotide #230.  
 DE  
 KW Human; Grb2-related with Insert Domain; GRID; T-cell;  
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;  
 KW leukaemia; cytostatic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200162911-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 23-FEB-2001; 2001WO-US005957.  
 XX  
 CC 24-FEB-2000; 2000US-0184594P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (GLAX ) GLAXO GROUP LTD.  
 PA  
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;  
 PI WPI; 2001-550088/61.  
 XX  
 DR New nucleic acid(s) for regulating the Grb2-related with Insert Domain  
 XX (GRID) gene comprises using antisense and enzymatic nucleic acid  
 PT molecules such as hammerhead ribozymes.  
 PT  
 XX Claim 4; Page 67; 108pp; English.  
 PS  
 XX The present invention relates to oligonucleotides that downregulate the  
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is  
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful  
 CC for modulating the expression of GRID, to treat conditions such as  
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be  
 CC administered in conjunction with other therapies such as radiation,  
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was  
 CC used to illustrate the invention  
 CC  
 XX Sequence 17 BP; 3 A; 2 C; 7 G; 0 T; 5 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 56.2%; Pred. No. 5.2e+02;

Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1632 GATGGGCTGTAGCA 1647  
 ||:|||| :|||  
 Db 2 GAUGGCAUGUGGCA 17

RESULT 680  
 ABL46486/c  
 ID ABL46486 standard; RNA; 17 BP.  
 XX AC ABL46486;  
 XX DT 27-JUN-2003 (first entry)  
 XX DE Human GRID hammerhead ribozyme substrate oligonucleotide #119.  
 XX KW Human; Grb2-related with Insert Domain; GRID; T-cell;  
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;  
 KW leukaemia; cytostatic; ss.  
 XX OS Homo sapiens.  
 XX PN WO200162911-A2.  
 XX PD 30-AUG-2001.  
 XX PF 23-FEB-2001; 2001WO-US005957.  
 XX PR 24-FEB-2000; 2000US-0184594P.  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 PA (GLAXO) GLAXO GROUP LTD.  
 XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;  
 XX WPI; 2001-550088/61.  
 DR New nucleic acid(s) for regulating the Grb2-related with Insert Domain  
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid  
 PT molecules such as hammerhead ribozymes.  
 XX PS Claim 4; Page 61; 108pp; English.  
 XX CC The present invention relates to oligonucleotides that downregulate the  
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is  
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful  
 CC for modulating the expression of GRID, to treat conditions such as  
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be  
 CC administered in conjunction with other therapies such as radiation,  
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was  
 CC used to illustrate the invention  
 XX SQ Sequence 17 BP; 5 A; 6 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGGC 1736  
 |||:|||||:|||||  
 Db 17 GGAGATGGAAATTGTC 2

RESULT 681  
 ABL92165  
 ID ABL92165 standard; cDNA; 17 BP.  
 XX AC ABL92165;  
 XX DT 30-MAY-2002 (first entry)  
 XX DE Long human Tumour Endothelial Marker SEQ ID NO 331.

XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
 KW psoriasis; ss.  
 XX OS Homo sapiens.  
 XX PN WO200210217-A2.  
 XX PD 07-FEB-2002.  
 XX PF 01-AUG-2001; 2001WO-US024031.  
 XX PR 02-AUG-2000; 2000US-0222599P.  
 PR 11-AUG-2000; 2000US-0224360P.  
 PR 11-APR-2001; 2001US-0282850P.  
 XX PA (UYJO) UNIV JOHNS HOPKINS.  
 XX PI St Croix B, Kinzler KW, Vogelstein B;  
 XX WPI; 2002-291856/33.  
 XX DR An isolated molecule comprising an antibody variable region which  
 PT specifically binds to an extracellular domain of a tumor endothelial  
 PT marker (TEM) protein, useful for inhibiting tumor growth.  
 XX PS Disclosure; Page 22; 331pp; English.  
 XX CC The invention relates to an isolated molecule comprising an antibody  
 CC variable region which specifically binds to an extracellular domain of a  
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,  
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.  
 CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
 CC bearing a vascularised tumour, polycystic kidney disease, diabetic  
 CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
 CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
 CC are disclosed, as are marker oligonucleotide sequences: tumour  
 CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
 CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
 CC (PEM) ABL91903-ABL91995. The present sequence is that of an  
 CC oligonucleotide marker useful to the invention  
 XX SQ Sequence 17 BP; 2 A; 9 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1741 AACTCTCCCTATCCT 1756  
 |||:|||||:|||||  
 Db 2 ACCACTCCCTTCT 17

RESULT 682  
 ABL10216  
 ID ABL10216 standard; DNA; 17 BP.  
 XX AC ABL10216;  
 XX DT 29-MAY-2002 (first entry)  
 XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10208.  
 XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX OS Homo sapiens.

PN WO200192524-A2.  
XX 06-DEC-2001.  
XX 25-MAY-2001; 2001WO-US016981.  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-026860P.  
XX (AEOM-) ABOmica INC.  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
PI WPI; 2002-179446/23.  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX Disclosure; SEQ ID NO 10208; 214pp; English.  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterize and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;  
SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1750 CTATCCTAAAGGCCCA 1765  
Db ||||| |||||  
2 CTATCGGAGGCCCA 17  
RESULT 683  
ABN00537  
ID ABN00537 standard; DNA; 17 BP.  
XX  
AC ABN00537;

XX 29-MAY-2002 (first entry)  
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:529.  
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX Homo sapiens.  
OS WO200192524-A2.  
PN 06-DEC-2001.  
XX 25-MAY-2001; 2001WO-US016981.  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-026860P.  
XX (AEOM-) ABOmica INC.  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX Disclosure; SEQ ID NO 529; 214pp; English.  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterize and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX Sequence 17 BP; 8 A; 4 C; 3 G; 2 T; 0 U; 0 Other;  
SQ Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1646 CAGAAGCAAGCACCA 1661  
 DB 1 CAGATGACAGCATCA 16  
 RESULT 684  
 ABN01271/c  
 ID ABN01271 standard; DNA; 17 BP.  
 AC ABN01271;  
 XX  
 XX 29-MAY-2002 (first entry)  
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1263.  
 DE  
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200192524-A2.  
 XX  
 XX 06-DEC-2001.  
 XX  
 XX 25-MAY-2001; 2001WO-US016981.  
 XX  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX WPI; 2002-179446/23.  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX  
 PS Disclosure; SEQ ID NO 1263; 214pp; English.  
 XX  
 XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 17 BP; 3 A; 3 C; 8 G; 3 T; 0 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1730 GATTGGCTCCCACTC 1745  
 DB 17 GATCGTCCCCCACTC 2  
 RESULT 685  
 ABN01293/c  
 ID ABN01293 standard; DNA; 17 BP.  
 XX  
 AC ABN01293;  
 XX  
 XX 29-MAY-2002 (first entry)  
 DT Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1285.  
 DE  
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 OS Homo sapiens.  
 XX  
 XX WO200192524-A2.  
 PN  
 XX 06-DEC-2001.  
 XX  
 XX 25-MAY-2001; 2001WO-US016981.  
 XX  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX WPI; 2002-179446/23.  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX  
 PS Disclosure; SEQ ID NO 1285; 214pp; English.  
 XX  
 XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 CC  
 CC Sequence 17 BP; 6 A; 1 C; 9 G; 1 T; 0 U; 0 Other;  
 CC  
 CC Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 CC Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 CC Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 CC  
 CC QY 1678 CCTGCTGCTCTCTCCA 1693  
 CC ||||| ||||| |||||  
 CC 17 CCTGCTTCTCTCCCA 2  
 CC  
 CC RESULT 686  
 CC ABN09665/c  
 CC ID ABN09665 standard; DNA; 17 BP.  
 CC AC ABN09665;  
 CC  
 CC DT 29-MAY-2002 (first entry)  
 CC DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9657.  
 CC KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 CC muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 CC skeletal muscle disorder; amplicon; screening; ss.  
 CC OS Homo sapiens.  
 CC PN WO200192524-A2.  
 CC PD 06-DEC-2001.  
 CC PF 25-MAY-2001; 2001WO-US016981.  
 CC PR 26-MAY-2000; 2000US-0207456P.  
 CC PR 21-SEP-2000; 2000US-0234687P.  
 CC PR 27-SEP-2000; 2000US-0236359P.  
 CC PR 04-OCT-2000; 2000GB-00024263.  
 CC PR 30-JAN-2001; 2001WO-US000661.  
 CC PR 30-JAN-2001; 2001WO-US000662.  
 CC PR 30-JAN-2001; 2001WO-US000663.  
 CC PR 30-JAN-2001; 2001WO-US000664.  
 CC PR 30-JAN-2001; 2001WO-US000665.  
 CC PR 30-JAN-2001; 2001WO-US000666.  
 CC PR 30-JAN-2001; 2001WO-US000667.  
 CC PR 30-JAN-2001; 2001WO-US000668.  
 CC PR 05-FEB-2001; 2001US-0266860P.  
 CC (AEOM-) ABOMICA INC.  
 CC Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 CC WPI; 2002-179446/23.  
 CC New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,

PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption/ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX Disclosure; SEQ ID NO 9657; 214pp; English.  
 XX  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 CC  
 CC Sequence 17 BP; 4 A; 4 C; 8 G; 1 T; 0 U; 0 Other;  
 CC  
 CC Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 CC Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 CC Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 CC  
 CC QY 1673 GGACCCCTGGTCTCTC 1688  
 CC ||||| ||||| |||||  
 CC 17 GGACCCCTGGCTCTCTC 2  
 CC  
 CC RESULT 687  
 CC ABN01294/c  
 CC ID ABN01294 standard; DNA; 17 BP.  
 CC AC ABN01294;  
 CC  
 CC DT 29-MAY-2002 (first entry)  
 CC DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1286.  
 CC KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 CC muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 CC skeletal muscle disorder; amplicon; screening; ss.  
 CC OS Homo sapiens.  
 CC PN WO200192524-A2.  
 CC PD 06-DEC-2001.  
 CC PF 25-MAY-2001; 2001WO-US016981.  
 CC PR 26-MAY-2000; 2000US-0207456P.  
 CC PR 21-SEP-2000; 2000US-0234687P.  
 CC PR 27-SEP-2000; 2000US-0236359P.  
 CC PR 04-OCT-2000; 2000GB-00024263.  
 CC PR 30-JAN-2001; 2001WO-US000661.  
 CC PR 30-JAN-2001; 2001WO-US000662.  
 CC PR 30-JAN-2001; 2001WO-US000663.  
 CC PR 30-JAN-2001; 2001WO-US000664.  
 CC PR 30-JAN-2001; 2001WO-US000665.  
 CC PR 30-JAN-2001; 2001WO-US000666.  
 CC PR 30-JAN-2001; 2001WO-US000667.  
 CC PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
XX 05-FEB-2001; 2001US-0266860P.  
PA (AEOM-) AEOMICA INC.  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX Disclosure; SEQ ID NO 1286; 214pp; English.  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterize and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX Sequence 17 BP; 5 A; 1 C; 9 G; 2 T; 0 U; 0 Other;  
XX  
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;  
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1678 CCTGGTGTCTCCGCCA 1693  
Db ||||| ||||| |||||  
16 CCTGCTTCTCCGCCA 1  
RESULT 688  
ABN10217  
ID AEN10217 standard; DNA; 17 BP.  
XX AC AEN10217;  
XX DT 29-MAY-2002 (first entry)  
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10209.  
XX DE Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;  
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
XX KW skeletal muscle disorder; amplicon; screening; ss.  
XX OS Homo sapiens.  
XX PN WO200192524-A2.  
XX PD 06-DEC-2001.  
XX PF 25-MAY-2001; 2001WO-US016981.  
XX PP 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX (AEOM-) AEOMICA INC.  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX Disclosure; SEQ ID NO 10209; 214pp; English.  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterize and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;  
XX  
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;  
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1750 CTATCTCTAAGGCCCA 1765  
Db ||||| ||||| |||||  
1 CTATCCGGAAGCCCA 16  
RESULT 689  
ABN01273/c  
ID AEN01273 standard; DNA; 17 BP.  
XX AC AEN01273;  
XX DT 29-MAY-2002 (first entry)  
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1265.  
XX DE Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;  
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW

KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

XX WO200192524-A2.

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US016981.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024283.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 05-FEB-2001; 2001US-0266860P.

XX PA (AEOM-) AEOMICA INC.

XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX DR WPI; 2002-179446/23.

XX PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,

XX PT or as specific biomolecule capture probes for surface-enhanced laser

XX PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

XX PS Disclosure; SEQ ID NO 1265; 214pp; English.

XX CC The present invention describes a human genome-derived myosin-like

XX CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-

XX CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1

XX CC nucleic acids can be used as probes to detect, characterize and quantify

XX CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to

XX CC provide initial substrates for the recombinant engineering of hGDMPLP-1

XX CC protein variants having desired phenotypic improvements, and for

XX CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be

XX CC used as immunogens to raise antibodies that specifically recognise hGDMPLP

XX CC -1 proteins, as standards in assays used to determine the concentration

XX CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule

XX CC capture probes for surface-enhanced laser desorption ionisation, as

XX CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1

XX CC production, and in vaccines or for replacement therapy. The

XX CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a

XX CC disorder associated with the expression of hGDMPLP-1, in particular heart

XX CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

ABN07992

ID ABN07992 standard; DNA; 17 BP.

XX AC ABN07992;

XX XX 29-MAY-2002 (first entry)

XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7984.

XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;

XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

XX KW skeletal muscle disorder; amplicon; screening; ss.

XX OS Homo sapiens.

XX PN WO200192524-A2.

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US016981.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024283.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 05-FEB-2001; 2001US-0266860P.

XX XX (AEOM-) AEOMICA INC.

XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX DR WPI; 2002-179446/23.

XX PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,

XX PT or as specific biomolecule capture probes for surface-enhanced laser

XX PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

XX PS Disclosure; SEQ ID NO 7984; 214pp; English.

XX CC The present invention describes a human genome-derived myosin-like

XX CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-

XX CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1

XX CC nucleic acids can be used as probes to detect, characterize and quantify

XX CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to

XX CC provide initial substrates for the recombinant engineering of hGDMPLP-1

XX CC protein variants having desired phenotypic improvements, and for

XX CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be

XX CC used as immunogens to raise antibodies that specifically recognise hGDMPLP

XX CC -1 proteins, as standards in assays used to determine the concentration

XX CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule

XX CC capture probes for surface-enhanced laser desorption ionisation, as

XX CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1

XX CC production, and in vaccines or for replacement therapy. The

XX CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a

XX CC disorder associated with the expression of hGDMPLP-1, in particular heart

XX CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

XX CC The present sequence represents an oligomer used in the screening of the

XX CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.

XX CC The sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published\_pct\_sequence

XX SQ Sequence 17 BP; 8 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1729 AGATTGGTCCCACT 1744

Db 16 AGATCGTCCCACT 1

RESULT 690

```
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1646 CAGAAGGCAAGCACCA 1661
Db 2 CAGCAGGAAAACACCA 17

RESULT 691
ABN07993
ID ABN07993 standard; DNA; 17 BP.
XX
AC ABN07993;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7985.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001WO-US000670.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 7985; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
```

```
CC production, and in vaccines or for replacement therapy. The
CC Polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 8 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1646 CAGAAGGCAAGCACCA 1661
Db 1 CAGCAGGAAAACACCA 16

RESULT 692
ABN09667/c
ID ABN09667 standard; DNA; 17 BP.
XX
AC ABN09667;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9659.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 9659; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
```



XX
PI Gu Y.
Ji Y.
Penn SG.
Hanzel DK.
Rank DR.
Chen W.
Shannon ME:

PR 30-JAN-2001; 2001WO-US000665.

```

PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 28-AUG-2001; 2001US-0315676P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhang J;
XX
XX WPI; 2002-479509/51.
XX
XX New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
PT acids encoding the protein, useful for treating subjects having defects
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
PT e.g., liver or bone.
XX
XX Example 2; Page 216; 418pp; English.
XX
XX The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to scan
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)
XX
XX Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1664 CTCACAGCTGGAACCC 1679
DB ||| ||||| |||
2 CTCACAGCTGGAGACC 17

RESULT 695
ABQ63739
ID ABQ63739 standard; DNA; 17 BP.
XX
XX AC ABQ63739;
XX
XX DT 20-AUG-2002 (first entry)
XX
XX DE Human KTOM1a portion (ABQ63232) probe # 452.
XX
XX Human; KTOM1a; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
XX OS Homo sapiens.
XX
XX WO200224750-A2.
XX
XX PD 28-MAR-2002.
XX
XX PF 21-SEP-2001; 2001WO-US029656.
XX
XX 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 28-AUG-2001; 2001US-0315676P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhang J;
XX
XX WPI; 2002-479509/51.
XX
XX New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
PT acids encoding the protein, useful for treating subjects having defects
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
PT e.g., liver or bone.
XX
XX Example 2; Page 216; 418pp; English.
XX
XX The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to scan
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)
XX
XX Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1664 CTCACAGCTGGAACCC 1679
DB ||| ||||| |||
2 CTCACAGCTGGAGACC 17

RESULT 696
ABK13146
ID ABK13146 standard; DNA; 17 BP.
XX
XX AC ABK13146;
XX
XX DT 23-APR-2002 (first entry)
XX
XX DE Oligonucleotide used to randomise amino acid sequence in Env protein.
XX
XX retroviral display library; retrovirus; Env protein; virus; gene therapy;
KW toxic gene delivery; tumour; viral infection; tissue regeneration;
KW receptor binding domain; receptor determining sequence; ss.
XX
XX OS Synthetic.
XX
XX WO200198514-A2.
XX
XX PD 27-DEC-2001.
XX
XX PF 15-JUN-2001; 2001WO-US019296.
XX
XX 16-JUN-2000; 2000US-0212239P.
PR 14-JUN-2001; 2001US-00881572.
XX
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
XX Roth MJ, Bupp K;
PI

```

XX WPI; 2002-147801/19.

XX Novel retroviral display library, useful for isolating a virus that can

PT transfer its nucleic acid to a host cell, i.e. for gene therapy,

PT comprises retroviruses which differ from each other in the Env protein

PT amino acid sequence.

XX Example 1; Fig 8; 59pp; English.

PS This invention relates to a method for creating a retroviral display

XX library, comprising several retroviruses, where each retrovirus in the

CC library differs in relation to other retroviruses in the amino acid

CC sequence of an Env protein and comprises a nucleic acid coding for both

CC the Env protein and a cell-selection marker. The method of the invention

CC is useful for isolating a virus that can transfer its nucleic acid to a

CC host cell. The libraries are useful as pools of viral vehicles from which

CC an appropriate vehicle can be selected to transfer a gene to a host cell.

CC The virus vectors created using the above mentioned methods are useful

CC for gene therapy applications, and can be used to target specific cell

CC types for gene therapy applications and for delivery of toxic genes to

CC tumours or virus infected cells for therapeutic applications. Selected

CC Env variants can also be used to target genes to heart cells to deliver

CC factors which promote tissue regeneration in diseased states. The library

CC allows direct selection of fully functional novel Env proteins. The

CC advantage of this approach over using prescreened ligands with known cell

CC -binding is that it does not require a predetermined conformationally

CC active orientation to fit onto the Env protein and does not necessarily

CC entail foreknowledge of a cell-type specific receptor. The random library

CC method entails minimal disruption of the Env structure due to the precise

CC substitution of the receptor binding domain by random amino acids. Using

CC this technique, more than one million different variant constructs can be

CC screened at a time for gene transfer function. The present sequence

CC represents a synthetic oligonucleotide used to create a randomised amino

CC acid sequence in the Env protein to create the retroviral display library

CC of the invention

XX

SQ Sequence 17 BP; 2 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1673 GGACCTCGGTGCTC 1688

DB 2 GGTCCCGAGGTCTC 17

RESULT 697

AAD42386

XX AAD42386 standard; DNA; 17 BP.

XX

AC AAD42386;

XX

DT 04-NOV-2002 (first entry)

XX

DE A. ochraceus 11 alpha hydroxylase DNA specific primer, 45624-for1.

XX

XX 11 alpha hydroxylase; enzyme; sitosterol; eplerenone; cell therapy;

KW steroid bioconversion; antiinflammatory; antiarthritic; cytostatic;

KW cardiant; cytochrome P450; oxidoreductase; primer; ss.

XX

OS Aspergillus ochraceus.

XX

XX WO200246386-A2.

PN

XX 13-JUN-2002.

XX

XX 26-OCT-2001; 2001WO-US051070.

PF

XX 30-OCT-2000; 2000US-0244300P.

PR

XX (PHAA ) PHARMACIA CORP.

PA

PA (BOLT/) BOLTON S.

PA (CLAY/) CLAYTON R.

PA (EAST/) EASTON A.

PA (ENGEL/) ENGEL L.

PA (MESS/) MESSING D.

XX Bolton S, Clayton R, Easton A, Engel L, Messing D;

PI

XX WPI; 2002-547772/58.

XX

XX New isolated Aspergillus ochraceus 11 alpha-hydroxylase or

PT oxidoreductase, for bioconversion of steroid substances to their 11 alpha

PT hydroxy counterparts in heterologous cells.

XX

XX Example 11; Page 164; 181pp; English.

XX

CC The present invention relates to novel cytochrome P450-like enzyme

CC (Aspergillus ochraceus 11 alpha hydroxylase protein), oxidoreductases and

CC polynucleotides encoding such proteins. Host cells comprising the

CC sequences of the invention are useful for making one or more enzymes from

CC the metabolic pathway for the synthesis of sitosterol to eplerenone. They

CC are useful for selective oxidation of a compound to an hydroxylated

CC product. Compositions of the invention are useful for producing spores

CC from A. ochraceus, A. niger, A. nidulans, Rhizopus oryzae, R. stolonifer,

CC R. arrhizus Trichothecium roseum, Fusarium oxysporum and M. olivaceum

CC etc, preferably to produce spores from A. ochraceus. Sequences of the

CC invention are useful in bioconversion of steroid substances to their 11

CC alpha-hydroxy counterparts. They are also used in cell therapy. The

CC present sequence is A. ochraceus 11 alpha hydroxylase DNA specific

CC primer. This sequence is used in the exemplification of the invention

XX

SQ Sequence 17 BP; 5 A; 3 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1722 GAGATGGAGATTGGCT 1737

DB 1 GAGATCAAGATTGGCT 16

RESULT 698

ABK27291

ID ABK27291 standard; DNA; 17 BP.

XX

AC ABK27291;

XX

DT 09-APR-2002 (first entry)

XX

DE Reduced linolenic acid production genome altering oligonucleotide #187.

XX

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;

KW o-methyl modification; DNA modification; phosphorothioate linkage;

KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;

KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;

KW amino acid over production; herbicide resistance; glyphosate resistance;

KW imidazolone herbicide resistance; sulphonylurea herbicide resistance;

KW porphyrin herbicide resistance; triazine resistance; disease resistance;

KW modified oil production; modified starch production; waxy starch;

KW altered floral morphology; male-sterile plant; albino mutant;

KW modified fatty acid content; reduced palmitate production; albino plant;

KW increased stearate production; reduced linolenic acid production;

KW photosynthetic process.

XX

OS Triticum aestivum.

XX Synthetic.

XX WO200192512-A2.

PN

XX 06-DEC-2001.

PD

XX 01-JUN-2001; 2001WO-US017672.

PF

XX 01-JUN-2000; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 PR 27-MAR-2001; 2001US-00818875.  
 XX  
 PA (UYDE ) UNIV DELAWARE.  
 XX  
 XX Kmiec BB, Gamper HB, Rice MC, Kim J;  
 PI WPI; 2002-106307/14.  
 XX  
 DR New oligonucleotides with modified nuclease-resistant termini, useful for  
 XX creating plants with desired phenotypes, e.g. stress tolerance, improved  
 PT nutritional value, herbicide or disease resistance, or modified oil  
 PT production.  
 PT  
 PT Claim 7; Page 201; 220pp; English.  
 PS  
 XX The invention relates to an oligonucleotide for targeted alteration of a  
 CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of o-methyl modification, an LNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention  
 XX  
 XX Sequence 17 BP; 4 A; 4 C; 8 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1642 GTAGCAGAGGCAAGC 1657  
 Db 2 GGAGCAGTAGGCGAGC 17  
 RESULT 699  
 ABK27292/C  
 ID ABK27292 standard; DNA; 17 BP.  
 XX  
 AC ABK27292;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 XX Reduced linolenic acid production genome altering oligonucleotide #188.  
 DE  
 XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
 KW o-methyl modification; LNA modification; phosphorothioate linkage;  
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
 KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;  
 KW amino acid over production; herbicide resistance; glyphosate resistance;  
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;  
 KW modified oil production; modified starch production; waxy starch;  
 KW altered floral morphology; male-sterile plant; albino mutant;  
 KW modified fatty acid content; reduced palmitate production; albino plant;  
 KW increased stearate production; reduced linolenic acid production;  
 KW

KW photosynthetic process.  
 XX  
 OS Triticum aestivum.  
 OS Synthetic.  
 XX  
 PN WO200192512-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 01-JUN-2001; 2001WO-US017672.  
 XX  
 XX 01-JUN-2000; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 PR 27-MAR-2001; 2001US-00818875.  
 XX  
 XX (UYDE ) UNIV DELAWARE.  
 PA  
 XX Kmiec BB, Gamper HB, Rice MC, Kim J;  
 PI WPI; 2002-106307/14.  
 XX  
 DR New oligonucleotides with modified nuclease-resistant termini, useful for  
 XX creating plants with desired phenotypes, e.g. stress tolerance, improved  
 PT nutritional value, herbicide or disease resistance, or modified oil  
 PT production.  
 PT  
 PT Claim 7; Page 201; 220pp; English.  
 PS  
 XX The invention relates to an oligonucleotide for targeted alteration of a  
 CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of o-methyl modification, an LNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention  
 XX  
 XX Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1642 GTAGCAGAGGCAAGC 1657  
 Db 16 GGAGCAGTAGGCGAGC 1  
 RESULT 700  
 ABV79505  
 ID ABV79505 standard; DNA; 17 BP.  
 XX  
 AC ABV79505;  
 XX  
 DT 03-JAN-2003 (first entry)  
 XX  
 XX Human HTPL scanning oligonucleotide SEQ ID 751.  
 DE Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
 KW

KW human testis expressed Patched like protein; testis; adrenal; liver;  
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.  
 XX Homo sapiens.  
 OS  
 EN EPI229046-A2.  
 XX  
 XX 07-AUG-2002.  
 XX  
 XX 28-JAN-2002; 2002EP-000011167.  
 XX  
 XX 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 09-OCT-2001; 2001US-0327898P.  
 XX  
 PA (ABOM-) ABOMICA INC.  
 XX  
 XX Zhan J;  
 PI  
 XX WPI; 2002-676582/73.  
 DR  
 XX  
 PT Novel isolated human testis expressed Patched like protein (HTPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPL.  
 XX  
 XX Example 2; Page 162; 718pp; English.  
 PS  
 XX The present invention relates to human testis expressed Patched like  
 CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was  
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention  
 XX  
 XX Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1662 GGCTCACAGCTGGAC 1677  
 DB | | | | | | | | | | | | | | | | | | | |  
 2 GACTCACTGCTGGACC 17  
 RESULT 701  
 ABV79023  
 ID ABV79023 standard; DNA; 17 BP.  
 XX  
 AC ABV79023;  
 XX  
 XX 03-JAN-2003 (first entry)  
 XX  
 DE Human HTPL scanning oligonucleotide SEQ ID 269.

XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
 KW human testis expressed Patched like protein; testis; adrenal; liver;  
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.  
 XX Homo sapiens.  
 OS  
 EN EPI229046-A2.  
 XX  
 XX 07-AUG-2002.  
 XX  
 XX 28-JAN-2002; 2002EP-000011167.  
 XX  
 XX 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 09-OCT-2001; 2001US-0327898P.  
 XX  
 PA (ABOM-) ABOMICA INC.  
 XX  
 XX Zhan J;  
 PI  
 XX WPI; 2002-676582/73.  
 DR  
 XX  
 PT Novel isolated human testis expressed Patched like protein (HTPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPL.  
 XX  
 XX Example 2; Page 99; 718pp; English.  
 PS  
 XX The present invention relates to human testis expressed Patched like  
 CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was  
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention  
 XX  
 XX Sequence 17 BP; 2 A; 7 C; 5 G; 3 T; 0 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1671 CTGGAACCTGCTGTC 1686  
 DB | | | | | | | | | | | | | | | | | | | |  
 2 CAGGACCCCTGGCGTC 17  
 RESULT 702  
 ABV79024  
 ID ABV79024 standard; DNA; 17 BP.  
 XX  
 AC ABV79024;  
 XX  
 XX 03-JAN-2003 (first entry)  
 XX  
 DE Human HTPL scanning oligonucleotide SEQ ID 269.

XX DE Human HTPL scanning oligonucleotide SEQ ID 270.

XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;

XX KW human testis expressed Patched like protein; testis; adrenal; liver;

XX KW male germ cell development; bone marrow; brain; kidney; lung; placenta;

XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

OS Homo sapiens.

XX PN BP1229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX DR WPI; 2002-676582/73.

XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful

XX PT for identifying agonist and antagonist and specific binding partners, and

XX PT for treating subjects having defects in HTPL.

XX PS Example 2; Page 99; 718pp; English.

XX CC The present invention relates to human testis expressed Patched like

XX CC protein (HTPL, see ABV78759 to ABV78762 and ABP38519 to ABP38520). HTPL

XX CC has two isoforms, with a few single base pair differences between the

XX CC two. One of the single base pair changes introduces a premature stop

XX CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL

XX CC shares an overall structure organisation with the Patched protein. The

XX CC shared structural features strongly imply that HTPL plays a role similar

XX CC to that of Patched, and is a potential tumour suppressor. HTPL is

XX CC important in regulating male germ cell development, and the HTPL gene was

XX CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are

XX CC useful for diagnosing a disorder caused by mutation in HTPL, and in

XX CC therapy and manufacture of a medicament for treatment or prevention of

XX CC such disorder associated with decreased expression or activity of human

XX CC HTPL. Such disorders include disorders of testis, or adrenal, adult and

XX CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,

XX CC skeletal muscle or colon function. HTPL proteins and nucleic acids are

XX CC clinically useful diagnostic markers and potential therapeutic agents for

XX CC male infertility and cancer. The present oligonucleotide was used in an

XX CC example from the invention

XX SQ Sequence 17 BP; 2 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1671 CTGGACCCCTGGTGC 1686

DB 1 CAGGACCCCTGGTGC 16

RESULT 703

ABK19420

ID ABK19420 standard; RNA; 17 BP.

XX AC

ABK19420;

XX DT 09-APR-2002 (first entry)

XX DE Human ERG Amberzyme target sequence Seq ID No 2067.

XX KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;

XX KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;

XX KW vulvar; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;

XX KW tumour angiogenesis; diabetic retinopathy; macular degeneration;

XX KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;

XX KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;

XX KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;

XX KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;

XX KW amberzyme.

XX OS Homo sapiens.

XX PN WO200188124-A2.

XX PD 22-NOV-2001.

XX PF 16-MAY-2001; 2001WO-US015866.

XX PR 16-MAY-2000; 2000US-00572021.

XX PR (RIBO-) RIBOZYME PHARM INC.

XX PA (GLAX ) GLAXO GROUP LTD.

XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;

XX DR WPI; 2002-082995/11.

XX PT Novel polynucleotide which down regulates expression of Ets-related gene,

XX PT useful for treating cancer, diabetic retinopathy, macular degeneration,

XX PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

XX PS Claim 4; Page 128; 149pp; English.

XX CC The invention relates to a nucleic acid molecule (I) which down regulates

XX CC expression of an Ets-related gene (ERG). (I) is useful for treating

XX CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,

XX CC tumour angiogenesis, diabetic retinopathy, macular degeneration,

XX CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca

XX CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge

XX CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu

XX CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for

XX CC treating a patient having a condition associated with the level of ERG,

XX CC by contacting cells of the patient with (I) under conditions suitable for

XX CC the treatment. The method comprises the use of one or more therapies

XX CC under conditions suitable for the treatment. Leukaemia or tumour

XX CC angiogenesis is treated by administering (I) to the patient in

XX CC conjunction with one or more of other therapies such as radiation or

XX CC chemotherapy treatment. (I) is useful for reducing ERG activity in a

XX CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of

XX CC ERG gene, by contacting (I) with RNA, in the presence of a divalent

XX CC cation such as Mg<sup>2+</sup>. (I) is useful for diagnosis of conditions and

XX CC diseases related to the expression of ERG, and as diagnostic tool to

XX CC examine genetic drift and mutations within diseased cells or to detect

XX CC the presence of ERG RNA in a cell. (I) is useful for specifically

XX CC targeting genes that share homology with ERG gene or ERG fusion genes.

XX CC ABK17354-ABK22719 represent nucleic acids, including antisense and

XX CC enzymatic nucleic acid molecules which regulate expression of ERG, and

XX CC related PCR primers of the invention

XX SQ Sequence 17 BP; 7 A; 1 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 68.8%; Pred. No. 5.2e+02;

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1710 GTTAGAGTACGAGA 1725

DB 2 GUTAGGAGAAAGGACA 17

RESULT 704  
ABK19419  
ID ABK19419 standard; RNA; 17 BP.  
XX  
AC ABK19419;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE Human ERG Amberzyme target sequence Seq ID No 2066.  
XX  
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;  
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;  
KW tumour; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;  
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;  
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;  
KW angiofibroma of tuberosus scleriosis; port-wine stain; wound healing;  
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;  
KW Oster-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;  
KW  
XX  
OS Homo sapiens.  
XX  
PN WO200198124-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 16-MAY-2001; 2001WO-US015866.  
XX  
PR 16-MAY-2000; 2000US-00572021.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (GLAXO) GLAXO GROUP LTD.  
XX  
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;  
XX  
XX WPI; 2002-082995/11.  
XX  
XX Novel polynucleotide which down regulates expression of Ets-related gene,  
XX useful for treating cancer, diabetic retinopathy, macular degeneration,  
XX arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.  
XX  
XX Claim 4; Page 128; 149pp; English.  
XX  
CC The invention relates to a nucleic acid molecule (I) which down regulates  
CC expression of an Ets-related gene (ERG). (I) is useful for treating  
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,  
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,  
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca  
CC vulgaris, angiofibroma of tuberosus scleriosis, port-wine stains, Sturge  
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu  
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for  
CC treating a patient having a condition associated with the level of ERG  
CC by contacting cells of the patient with (I) under conditions suitable for  
CC the treatment. The method comprises the use of one or more therapies  
CC under conditions suitable for the treatment. Leukaemia or tumour  
CC angiogenesis is treated by administering (I) to the patient in  
CC conjunction with one or more of other therapies such as radiation or  
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a  
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of  
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent  
CC cation such as Mg<sup>2+</sup>. (I) is useful for diagnosis of conditions and  
CC diseases related to the expression of ERG, and as diagnostic tool to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of ERG RNA in a cell. (I) is useful for specifically  
CC targeting genes that share homology with ERG gene or ERG fusion genes.  
CC ABK17354-ABK22719 represent nucleic acids, including antisense and  
CC enzymatic nucleic acid molecules which regulate expression of ERG, and  
XX related PCR primers of the invention  
XX  
XX Sequence 17 BP; 7 A; 0 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 68.8%; Pred. NO. 5.2e+02;  
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1708 GGGTTAGGAGTACGGA 1723  
Db |:::|||||  
2 GUGUAGGAGGAAGGA 17  
  
RESULT 705  
ABV90072  
ID ABV90072 standard; DNA; 17 BP.  
XX  
AC ABV90072;  
XX  
DT 23-DEC-2002 (first entry)  
XX  
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 785.  
XX  
KW Human; POSHL1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
KW gene therapy; transgenic; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1239051-A2.  
XX  
PD 11-SEP-2002.  
XX  
PF 28-JAN-2002; 2002EP-00001165.  
XX  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-00864761.  
PR 10-OCT-2001; 2001US-0328205P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
XX Shannon M;  
XX  
XX WPI; 2002-684061/74.  
XX  
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
XX -1, useful for treating disorders associated with decreased expression or  
XX activity of human POSHL1.  
XX  
XX Example 2; SEQ ID NO 785; 60pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated SH3 domain (POSH)-like signalling  
CC protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino  
CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),  
CC (SI) having 95% deviations, especially conservative substitutions or a  
CC fragment of the sequences comprising at least 8 contiguous amino acids.  
CC Human POSHL1 is a proto-oncogene/oncogene product that functions as an  
CC adaptor protein that interacts with Rho family small GTPases as well as  
CC downstream components of the signal transduction pathway. (I) is useful  
CC for identifying a specific binding partner. (I) and nucleic acids (II)  
CC encoding (I) are useful for diagnosing, monitoring disease and treating  
CC caused by altered expression of human POSHL1 including diagnosing and  
CC treating cancer, they are useful in the development of vaccines and (II) is  
CC useful in gene therapy. (II) is useful for constructing microarrays which  
CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present sequence is that of a scanning oligonucleotide useful in examples  
CC of the invention. Note: The present sequence did not form part of the  
CC printed specification, but is based on sequence information supplied to  
CC Derwent by the European Patent Office

XX SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1691 CCAGCGTGGTGAAGT 1706  
|||||  
Db 2 CCAGTCCGTGAAGT 17

RESULT 706  
ABV91247  
ID ABV91247 standard; DNA; 17 BP.  
XX AC ABV91247;  
XX DT 23-DEC-2002 (first entry)  
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1960.  
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
KW gene therapy; transgenic; ss.  
XX OS Homo sapiens.  
XX XN EP1239051-A2.  
XX PD 11-SEP-2002.  
XX PF 28-JAN-2002; 2002EP-00001165.  
XX PR 30-JAN-2001; 2001WO-US000663.  
XX PR 30-JAN-2001; 2001WO-US000664.  
XX PR 30-JAN-2001; 2001WO-US000665.  
XX PR 30-JAN-2001; 2001WO-US000666.  
XX PR 30-JAN-2001; 2001WO-US000667.  
XX PR 30-JAN-2001; 2001WO-US000668.  
XX PR 30-JAN-2001; 2001WO-US000669.  
XX PR 30-JAN-2001; 2001WO-US000670.  
XX PR 23-MAY-2001; 2001US-00864761.  
XX PR 10-OCT-2001; 2001US-0328205P.  
XX PA (AEOM-) AEOMICA INC.  
XX PI Shannon M;  
XX DR WPI; 2002-684061/74.  
XX PT Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
PT -1, useful for treating disorders associated with decreased expression or  
PT activity of human POSHL1.  
XX Example 2; SEQ ID NO 1960; 60pp + Sequence Listing; English.  
XX The invention relates to an isolated SH3 domain (POSH)-like signalling  
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
CC acids (SI, AB83999), a sequence having 65% sequence identity to (SI),  
CC (SI) having 95% deviations, especially conservative substitutions or a  
CC fragment of the sequences comprising at least 8 contiguous amino acids.  
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
CC adaptor protein that interacts with Rho family small GTPases as well as  
CC downstream components of the signal transduction pathway. (I) is useful  
CC for identifying a specific binding partner. (I) and nucleic acids (II)  
CC encoding (I) are useful for diagnosing, monitoring disease and treating  
CC caused by altered expression of human POSHL1 including diagnosing and  
CC treating cancer, they useful in the development of vaccines and (II) is  
CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present sequence is that of a scanning oligonucleotide useful in examples

CC of the invention. Note: The present sequence did not form part of the  
CC printed specification, but is based on sequence information supplied to  
CC Derwent by the European Patent Office  
XX SQ Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1724 GATGGAGATTGGTCC 1739  
|||||  
Db 1 GGTGGAGATGGGTCC 16

RESULT 707  
ABV90073  
ID ABV90073 standard; DNA; 17 BP.  
XX AC ABV90073;  
XX DT 23-DEC-2002 (first entry)  
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 786.  
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
KW gene therapy; transgenic; ss.  
XX OS Homo sapiens.  
XX XN EP1239051-A2.  
XX PD 11-SEP-2002.  
XX PF 28-JAN-2002; 2002EP-00001165.  
XX PR 30-JAN-2001; 2001WO-US000663.  
XX PR 30-JAN-2001; 2001WO-US000664.  
XX PR 30-JAN-2001; 2001WO-US000665.  
XX PR 30-JAN-2001; 2001WO-US000666.  
XX PR 30-JAN-2001; 2001WO-US000667.  
XX PR 30-JAN-2001; 2001WO-US000668.  
XX PR 30-JAN-2001; 2001WO-US000669.  
XX PR 30-JAN-2001; 2001WO-US000670.  
XX PR 23-MAY-2001; 2001US-00864761.  
XX PR 10-OCT-2001; 2001US-0328205P.  
XX PA (AEOM-) AEOMICA INC.  
XX PI Shannon M;  
XX DR WPI; 2002-684061/74.  
XX PT Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
PT -1, useful for treating disorders associated with decreased expression or  
PT activity of human POSHL1.  
XX Example 2; SEQ ID NO 786; 60pp + Sequence Listing; English.  
XX The invention relates to an isolated SH3 domain (POSH)-like signalling  
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
CC acids (SI, AB83999), a sequence having 65% sequence identity to (SI),  
CC (SI) having 95% deviations, especially conservative substitutions or a  
CC fragment of the sequences comprising at least 8 contiguous amino acids.  
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
CC adaptor protein that interacts with Rho family small GTPases as well as  
CC downstream components of the signal transduction pathway. (I) is useful  
CC for identifying a specific binding partner. (I) and nucleic acids (II)  
CC encoding (I) are useful for diagnosing, monitoring disease and treating  
CC caused by altered expression of human POSHL1 including diagnosing and  
CC treating cancer, they useful in the development of vaccines and (II) is  
CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present sequence is that of a scanning oligonucleotide useful in examples



CC caused by altered expression of human POSHL1 including diagnosing and  
CC treating cancer, they useful in the development of vaccines and (II) is  
CC useful in gene therapy. (II) is useful for constructing microarrays which  
CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present sequence is that of a scanning oligonucleotide useful in examples  
CC of the invention. Note: The present sequence did not form part of the  
CC printed specification, but is based on sequence information supplied to  
CC Derwent by the European Patent Office

XX  
SQ Sequence 17 BP; 1 A; 8 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1671 CTGGACCCCTGGTCTC 1686  
Db 2 CCGGAGCCCTGGTCTC 17

RESULT 709  
ABV91245  
ID ABV91245 standard; DNA; 17 BP.  
XX AC ABV91245;  
XX DT 23-DEC-2002 (first entry)  
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1958.  
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
XX KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
XX KW gene therapy; transgenic; ss.  
XX OS Homo sapiens.  
XX PN EP1239051-A2.  
XX PD 11-SEP-2002.  
XX PF 28-JAN-2001; 2002EP-00001165.  
XX PR 30-JAN-2001; 2001WO-US000663.  
XX PR 30-JAN-2001; 2001WO-US000664.  
XX PR 30-JAN-2001; 2001WO-US000665.  
XX PR 30-JAN-2001; 2001WO-US000666.  
XX PR 30-JAN-2001; 2001WO-US000667.  
XX PR 30-JAN-2001; 2001WO-US000668.  
XX PR 30-JAN-2001; 2001WO-US000669.  
XX PR 30-JAN-2001; 2001WO-US000670.  
XX PR 23-MAY-2001; 2001US-00864761.  
XX PR 10-OCT-2001; 2001US-0328205P.  
XX PA (AEOM-) AEOMICA INC.  
XX PI Shannon M;  
XX WPI; 2002-684061/74.  
XX DR Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
XX PT -1, useful for treating disorders associated with decreased expression or  
XX PT activity of human POSHL1.  
XX PS Example 2; SEQ ID NO 1958; 60pp + Sequence Listing; English.  
XX The invention relates to an isolated SH3 domain (POSH)-like signalling  
XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
XX acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),  
XX (S1) having 95% deviations, especially conservative substitutions or a  
XX fragment of the sequences comprising at least 8 contiguous amino acids.  
XX Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
XX adaptor protein that interacts with Rho family small GTPases as well as  
XX downstream components of the signal transduction pathway. (I) is useful  
XX for identifying a specific binding partner. (II) and nucleic acids (II)  
XX encoding (I) are useful for diagnosing, monitoring disease and treating

CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present sequence is that of a scanning oligonucleotide useful in examples  
CC of the invention. Note: The present sequence did not form part of the  
CC printed specification, but is based on sequence information supplied to  
CC Derwent by the European Patent Office

XX  
SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1691 CCAGCTGGTGGAGT 1706  
Db 1 CCAGCTGGTGGAGT 16

RESULT 708  
ABV90892  
ID ABV90892 standard; DNA; 17 BP.  
XX AC ABV90892;  
XX DT 23-DEC-2002 (first entry)  
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1605.  
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
XX KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
XX KW gene therapy; transgenic; ss.  
XX OS Homo sapiens.  
XX PN EP1239051-A2.  
XX PD 11-SEP-2002.  
XX PF 28-JAN-2001; 2002EP-00001165.  
XX PR 30-JAN-2001; 2001WO-US000663.  
XX PR 30-JAN-2001; 2001WO-US000664.  
XX PR 30-JAN-2001; 2001WO-US000665.  
XX PR 30-JAN-2001; 2001WO-US000666.  
XX PR 30-JAN-2001; 2001WO-US000667.  
XX PR 30-JAN-2001; 2001WO-US000668.  
XX PR 30-JAN-2001; 2001WO-US000669.  
XX PR 30-JAN-2001; 2001WO-US000670.  
XX PR 23-MAY-2001; 2001US-00864761.  
XX PR 10-OCT-2001; 2001US-0328205P.  
XX PA (AEOM-) AEOMICA INC.  
XX PI Shannon M;  
XX WPI; 2002-684061/74.  
XX DR Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
XX PT -1, useful for treating disorders associated with decreased expression or  
XX PT activity of human POSHL1.  
XX PS Example 2; SEQ ID NO 1605; 60pp + Sequence Listing; English.  
XX The invention relates to an isolated SH3 domain (POSH)-like signalling  
XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
XX acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),  
XX (S1) having 95% deviations, especially conservative substitutions or a  
XX fragment of the sequences comprising at least 8 contiguous amino acids.  
XX Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
XX adaptor protein that interacts with Rho family small GTPases as well as  
XX downstream components of the signal transduction pathway. (I) is useful  
XX for identifying a specific binding partner. (II) and nucleic acids (II)  
XX encoding (I) are useful for diagnosing, monitoring disease and treating

CC downstream components of the signal transduction pathway. (I) is useful  
 CC for identifying a specific binding partner. (II) and nucleic acids (II)  
 CC encoding (I) are useful for diagnosing, monitoring disease and treating  
 CC caused by altered expression of human POSHL1 including diagnosing and  
 CC treating cancer, they are useful in the development of vaccines and (II) is  
 CC useful in gene therapy. (II) is useful for constructing microarrays which  
 CC are useful for measuring and for surveying gene expression and creating  
 CC transgenic non-human animals capable of producing the proteins. The  
 CC present sequence is that of a scanning oligonucleotide useful in examples  
 CC of the invention. Note: The present sequence did not form part of the  
 CC printed specification, but is based on sequence information supplied to  
 CC Derwent by the European Patent Office  
 CC  
 CC Sequence 17 BP; 2 A; 1 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1696 GTGGTGGAGTGGGT 1711  
 Db 1 GTGGTGGAGTGGGT 16

RESULT 710  
 ABV91051/c  
 ID ABV91051 standard; DNA; 17 BP.

AC ABV91051;

XX 23-DEC-2002 (first entry)

DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1764.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
 KW gene therapy; transgenic; ss.

XX Homo sapiens.

XX EP1239051-A2.

XX 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 23-MAY-2001; 2001WO-US000670.

XX 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.

XX Shannon M;

XX WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL

XX -1, useful for treating disorders associated with decreased expression or

XX activity of human POSHL1.

XX Example 2; SEQ ID NO 1764; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling

XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino

XX acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),

XX (SI) having 95% deviations, especially conservative substitutions or a

CC fragment of the sequences comprising at least 8 contiguous amino acids.  
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
 CC adaptor protein that interacts with Rho family small GTPases as well as  
 CC downstream components of the signal transduction pathway. (I) is useful  
 CC for identifying a specific binding partner. (II) and nucleic acids (II)  
 CC encoding (I) are useful for diagnosing, monitoring disease and treating  
 CC caused by altered expression of human POSHL1 including diagnosing and  
 CC treating cancer, they are useful in the development of vaccines and (II) is  
 CC useful in gene therapy. (II) is useful for constructing microarrays which  
 CC are useful for measuring and for surveying gene expression and creating  
 CC transgenic non-human animals capable of producing the proteins. The  
 CC present sequence is that of a scanning oligonucleotide useful in examples  
 CC of the invention. Note: The present sequence did not form part of the  
 CC printed specification, but is based on sequence information supplied to  
 CC Derwent by the European Patent Office  
 CC  
 CC Sequence 17 BP; 5 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1748 CCTATCTCTAAAG3CC 1763  
 Db 16 CCTGTCTCTAAAGTCC 1

RESULT 711

ID ABV91071/c

XX ABV91071 standard; DNA; 17 BP.

XX AC ABV91071;

XX 23-DEC-2002 (first entry)

DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1784.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
 KW gene therapy; transgenic; ss.

XX Homo sapiens.

XX EP1239051-A2.

XX 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 23-MAY-2001; 2001WO-US000670.

XX 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.

XX Shannon M;

XX WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL

XX -1, useful for treating disorders associated with decreased expression or

XX activity of human POSHL1.

XX Example 2; SEQ ID NO 1784; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling



PT -1, useful for treating disorders associated with decreased expression or  
PT activity of human POSHL1.  
PS Example 2; SEQ ID NO 1609; 60pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated SH3 domain (POSH)-like signalling  
CC protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino  
CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),  
CC (SI) having 95% deviations, especially conservative substitutions or a  
CC fragment of the sequences comprising at least 8 contiguous amino acids.  
CC Human POSHL1 is a proto-oncogene/oncogene product that functions as an  
CC adaptor protein that interacts with Rho family small GTPases as well as  
CC downstream components of the signal transduction pathway. (I) is useful  
CC for identifying a specific binding partner. (I) and nucleic acids (II)  
CC encoding (I) are useful for diagnosing, monitoring disease and treating  
CC caused by altered expression of human POSHL1 including diagnosing and  
CC treating cancer, they useful in the development of vaccines and (II) is  
CC useful in gene therapy. (II) is useful for constructing microarrays which  
CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present sequence is that of a scanning oligonucleotide useful in examples  
CC of the invention. Note: The present sequence did not form part of the  
CC printed specification, but is based on sequence information supplied to  
CC Derwent by the European Patent Office  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1674 GAACCTGGTGTCTCC 1699  
Db 1 GAGCCCTGGTCTCTAC 16  
RESULT 714  
ABV90900  
ID ABV90900 standard; DNA; 17 BP.  
AC ABV90900;  
XX  
XX 23-DEC-2002 (first entry)  
DT Human POSHL1 scanning oligonucleotide SEQ ID NO 1613.  
DE Human; POSHL1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
KW gene therapy; transgenic; ss.  
XX Homo sapiens.  
OS EP1239051-A2.  
XX  
XX 11-SEP-2002.  
PD  
XX 28-JAN-2002; 2002EP-00001165.  
PF 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-00864761.  
PR 10-OCT-2001; 2001US-0328205P.  
XX (AEOM-) AEOMICA INC.  
PA Shannon M;  
PI

DR WPI; 2002-684061/74.  
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
PT -1, useful for treating disorders associated with decreased expression or  
PT activity of human POSHL1.  
XX  
XX Example 2; SEQ ID NO 1613; 60pp + Sequence Listing; English.  
PS  
XX The invention relates to an isolated SH3 domain (POSH)-like signalling  
CC protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino  
CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),  
CC (SI) having 95% deviations, especially conservative substitutions or a  
CC fragment of the sequences comprising at least 8 contiguous amino acids.  
CC Human POSHL1 is a proto-oncogene/oncogene product that functions as an  
CC adaptor protein that interacts with Rho family small GTPases as well as  
CC downstream components of the signal transduction pathway. (I) is useful  
CC for identifying a specific binding partner. (I) and nucleic acids (II)  
CC encoding (I) are useful for diagnosing, monitoring disease and treating  
CC caused by altered expression of human POSHL1 including diagnosing and  
CC treating cancer, they useful in the development of vaccines and (II) is  
CC useful in gene therapy. (II) is useful for constructing microarrays which  
CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present sequence is that of a scanning oligonucleotide useful in examples  
CC of the invention. Note: The present sequence did not form part of the  
CC printed specification, but is based on sequence information supplied to  
CC Derwent by the European Patent Office  
XX  
SQ Sequence 17 BP; 3 A; 8 C; 2 G; 4 T; 0 U; 0 Other;  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1678 CCTGGTGTCTCTCTCA 1693  
Db 1 CCTGGTGTCTCTACCA 16  
RESULT 715  
ABV91072/c  
ID ABV91072 standard; DNA; 17 BP.  
AC ABV91072;  
XX  
XX 23-DEC-2002 (first entry)  
DT Human POSHL1 scanning oligonucleotide SEQ ID NO 1785.  
DE Human; POSHL1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
KW gene therapy; transgenic; ss.  
XX Homo sapiens.  
OS EP1239051-A2.  
XX  
XX 11-SEP-2002.  
PD  
XX 28-JAN-2002; 2002EP-00001165.  
PF 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-00864761.  
PR 10-OCT-2001; 2001US-0328205P.  
XX (AEOM-) AEOMICA INC.  
PA

```
XX
PI Shannon M;
XX
DR WPI; 2002-684061/74.
XX
XX
PT Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
PS Example 2; SEQ ID NO 1785; 60pp + Sequence Listing; English.
XX
CC The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, AB883999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;
XX
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1743 CTCCTCCCTATCTCTAA 1758
Db ||||| |||||
16 CTCGCCCTTCGGAA 1
RESULT 716
ABV91244
ID ABV91244 standard; DNA; 17 BP.
XX
XX ABV91244;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1957.
XX
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
XX
XX Homo sapiens.
XX
XX EP1239051-A2.
XX
XX 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 23-MAY-2001; 2001US-00864761.
PI Shannon M;
XX
DR WPI; 2002-684061/74.
XX
XX
PT Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
PS Example 2; SEQ ID NO 1957; 60pp + Sequence Listing; English.
XX
CC The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, AB883999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 2 A; 0 C; 11 G; 4 T; 0 U; 0 Other;
XX
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1696 GTGGTGGAGTTGGGT 1711
Db ||||| |||||
2 GTGGTGGAGATGGGT 17
RESULT 717
ABV91246
ID ABV91246 standard; DNA; 17 BP.
XX
XX ABV91246;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1959.
XX
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
XX
XX Homo sapiens.
XX
XX EP1239051-A2.
XX
XX 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
```



PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-00864761.  
PR 10-OCT-2001; 2001US-0328205P.  
XX  
XX (AEOM-) AEOMICA INC.  
XX Shannon M;  
XX WPI; 2002-684061/74.  
XX  
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
PT -1, useful for treating disorders associated with decreased expression or  
PT activity of human POSHL.  
XX  
XX Example 2; SEQ ID NO 1611; 60pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated SH3 domain (POSH)-like signalling  
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
CC acids (S1, AB883999), a sequence having 65% sequence identity to (S1),  
CC (S1) having 95% deviations, especially conservative substitutions or a  
CC fragment of the sequences comprising at least 8 contiguous amino acids.  
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
CC adaptor protein that interacts with Rho family small GTPases as well as  
CC downstream components of the signal transduction pathway. (I) is useful  
CC for identifying a specific binding partner. (I) and nucleic acids (II)  
CC encoding (I) are useful for diagnosing, monitoring disease and treating  
CC caused by altered expression of human POSHL1 including diagnosing and  
CC treating cancer, they useful in the development of vaccines and (II) is  
CC useful in gene therapy. (II) is useful for constructing microarrays which  
CC are useful for measuring and for surveying gene expression and creating  
CC transgenic non-human animals capable of producing the proteins. The  
CC present invention is that of a scanning oligonucleotide useful in examples  
CC of the invention. Note: The present sequence did not form part of the  
CC printed specification, but is based on sequence information supplied to  
CC Derwent by the European Patent Office  
XX  
XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
XX 1677 CCTGTGTCTCTCTCC 1692  
Db 2 CCTGTGTCTCTACAC 17  
XX  
RESULT 720  
ABL30789  
ID ABL30789 standard; DNA; 17 BP.  
XX  
XX ABL30789;  
XX  
XX 21-MAR-2002 (first entry)  
XX  
XX Human HLA genotyping oligonucleotide SEQ ID NO 278.  
XX  
XX Human; human leukocyte antigen; HLA; genotype; polymorphism;  
KW immunogenetic; transplantation; genetic disease; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200192572-A1.  
XX  
XX 06-DEC-2001.  
XX  
XX

PF 01-JUN-2001; 2001WO-JP004662.  
XX  
XX 01-JUN-2000; 2000JP-00164798.  
XX  
XX (NISN) NISSHINBO IND INC.  
PA (SYST-) SYSTEM RES INC.  
XX  
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;  
PI WPI; 2002-122074/16.  
XX  
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of  
PT individuals e.g. by determining immunogenetic differences when  
PT transplanting them.  
XX  
XX Claim 10; Page 146; 345pp; Japanese.  
XX  
XX The invention relates to a typing kit for judging human leukocyte antigen  
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base  
CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of  
CC genes e.g. belonging to HLA class I antigens on human genome and  
CC containing gene polymorphisms as alloantigens have been immobilised as  
CC primers for amplification of cleaved nucleic acids relating to gene  
CC polymorphisms. The method is useful for judging HLA genotypes of  
CC individuals by determining immunogenetic differences before transplanting  
CC between them, providing genetic information to decide compatibility of  
CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,  
CC pancreas, Langerhans islet in pancreas and cornea, susceptibility  
CC diagnosis of genetic diseases and identifying individuals  
XX  
XX Sequence 17 BP; 5 A; 2 C; 6 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
XX 1716 ACTACGGAGTGTGAGA 1731  
Db 2 ACTACGGAGTGTGTGA 17  
XX  
RESULT 721  
ABL31672/C  
ID ABL31672 standard; DNA; 17 BP.  
XX  
XX ABL31672;  
XX  
XX 21-MAR-2002 (first entry)  
XX  
XX Human HLA genotyping oligonucleotide SEQ ID NO 1161.  
XX  
XX Human; human leukocyte antigen; HLA; genotype; polymorphism;  
KW immunogenetic; transplantation; genetic disease; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200192572-A1.  
XX  
XX 06-DEC-2001.  
XX  
XX 01-JUN-2001; 2001WO-JP004662.  
XX  
XX 01-JUN-2000; 2000JP-00164798.  
XX  
XX (NISN) NISSHINBO IND INC.  
PA (SYST-) SYSTEM RES INC.  
XX  
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;  
PI WPI; 2002-122074/16.  
XX  
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of  
PT individuals e.g. by determining immunogenetic differences when

The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic

The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or



CC	determining whether a subject has a genetic deficiency for metabolising a
CC	drug, evaluating therapy with a drug metabolised by P450 CYP2D6, and
CC	determining if an individual is susceptible to being a poor metaboliser
CC	of drugs. The nucleic acids are useful as probes or primers for
CC	determining whether a subject has a genetic deficiency for metabolising
CC	drugs that are substrates of P450 CYP2D6. The methods are useful for
CC	determining if a subject has or is at risk of developing a drug
CC	sensitivity condition or disorder that is associated with an aberrant
CC	CYP2D6 activity, e.g. an aberrant level of a CYP2D6 protein or an
CC	aberrant CYP2D6 bioactivity. The methods are also useful in selecting the
CC	appropriate drugs or determining the course of treatment to administer to
CC	a subject to treat cardiovascular or psychiatric disorders, or for
CC	treating a subject with a drug sensitivity or disorder associated with a
CC	specific allelic variant of a polymorphic region of the CYP2D6 gene. The
CC	specificities are useful for monitoring CYP2D6 protein levels in an
CC	individual for determining whether a subject has a disease or conditions
CC	associated with an aberrant CYP2D6 protein level. The gene is located on
CC	human chromosome 22. The present sequence is an allele specific
CC	oligonucleotide (ASO) probe used to detect the wild-type CYP2D6 gene at
CC	polymorphic site 5816
XX	
SQ	Sequence 17 BP; 2 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
	Query Match 8.1%; Score 11.2; DB 1; Length 17;
	Best Local Similarity 81.2%; Pred.No. 5.2e+02;
	Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1655 AGCACAGGCTCACAG 1670
Db	 17 AGCACAAAGTCTATAG 2
RESULT 725	
ACA61317	
ID	ACA61317 standard; DNA; 17 BP.
XX	
AC	ACA61317;
XX	
DT	16-JUL-2003 (first entry)
XX	
DE	Human cytochrome p450 gene CYP2D6, ASO probe WT C5816-3'.
KW	Human; ss; cytochrome P450; CYP2D6; chromosome 22; probe; ASO;
KW	drug metabolism; cardiovascular disorder; psychiatric disorder;
KW	drug sensitivity; allele specific oligonucleotide.
XX	
OS	Homo sapiens.
PX	
PN	EP1281755-A2.
XX	
PD	05-FEB-2003.
XX	
PF	16-JUL-2002; 2002EP-00254972.
XX	
PR	31-JUL-2001; 2001US-0309111P.
XX	(PFIZ ) PFIZER PROD INC.
PA	
XX	
PI	Milos PM, Webb SM;
XX	
DR	WPI; 2003-373769/36.
XX	
PT	New cytochrome P450 2D6 gene variants and polypeptides, useful for
PT	determining if a subject has or is at risk of developing a drug
PT	sensitivity condition or disorder that is associated with an aberrant
PT	CYP2D6 activity.
XX	
PS	Disclosure; Page 13; 88pp; English.
XX	
CC	The invention relates to an isolated nucleic acid comprising a cytochrome
CC	P450 2D6 gene variant, e.g. G5799C or C5816AT (referring to the genomic
CC	sequence or the same variant nucleotide in the corresponding cDNA
CC	sequences). Also included are probes, primers (allele specific

oligonucleotides) and arrays used to detect and or amplify the CYP2D6 gene polymorphic regions, the variant polypeptides, antibodies which are capable of distinguishing between the variant and wild-type polypeptides, determining whether a subject has a genetic deficiency for metabolising a drug, evaluating therapy with a drug metabolised by P450 CYP2D6 and determining whether an individual is susceptible to being a poor metaboliser of drugs. The DNA probe is useful for hybridising to a variant form of the CYP2D6 gene. The primer is useful for amplifying the C58167A allelic variant. The allele specific nucleotide is useful for the detection of the C58167A allelic variant. The methods are useful for determining whether a subject has a genetic deficiency for metabolising a drug, evaluating therapy with a drug metabolised by P450 CYP2D6, and determining if an individual is susceptible to being a poor metaboliser of drugs. The nucleic acids are useful as probes or primers for determining whether a subject has a genetic deficiency for metabolising drugs that are substrates of P450 CYP2D6. The methods are useful for determining if a subject has or is at risk of developing a drug sensitivity condition or disorder that is associated with an aberrant CYP2D6 activity, e.g. an aberrant level of a CYP2D6 protein or an aberrant CYP2D6 bioactivity. The methods are also useful in selecting the appropriate drugs or determining the course of treatment to administer to a subject to treat cardiovascular or psychiatric disorders, or for treating a subject with a drug sensitivity or disorder associated with a specific allelic variant of a polymorphic region of the CYP2D6 gene. The antibodies are useful for monitoring CYP2D6 protein levels in an individual for determining whether a subject has a disease or conditions associated with an aberrant CYP2D6 protein level. The gene is located on human chromosome 22. The present sequence is an allele specific oligonucleotide (ASO) probe used to detect the wild-type CYP2D6 gene at polymorphic site 5816

SQ Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCAG 1670  
||||| |||||  
Db 1 AGCACAAAGCTCATAG 16

RESULT 726  
ACCS2643  
ID ACCS2643 standard; DNA; 17 BP.  
AC ACS2643;  
DT 27-JUN-2003 (first entry)  
DE Human tumour suppressor sequence #1410.  
KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;  
KW tumour regression; apoptosis; virus resistance; diagnosis;  
KW cellular degeneration.

OS Homo sapiens.  
XX FR2826373-A1.  
XX 27-DEC-2002.  
XX 20-JUN-2001; 2001PR-00008139.  
XX 20-JUN-2001; 2001PR-00008139.  
XX (MOLE-) MOLECULAR ENGINES LAB SA.  
XX Tuijnder M, Telerman A, Amson R;  
XX WPI; 2003-250498/25.  
XX New nucleic acid sequences associated with tumor suppression, regression,

PT apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.

PT apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.  
PT Claim 1; Page 366; 798pp; French.  
XX This sequence represents an isolated nucleic acid sequence associated with tumour suppression or regression, apoptosis or virus resistance. The invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration  
XX SQ Sequence 17 BP; 4 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1735 GCTCCCAACTCTCTCC 1750  
||||| |||||  
Db 1 GATCCCAAGCTACTCCC 16

RESULT 727  
ACCS2645  
ID ACCS2645 standard; DNA; 17 BP.  
XX AC ACS2645;  
XX 27-JUN-2003 (first entry)  
XX Human tumour suppressor sequence #1412.

XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;  
KW tumour regression; apoptosis; virus resistance; diagnosis;  
KW cellular degeneration.

OS Homo sapiens.  
XX FR2826373-A1.  
XX 27-DEC-2002.  
XX 20-JUN-2001; 2001PR-00008139.  
XX 20-JUN-2001; 2001PR-00008139.  
XX (MOLE-) MOLECULAR ENGINES LAB SA.  
XX Tuijnder M, Telerman A, Amson R;  
XX WPI; 2003-250498/25.

PT New nucleic acid sequences associated with tumor suppression, regression, apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.

XX Claim 1; Page 366; 798pp; French.  
XX This sequence represents an isolated nucleic acid sequence associated with tumour suppression or regression, apoptosis or virus resistance. The invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration  
XX SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY      1663 GCTCACAGCTGGACC 1678
Db      1 GATCCCAGCTGGGACC 16
RESULT 728
ACCS1350
ID      ACCS1350 standard; DNA; 17 BP.
XX      AC
XX      ACCS1350;
XX      DT
XX      27-JUN-2003 (first entry)
XX      DE
XX      Human tumour suppressor sequence #117.
XX      ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX      tumour regression; apoptosis; virus resistance; diagnosis;
XX      cellular degeneration.
XX      OS
XX      Homo sapiens.
XX      PN
XX      FR2826373-A1.
XX      PD
XX      27-DEC-2002.
XX      PF
XX      20-JUN-2001; 2001FR-00008139.
XX      PR
XX      20-JUN-2001; 2001FR-00008139.
XX      PA
XX      (MOLE-) MOLECULAR ENGINES LAB SA.
XX      PI
XX      Tuijnder M, Telerman A, Amson R;
XX      WPI; 2003-250498/25.
XX      New nucleic acid sequences associated with tumor suppression, regression,
XX      apoptosis or virus resistance are useful to diagnose and treat viral
XX      disease, development of tumor cells and cell degeneration.
XX      Claim 1; Page 67; 798pp; French.
XX      This sequence represents an isolated nucleic acid sequence associated
XX      with tumour suppression or regression, apoptosis or virus resistance. The
XX      invention relates to these sequences or sequences having at least 80%
XX      identity to them, and polypeptides encoded by the sequences or
XX      polypeptides having 80% identity to the polypeptide sequences. The
XX      invention is used to diagnose or treat viral disease or disease
XX      characterized by development of tumour cells or cellular degeneration
XX      Sequence 17 BP; 6 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
XX      Query Match      8.1%; Score 11.2; DB 1; Length 17;
XX      Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX      Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX      QY      1655 AGCACACGGCTCAG 1670
XX      Db      2 ATCACACGGCTTACAG 17
RESULT 729
ACCS2642
ID      ACCS2642 standard; DNA; 17 BP.
XX      AC
XX      ACCS2642;
XX      DT
XX      27-JUN-2003 (first entry)
XX      DE
XX      Human tumour suppressor sequence #1409.
XX      ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX      tumour regression; apoptosis; virus resistance; diagnosis;
```

```
KW      cellular degeneration.
XX      Homo sapiens.
XX      PN
XX      FR2826373-A1.
XX      PD
XX      27-DEC-2002.
XX      PF
XX      20-JUN-2001; 2001FR-00008139.
XX      PR
XX      20-JUN-2001; 2001FR-00008139.
XX      PA
XX      (MOLE-) MOLECULAR ENGINES LAB SA.
XX      PI
XX      Tuijnder M, Telerman A, Amson R;
XX      WPI; 2003-250498/25.
XX      New nucleic acid sequences associated with tumor suppression, regression,
XX      apoptosis or virus resistance are useful to diagnose and treat viral
XX      disease, development of tumor cells and cell degeneration.
XX      Claim 1; Page 365; 798pp; French.
XX      This sequence represents an isolated nucleic acid sequence associated
XX      with tumour suppression or regression, apoptosis or virus resistance. The
XX      invention relates to these sequences or sequences having at least 80%
XX      identity to them, and polypeptides encoded by the sequences or
XX      polypeptides having 80% identity to the polypeptide sequences. The
XX      invention is used to diagnose or treat viral disease or disease
XX      characterized by development of tumour cells or cellular degeneration
XX      Sequence 17 BP; 2 A; 11 C; 2 G; 2 T; 0 U; 0 Other;
XX      Query Match      8.1%; Score 11.2; DB 1; Length 17;
XX      Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX      Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX      QY      1735 GCTCCCCAACTCTCTCCC 1750
XX      Db      1 GATCCCCAGCCCCCTCCC 16
RESULT 730
ACCS1413/c
ID      ACCS1413 standard; DNA; 17 BP.
XX      AC
XX      ACCS1413;
XX      DT
XX      27-JUN-2003 (first entry)
XX      DE
XX      Human tumour suppressor sequence #180.
XX      ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX      tumour regression; apoptosis; virus resistance; diagnosis;
XX      cellular degeneration.
XX      OS
XX      Homo sapiens.
XX      PN
XX      FR2826373-A1.
XX      PD
XX      27-DEC-2002.
XX      PF
XX      20-JUN-2001; 2001FR-00008139.
XX      PR
XX      20-JUN-2001; 2001FR-00008139.
XX      PA
XX      (MOLE-) MOLECULAR ENGINES LAB SA.
XX      PI
XX      Tuijnder M, Telerman A, Amson R;
XX      WPI; 2003-250498/25.
XX
```

PT New nucleic acid sequences associated with tumor suppression, regression, apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.

XX Claim 1; Page 81; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated with tumor suppression or regression, apoptosis or virus resistance. The invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumor cells or cellular degeneration

XX Sequence 17 BP; 6 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCAGCTGGGAC 1677  
16 GTCTCAGCTGTGATC 1

Db

RESULT 731

ABX72090

ID ABX72090 standard; DNA; 17 BP.

AC

XX ABX72090;

XX

DT 12-MAR-2003 (first entry)

XX

DE Human tumour endothelial marker TEM 21 DNA long tag #1.

XX

KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
tumour endothelial marker; normal endothelial marker; PEM;  
pan-endothelial marker; polycystic kidney disease; psoriasis;  
diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
neovascularization; immune response; cytostatic; antidiabetic;  
ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.

XX

OS Homo sapiens.

XX

FN WO200283874-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US008253.

XX

PR 11-APR-2001; 2001US-0282850P.

PR 06-FEB-2002; 2002US-0354262P.

PA (UYJO ) UNIV JOHNS HOPKINS.

XX

XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;  
WPI; 2003-093016/08.

DR

XX New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.

XX

PS Disclosure; Page 361; 374pp; English.

XX The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (NEM), and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease,

CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neovascularization or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. ABX72067-ABX72116 represent human TEM DNA tags

XX Sequence 17 BP; 2 A; 9 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1741 AACTCCTCCCTATCT 1756  
2 ACCACCTCCCTTCT 17

Db

RESULT 732

ABT40040

ID ABT40040 standard; DNA; 17 BP.

XX

AC ABT40040;

XX

DT 13-JUN-2003 (first entry)

XX

DE Tumour suppression related human fukutin oligo SEQ ID No 5677.

XX

KW Cytostatic; virucide; neuroprotective; neuroleptic; gene chip;  
antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
schizophrenia; protein chip; gene therapy; tumour suppression;  
human fukutin; ds.

XX

OS Homo sapiens.

XX

FN WO2003025175-A2.

XX

PD 27-MAR-2003.

XX

PF 17-SEP-2002; 2002WO-IB034208.

XX

PR 17-SEP-2001; 2001FR-00011978.

XX

PA (MOLE-) MOLECULAR ENGINES LAB.

XX

PI Telerman A, Amson R, Tuijnder M;

XX

DR WPI; 2003-313353/30.

XX

PT New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.

PT

XX Disclosure; Page 697; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein

CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
CC related human fukutin oligonucleotide of the invention  
XX  
SQ Sequence 17 BP; 6 A; 4 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1655 AGCACCAGGCTCACAG 1670  
| | | | | | | | | |  
Db 2 ATCACAGGCTTACAG 17  
RESULT 733  
ABT34526/c  
ID ABT34526 standard; DNA; 17 BP.  
XX  
XX AC ABT34526;  
XX  
XX DT 12-JUN-2003 (first entry)  
XX  
XX Tumour suppression related human fukutin oligo SEQ ID No 163.  
XX  
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
XX schizophrania; protein chip; gene therapy; tumour suppression;  
XX human fukutin; ds.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO2003025175-A2.  
XX  
XX PD 27-MAR-2003.  
XX  
XX PF 17-SEP-2002; 2002WO-IB004208.  
XX  
XX PR 17-SEP-2001; 2001FR-00011978.  
XX  
XX PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
XX PI Telerman A, Amson R, Tuijnder M;  
XX  
XX WPI; 2003-313353/30.  
XX  
XX DR New isolated nucleic acid, useful for treating viral diseases associated  
XX with tumors and cell degeneration, also related polypeptides, antibodies  
XX and transfected cells.  
XX  
XX PS Disclosure; Page 53; 720pp; French.  
XX  
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,  
XX given in the specification, a sequence containing at least 15 consecutive  
XX nucleotides from the 17 mer sequence, a sequence with, after optimal  
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
XX hybridizes to them under highly stringent conditions, or the complement  
XX of any of them, or the corresponding RNA. The novel isolated nucleic  
XX acids of the invention are useful as probes and primers for detecting,  
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
XX component of a gene chip, in vitro as (anti)sense reagents, and for  
XX production of recombinant polypeptides. Any of the nucleic acids,  
XX polypeptides, vectors containing the nucleic acids, cells containing the  
XX vector or antibodies directed against the polypeptides are useful for  
XX preparation of pharmaceuticals for prevention and/or treatment of viral  
XX diseases that are characterised by development of tumours or cell  
XX degeneration, specifically cancer but also Alzheimer's disease and  
XX schizophrania. Analysis of the expression of the 17 mer nucleic acids in  
XX patient samples is useful for diagnosis and/or prognosis of these  
XX diseases. The polypeptides can also be used to generate antibodies, and  
XX both the polypeptide and antibodies are useful as components of protein  
XX chips. The nucleic acid sequences of the invention can be used in gene  
XX therapy. This polynucleotide sequence represents a tumour suppression

CC related human fukutin oligonucleotide of the invention  
XX  
SQ Sequence 17 BP; 3 A; 9 C; 1 G; 4 T; 0 U; 0 Other;  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1717 GTACGGAGATGGAGAT 1732  
| | | | | | | | | |  
Db 17 GGATGGGGATGGAGAT 2  
RESULT 734  
ABT37658/c  
ID ABT37658 standard; DNA; 17 BP.  
XX  
XX AC ABT37658;  
XX  
XX DT 12-JUN-2003 (first entry)  
XX  
XX Tumour suppression related human fukutin oligo SEQ ID No 3295.  
XX  
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
XX schizophrania; protein chip; gene therapy; tumour suppression;  
XX human fukutin; ds.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO2003025175-A2.  
XX  
XX PD 27-MAR-2003.  
XX  
XX PF 17-SEP-2002; 2002WO-IB004208.  
XX  
XX PR 17-SEP-2001; 2001FR-00011978.  
XX  
XX PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
XX PI Telerman A, Amson R, Tuijnder M;  
XX  
XX WPI; 2003-313353/30.  
XX  
XX DR New isolated nucleic acid, useful for treating viral diseases associated  
XX with tumors and cell degeneration, also related polypeptides, antibodies  
XX and transfected cells.  
XX  
XX PS Disclosure; Page 419; 720pp; French.  
XX  
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,  
XX given in the specification, a sequence containing at least 15 consecutive  
XX nucleotides from the 17 mer sequence, a sequence with, after optimal  
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
XX hybridizes to them under highly stringent conditions, or the complement  
XX of any of them, or the corresponding RNA. The novel isolated nucleic  
XX acids of the invention are useful as probes and primers for detecting,  
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
XX component of a gene chip, in vitro as (anti)sense reagents, and for  
XX production of recombinant polypeptides. Any of the nucleic acids,  
XX polypeptides, vectors containing the nucleic acids, cells containing the  
XX vector or antibodies directed against the polypeptides are useful for  
XX preparation of pharmaceuticals for prevention and/or treatment of viral  
XX diseases that are characterised by development of tumours or cell  
XX degeneration, specifically cancer but also Alzheimer's disease and  
XX schizophrania. Analysis of the expression of the 17 mer nucleic acids in  
XX patient samples is useful for diagnosis and/or prognosis of these  
XX diseases. The polypeptides can also be used to generate antibodies, and  
XX both the polypeptide and antibodies are useful as components of protein  
XX chips. The nucleic acid sequences of the invention can be used in gene  
XX therapy. This polynucleotide sequence represents a tumour suppression

```
SQ Sequence 17 BP; 2 A; 8 C; 2 G; 5 T; 0 U; 0 Other;
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1717 GTACGGAGATGGAGAT 1732
    |||||
Db 17 GGAAGAGCTGGAGAT 2

RESULT 735
ABT38730/c
ID ABT38730 standard; DNA; 17 BP.
XX
AC ABT38730;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 4367.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
New isolated nucleic acid, useful for treating viral diseases associated
with tumors and cell degeneration, also related polypeptides, antibodies
and transfected cells.
PS Disclosure; Page 544; 720pp; French.
XX
The invention relates to a novel isolated 17 mer nucleic acid sequence,
given in the specification, a sequence containing at least 15 consecutive
nucleotides from the 17 mer sequence, a sequence with, after optimal
alignment, at least 80 % identity to the 17 mer sequence, a sequence that
hybridizes to them under highly stringent conditions, or the complement
of any of them, or the corresponding RNA. The novel isolated nucleic
acids of the invention are useful as probes and primers for detecting,
identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
component of a gene chip, in vitro as (anti)sense reagents, and for
production of recombinant polypeptides. Any of the nucleic acids,
polypeptides, vectors containing the nucleic acids, cells containing the
vector or antibodies directed against the polypeptides are useful for
preparation of pharmaceuticals for prevention and/or treatment of viral
diseases that are characterised by development of tumours or cell
degeneration, specifically cancer but also Alzheimer's disease and
schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
patient samples is useful for diagnosis and/or prognosis of these
diseases. The polypeptides can also be used to generate antibodies, and
both the polypeptide and antibodies are useful as components of protein
chips. The nucleic acid sequences of the invention can be used in gene
therapy. This polynucleotide sequence represents a tumour suppression
related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1651 GGCAAGCACCAGGCTC 1666
    |||||
Db 16 GTCCAGACCAGGATC 1

RESULT 736
ABT37668/c
ID ABT37668 standard; DNA; 17 BP.
XX
AC ABT37668;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 3305.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
New isolated nucleic acid, useful for treating viral diseases associated
with tumors and cell degeneration, also related polypeptides, antibodies
and transfected cells.
PS Disclosure; Page 420; 720pp; French.
XX
The invention relates to a novel isolated 17 mer nucleic acid sequence,
given in the specification, a sequence containing at least 15 consecutive
nucleotides from the 17 mer sequence, a sequence with, after optimal
alignment, at least 80 % identity to the 17 mer sequence, a sequence that
hybridizes to them under highly stringent conditions, or the complement
of any of them, or the corresponding RNA. The novel isolated nucleic
acids of the invention are useful as probes and primers for detecting,
identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
component of a gene chip, in vitro as (anti)sense reagents, and for
production of recombinant polypeptides. Any of the nucleic acids,
polypeptides, vectors containing the nucleic acids, cells containing the
vector or antibodies directed against the polypeptides are useful for
preparation of pharmaceuticals for prevention and/or treatment of viral
diseases that are characterised by development of tumours or cell
degeneration, specifically cancer but also Alzheimer's disease and
schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
patient samples is useful for diagnosis and/or prognosis of these
diseases. The polypeptides can also be used to generate antibodies, and
both the polypeptide and antibodies are useful as components of protein
chips. The nucleic acid sequences of the invention can be used in gene
therapy. This polynucleotide sequence represents a tumour suppression
related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 2 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
```

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1711 TTAGAGTACGAGAT 1726  
| | | | | | | | | |  
Db 17 TCAGGAGCGGAGAT 2

RESULT 737  
ABT37550  
ID ABT37550 standard; DNA; 17 BP.  
XX AC ABT37550;  
XX DT 12-JUN-2003 (first entry)  
XX DE Tumour suppression related human fukutin oligo SEQ ID No 3187.  
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
XX KW schizophrenia; protein chip; gene therapy; tumour suppression;  
XX KW human fukutin; ds.  
XX OS Homo sapiens.  
XX PN WO2003025175-A2.  
XX PD 27-MAR-2003.  
XX PF 17-SEP-2002; 2002WO-IB004208.  
XX PR 17-SEP-2001; 2001FR-00011978.  
XX PA (MOLE-) MOLECULAR ENGINES LAB.  
XX PI Telerman A, Amson R, Tuijnder M;  
XX WPI; 2003-313353/30.  
XX PT New isolated nucleic acid, useful for treating viral diseases associated  
XX PT with tumors and cell degeneration, also related polypeptides, antibodies  
XX PT and transfected cells.  
XX PS Disclosure; Page 406; 720pp; French.  
XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,  
XX CC given in the specification, a sequence containing at least 15 consecutive  
XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
XX CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
XX CC hybridizes to them under highly stringent conditions, or the complement  
XX CC of any of them, or the corresponding RNA. The novel isolated nucleic  
XX CC acids of the invention are useful as probes and primers for detecting,  
XX CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
XX CC component of a gene chip, in vitro as (anti)sense reagents, and for  
XX CC production of recombinant polypeptides. Any of the nucleic acids,  
XX CC polypeptides, vectors containing the nucleic acids, cells containing the  
XX CC vector or antibodies directed against the polypeptides are useful for  
XX CC preparation of pharmaceuticals for prevention and/or treatment of viral  
XX CC diseases that are characterised by development of tumours or cell  
XX CC degeneration, specifically cancer but also Alzheimer's disease and  
XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
XX CC patient samples is useful for diagnosis and/or prognosis of these  
XX CC diseases. The polypeptides can also be used to generate antibodies, and  
XX CC both the polypeptide and antibodies are useful as components of protein  
XX CC chips. The nucleic acid sequences of the invention can be used in gene  
XX CC therapy. This polynucleotide sequence represents a tumour suppression  
XX CC related human fukutin oligonucleotide of the invention  
XX SQ Sequence 17 BP; 8 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1752 ATCTAAAGCCCACT 1767  
| | | | | | | | | |  
Db 2 ATCATAAAGACCACT 17

RESULT 738  
ABT40013/C  
ID ABT40013 standard; DNA; 17 BP.  
XX AC ABT40013;  
XX DT 13-JUN-2003 (first entry)  
XX DE Tumour suppression related human fukutin oligo SEQ ID No 5650.  
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
XX KW schizophrenia; protein chip; gene therapy; tumour suppression;  
XX KW human fukutin; ds.  
XX OS Homo sapiens.  
XX PN WO2003025175-A2.  
XX PD 27-MAR-2003.  
XX PF 17-SEP-2002; 2002WO-IB004208.  
XX PR 17-SEP-2001; 2001FR-00011978.  
XX PA (MOLE-) MOLECULAR ENGINES LAB.  
XX PI Telerman A, Amson R, Tuijnder M;  
XX WPI; 2003-313353/30.  
XX PT New isolated nucleic acid, useful for treating viral diseases associated  
XX PT with tumors and cell degeneration, also related polypeptides, antibodies  
XX PT and transfected cells.  
XX PS Disclosure; Page 694; 720pp; French.  
XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,  
XX CC given in the specification, a sequence containing at least 15 consecutive  
XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
XX CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
XX CC hybridizes to them under highly stringent conditions, or the complement  
XX CC of any of them, or the corresponding RNA. The novel isolated nucleic  
XX CC acids of the invention are useful as probes and primers for detecting,  
XX CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
XX CC component of a gene chip, in vitro as (anti)sense reagents, and for  
XX CC production of recombinant polypeptides. Any of the nucleic acids,  
XX CC polypeptides, vectors containing the nucleic acids, cells containing the  
XX CC vector or antibodies directed against the polypeptides are useful for  
XX CC preparation of pharmaceuticals for prevention and/or treatment of viral  
XX CC diseases that are characterised by development of tumours or cell  
XX CC degeneration, specifically cancer but also Alzheimer's disease and  
XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
XX CC patient samples is useful for diagnosis and/or prognosis of these  
XX CC diseases. The polypeptides can also be used to generate antibodies, and  
XX CC both the polypeptide and antibodies are useful as components of protein  
XX CC chips. The nucleic acid sequences of the invention can be used in gene  
XX CC therapy. This polynucleotide sequence represents a tumour suppression  
XX CC related human fukutin oligonucleotide of the invention  
XX SQ Sequence 17 BP; 5 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 16 GCTCACTGCTGGATC 1

RESULT 739  
ACA09101/c

ID ACA09101 standard, RNA; 17 BP.

XX ACA09101;

AC ACA09101;

XX 03-JUN-2003 (first entry)

XX NFKB sub-unit modulating amberzyme substrate #264.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate; gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes; rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX Homo sapiens.

OS US2002177568-A1.

XX 28-NOV-2002.

PD 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

PR 18-MAY-1994; 94US-00245466.

PR 15-AUG-1994; 94US-00291932.

PR 23-DEC-1996; 96US-00777916.

XX (STIN/) STINCHCOMB D T.

PA (MCSW/) MCSWIGGEN J.

PA (DRAP/) DRAPER K G.

XX Stinchcomb DT, Mcswiggen J, Draper KG;

XX WPI; 2003-340953/32.

XX Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.

PS Claim 3; Page 56; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and antisense nucleic acid molecules are useful for treating breast lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft

CC rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents the substrate of a novel enzymatic nucleic acid molecule

XX Sequence 17 BP; 4 A; 1 C; 10 G; 0 T; 2 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1740 CAATCTCTCCCTATCC 1755

Db 17 CAGCTCCCCCTTTC 2

RESULT 740

ACA06383

ID ACA06383 standard, RNA; 17 BP.

XX ACA06383;

AC ACA06383;

XX 03-JUN-2003 (first entry)

XX NFKB sub-unit modulating inozyme substrate #202.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate; gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes; rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX Homo sapiens.

OS US2002177568-A1.

XX 28-NOV-2002.

PD 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

PR 18-MAY-1994; 94US-00245466.

PR 15-AUG-1994; 94US-00291932.

PR 23-DEC-1996; 96US-00777916.

XX (STIN/) STINCHCOMB D T.

PA (MCSW/) MCSWIGGEN J.

PA (DRAP/) DRAPER K G.

XX Stinchcomb DT, Mcswiggen J, Draper KG;

XX WPI; 2003-340953/32.

XX Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.

PS Claim 3; Page 30; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and antisense nucleic acid molecules are useful for treating breast lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft



PI Stinchcomb DT, Mcswiggen J, Draper KG;

US2002177568-A1.





CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 17 BP; 3 A; 4 C; 8 G; 2 T; 0 U; 0 Other;  
  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1687 TCCTCAGCGTGGTGG 1702  
Db 17 TCCTCCACCATGGCGG 2  
|||||  
17 TCCTCCACCATGGCGG 2  
  
RESULT 747  
ADB03481  
ID ADB03481 standard; DNA; 17 BP.  
AC ADB03481;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human MDZ7 scanning oligonucleotide SEQ ID 4467.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1281758-A2.  
XX  
PD 05-FEB-2003.  
XX  
PF 30-JUL-2002; 2002EP-00016874.  
XX  
PR 02-AUG-2001; 2001US-00922181.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M, Gu Y, Nguyen C;  
XX  
DR WPI; 2003-423107/40.  
XX  
PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 4467; 103pp; English.  
XX  
CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic

CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 17 BP; 4 A; 4 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1663 GCTCAGCGTGGAAACC 1678  
Db 1 GCTCAAGCTGGGATC 16  
|||||  
1 GCTCAAGCTGGGATC 16  
  
RESULT 748  
ADA99486/C  
ID ADA99486 standard; DNA; 17 BP.  
XX  
AC ADA99486;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human MDZ3 scanning oligonucleotide SEQ ID 475.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1281758-A2.  
XX  
PD 05-FEB-2003.  
XX  
PF 30-JUL-2002; 2002EP-00016874.  
XX  
PR 02-AUG-2001; 2001US-00922181.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M, Gu Y, Nguyen C;  
XX  
DR WPI; 2003-423107/40.  
XX  
PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 475; 103pp; English.  
XX  
CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX

```
SQ Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1687 TCTCCAGCGTGGTGG 1702
DB 16 TCTCCACCATGGCG 1

RESULT 749
ADB03480
ID ADB03480 standard; DNA; 17 BP.
XX
AC ADB03480;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 4466.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (ABOM-) ABOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 4466; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1663 GCTCAGCTGGAAC 1678
DB 16 TCTCCACCATGGCG 1

RESULT 750
ADA99594/c
ID ADA99594 standard; DNA; 17 BP.
XX
AC ADA99594;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ3 scanning oligonucleotide SEQ ID 583.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (ABOM-) ABOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 583; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
Query Match      8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1666 CACAGCTGGAACCTG 1681
DB 16 CCGAGCTGGATGCTG 1

RESULT 751
ADA99555/c
ID ADA99555 standard; DNA; 17 BP.
XX
AC ADA99555;
```

```
XX 20-NOV-2003 (first entry)
XX Human MDZ3 scanning oligonucleotide SEQ ID 544.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX Homo sapiens.
XX EP1281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX Example 8; SEQ ID NO 544; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX Sequence 17 BP; 8 A; 3 C; 6 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1680 TGCTGTCTCTCTCCAGC 1695
XX |||||
XX Db 17 TGCTGTCTCTCTCTGC 2
XX
XX RESULT 752
XX ADA99409
XX ID ADA99409 standard; DNA; 17 BP.
XX AC ADA99409;
XX
XX 20-NOV-2003 (first entry)
XX Human MDZ3 scanning oligonucleotide SEQ ID 398.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX
```

```
XX developmental disorder; ss.
XX Homo sapiens.
XX EP1281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX Example 8; SEQ ID NO 398; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX Sequence 17 BP; 3 A; 7 C; 2 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1740 CAACTCTCTCTCTATCC 1755
XX |||||
XX Db 2 CAGTCTCTCACTATCC 17
XX
XX RESULT 753
XX ABZ61824/c
XX ID ABZ61824 standard; RNA; 17 BP.
XX AC ABZ61824;
XX
XX 21-MAR-2003 (first entry)
XX Human H-Ras DNazyme target #615.
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX Homo sapiens.
XX WO200297114-A2.
XX 05-DEC-2002.
XX 29-MAY-2002; 2002WO-US016840.
```

XX 29-MAY-2001; 2001US-0294140P.  
 PR 06-JUN-2001; 2001US-0296249P.  
 PR 10-SEP-2001; 2001US-0318471P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX PA  
 XX Mcswiggen J;  
 XX WPI; 2003-140484/13.  
 DR  
 XX Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
 XX  
 XX Claim 58; Page 122; 185pp; English.  
 XX  
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
 CC rheumatic activity. The nucleic acid molecules are useful for reducing  
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
 CC ribozymes of the invention  
 XX  
 SQ Sequence 17 BP; 4 A; 0 C; 11 G; 0 T; 2 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1736 CTCCTCACTCTCCCT 1751  
 |||||  
 DB 16 CTCCTCACTCTCCCT 1  
 |||||  
 RESULT 754  
 ABZ64589  
 ID ABZ64589 standard; RNA; 17 BP.  
 XX  
 AC ABZ64589;  
 XX  
 XX 21-MAR-2003 (first entry)  
 XX  
 DE Human HER2 DNzyme substrate #46.  
 XX  
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
 KW anti-rheumatic; cancer; AIDS; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200297114-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 29-MAY-2002; 2002WO-US016840.  
 XX  
 PR 29-MAY-2001; 2001US-0294140P.  
 PR 06-JUN-2001; 2001US-0296249P.  
 PR 10-SEP-2001; 2001US-0318471P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX PA  
 XX Mcswiggen J;  
 XX WPI; 2003-140484/13.  
 DR  
 XX Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
 XX  
 XX Claim 58; Page 122; 185pp; English.  
 XX  
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
 CC rheumatic activity. The nucleic acid molecules are useful for reducing  
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
 CC ribozymes of the invention  
 XX  
 SQ Sequence 17 BP; 4 A; 0 C; 11 G; 0 T; 2 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1736 CTCCTCACTCTCCCT 1751  
 |||||  
 DB 16 CTCCTCACTCTCCCT 1  
 |||||

PT Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
 XX  
 XX Claim 4; Page 133; 185pp; English.  
 XX  
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
 CC rheumatic activity. The nucleic acid molecules are useful for reducing  
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
 CC ribozymes of the invention  
 XX  
 SQ Sequence 17 BP; 0 A; 7 C; 6 G; 0 T; 4 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 5.2e+02;  
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1677 CCTGTGTCTCTCTCC 1692  
 |||||  
 DB 1 CGCUGGGGCGCCUCC 16  
 |||||  
 RESULT 755  
 ABZ60463/c  
 ID ABZ60463 standard; RNA; 17 BP.  
 XX  
 AC ABZ60463;  
 XX  
 XX 21-MAR-2003 (first entry)  
 XX  
 DE Human K-Ras DNzyme substrate #575.  
 XX  
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
 KW anti-rheumatic; cancer; AIDS; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200297114-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 29-MAY-2002; 2002WO-US016840.  
 XX  
 PR 29-MAY-2001; 2001US-0294140P.  
 PR 06-JUN-2001; 2001US-0296249P.  
 PR 10-SEP-2001; 2001US-0318471P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX PA  
 XX Mcswiggen J;  
 XX WPI; 2003-140484/13.  
 DR  
 XX Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
 XX  
 XX Claim 58; Page 96; 185pp; English.  
 XX  
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-

CC rheumatic activity. The nucleic acid molecules are useful for reducing  
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
CC ribozymes of the invention

XX SQ Sequence 17 BP; 3 A; 9 C; 1 G; 0 T; 4 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1633 ATGGGGCTGTGTAGCAG 1648  
DB 17 ATGGGGCATGTGGAAG 2

RESULT 756

ABZ65103

ID ABZ65103 standard; RNA; 17 BP.

XX AC ABZ65103;

XX DT 21-MAR-2003 (first entry)

XX DE Human HER2 DNzyme substrate #560.

XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

XX KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;

XX KW anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX PN WO200297114-A2.

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US016840.

XX PR 29-MAY-2001; 2001US-0294140P.

XX PR 06-JUN-2001; 2001US-0296249P.

XX PR 10-SEP-2001; 2001US-0318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswiggen J;

XX DR WPI; 2003-140484/13.

XX PT Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
XX PS Claim 4; Page 143; 185pp; English.  
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
CC rheumatic activity. The nucleic acid molecules are useful for reducing  
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
CC ribozymes of the invention

XX SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 62.5%; Pred. No. 5.2e+02;  
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1668 CAGCTGGAAACCTGGT 1683

DB 2 CAUCUGGAUCCCGAU 17

RESULT 757

ABZ65446

ID ABZ65446 standard; RNA; 17 BP.

XX AC ABZ65446;

XX DT 21-MAR-2003 (first entry)

XX DE Human HER2 DNzyme substrate #903.

XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

XX KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;

XX KW anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX PN WO200297114-A2.

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US016840.

XX PR 29-MAY-2001; 2001US-0294140P.

XX PR 06-JUN-2001; 2001US-0296249P.

XX PR 10-SEP-2001; 2001US-0318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswiggen J;

XX DR WPI; 2003-140484/13.

XX PT Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
XX PS Claim 4; Page 150; 185pp; English.  
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
CC rheumatic activity. The nucleic acid molecules are useful for reducing  
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
CC ribozymes of the invention

XX SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 50.0%; Pred. No. 5.2e+02;  
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1675 AACCTGGTGTCTCCT 1690

DB 2 AGCCUGAUGUGUCCU 17

RESULT 758

ABZ60377/c

ID ABZ60977 standard; RNA; 17 BP.





XX AC ACD55658;  
 XX DT 23-SEP-2003 (first entry)  
 XX DE HBV amberzyme substrate sequence #168.  
 XX  
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 OS Hepatitis B virus.  
 XX  
 XX WO200281494-A1.  
 XX 17-OCT-2002.  
 XX  
 XX 26-MAR-2002; 2002WO-US009187.  
 XX  
 XX 26-MAR-2001; 2001US-00817879.  
 XX 08-JUN-2001; 2001US-00877478.  
 XX 08-JUN-2001; 2001US-0296876P.  
 XX 24-OCT-2001; 2001US-0335059P.  
 XX 05-DEC-2001; 2001US-0337055P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX (BLAT/) BLATT L.  
 XX (MACE/) MACEJAK D.  
 XX (MCSW/) MCSWIGGEN J.  
 XX (MORR/) MORRISSEY D.  
 XX (PAVC/) PAVCO P.  
 XX (LEEP/) LEE P.  
 XX (DRAP/) DRAPER K.  
 XX (ROBE/) ROBERTS E.  
 XX  
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;  
 XX Draper K, Roberts E;  
 XX WPI; 2003-229207/22.  
 XX  
 XX Novel compound useful for treating cirrhosis, liver failure,  
 XX hepatocellular carcinoma, or condition associated with hepatitis C virus  
 XX infection.  
 XX  
 XX Example 1; Page 206; 387pp; English.  
 XX  
 XX The present invention relates to nucleic acid molecules which modulate  
 XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 XX and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,  
 XX inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 XX transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 XX as oligonucleotides that specifically bind the Enhancer I region of HBV  
 XX DNA. The nucleic acids may be used to modulate the expression of HBV  
 XX genes and HBV viral replication. Also disclosed is a method for screening  
 XX compounds and/or potential therapies directed against HBV, and compounds  
 XX that modulate the expression and/or replication of HCV. The compounds  
 XX methods of the invention are useful for the treatment of degenerative and  
 XX disease states related to HBV and HCV infection, replication and gene  
 XX expression such as cirrhosis, liver failure, and hepatocellular  
 XX carcinoma. The present sequence represents a substrate for one of the HBV  
 XX ribozyme, inozyme, G-cleaver, zinzyme, DNzyme or amberzyme sequences  
 XX disclosed in the present invention

SQ Sequence 17 BP; 4 A; 0 C; 11 G; 0 T; 2 U; 0 Other;

Query Match

8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 68.8%; Pred. No. 5.2e+02;  
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1702 GAA GTTGGT TAGGAG 1717  
 |||::||| |||||  
 DB 2 GCAGUUGGGGAGGAG 17

# RESULT 761

ACD58401/C

ID ACD58401 standard; RNA; 17 BP.

XX AC ACD58401;

XX DT 24-SEP-2003 (first entry)

XX DE HCV DNzyme substrate sequence #819.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.

OS Hepatitis C virus.

XX WO200281494-A1.

XX 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-0087879.

XX 08-JUN-2001; 2001US-00877478.

XX 08-JUN-2001; 2001US-0296876P.

XX 24-OCT-2001; 2001US-0335059P.

XX 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MACE/) MACEJAK D.

XX (MCSW/) MCSWIGGEN J.

XX (MORR/) MORRISSEY D.

XX (PAVC/) PAVCO P.

XX (LEEP/) LEE P.

XX (DRAP/) DRAPER K.

XX (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;  
 XX Draper K, Roberts E;

XX WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,  
 XX hepatocellular carcinoma, or condition associated with hepatitis C virus  
 XX infection.

XX Claim 1; Page 248; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate  
 XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 XX and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,  
 XX inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 XX transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 XX as oligonucleotides that specifically bind the Enhancer I region of HBV  
 XX DNA. The nucleic acids may be used to modulate the expression of HBV  
 XX genes and HBV viral replication. Also disclosed is a method for screening  
 XX compounds and/or potential therapies directed against HBV, and compounds

CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HCV  
CC DNAzyme or minus strand DNAzyme sequences disclosed in the present  
CC invention  
XX  
SQ Sequence 17 BP; 3 A; 4 C; 10 G; 0 T; 0 U; 0 Other;  
  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1677 CCGTGGTGTCCTCC 1692  
DB 17 CCGCGGTGTCCTCCC 2  
  
RESULT 762  
ACD51379  
ID ACD51379 standard; RNA; 17 BP.  
XX  
AC ACD51379;  
XX  
DT 23-SEP-2003 (first entry)  
XX  
DE HBV hammerhead ribozyme substrate sequence #539.  
XX  
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;  
KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX  
OS Hepatitis B virus.  
XX  
PN WO200281494-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 26-MAR-2002; 2002WO-US009187.  
XX  
PR 26-MAR-2001; 2001US-00817879.  
PR 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX  
XX WPI; 2003-229207/22.  
XX  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
XX Example 1; Page 146; 387pp; English.

CC The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HBV  
CC ribozyme, inozyme, G-cleaver, zinzyme, DNzyme or amberyne sequences  
CC disclosed in the present invention  
XX  
SQ Sequence 17 BP; 2 A; 6 C; 1 G; 0 T; 8 U; 0 Other;  
  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 50.0%; Pred. No. 5.2e+02;  
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1741 AACTCCTCCTATCCT 1756  
DB 1 AACUCCUUCUUUCCU 16  
  
RESULT 763  
ACD55659  
ID ACD55659 standard; RNA; 17 BP.  
XX  
AC ACD55659;  
XX  
DT 23-SEP-2003 (first entry)  
XX  
DE HBV amberyne substrate sequence #169.  
XX  
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;  
KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX  
OS Hepatitis B virus.  
XX  
PN WO200281494-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 26-MAR-2002; 2002WO-US009187.  
XX  
PR 26-MAR-2001; 2001US-00817879.  
PR 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX

PI Blatt L, Macejak D, McSwiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX WPI; 2003-229207/22.  
 XX Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX Example 1; Page 206; 387pp; English.  
 XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HBV  
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberyzyme sequences  
 CC disclosed in the present invention  
 XX Sequence 17 BP; 3 A; 0 C; 12 G; 0 T; 2 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 68.8%; Pred. No. 5.2e+02;  
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1702 GAAGTGGGTAGGAG 1717  
 Db 1 GGAGTUGGGGAGGAG 16  
 |||||:|||||  
 |||||:|||||  
 RESULT 764  
 ACDS8497  
 ID ACD58497 standard; RNA; 17 BP.  
 AC ACD58497;  
 XX  
 DT 24-SEP-2003 (first entry)  
 XX HCV DNazyme substrate sequence #859.  
 XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberyzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX Hepatitis C virus.  
 OS  
 XX WO200281494-A1.  
 PN 17-OCT-2002.  
 XX  
 XX 26-MAR-2002; 2002WO-US009187.  
 PF  
 XX 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEF/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX Blatt L, Macejak D, McSwiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX WPI; 2003-229207/22.  
 DR Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX Claim 1; Page 249; 387pp; English.  
 XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNazyme or minus strand DNazyme sequences disclosed in the present  
 CC invention  
 XX Sequence 17 BP; 4 A; 7 C; 3 G; 0 T; 3 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 5.2e+02;  
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1655 AGCACCAGGTCACAG 1670  
 Db 2 AUCACCAGCCUACCG 17  
 |||||:|||||  
 |||||:|||||  
 RESULT 765  
 ACDS3921  
 ID ACD53921 standard; RNA; 17 BP.  
 XX ACD53921;  
 AC ACD53921;  
 XX  
 DT 24-SEP-2003 (first entry)  
 XX HBV zinzyme substrate sequence #91.  
 DE  
 XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberyzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX Hepatitis B virus.  
 OS  
 XX

PN WO200281494-A1.  
 XX 17-OCT-2002.  
 XX 26-MAR-2002; 2002WO-US009187.  
 XX 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORE/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX WPI; 2003-229207/22.  
 XX Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX Example 1; Page 175; 387pp; English.  
 XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HBV  
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences  
 CC disclosed in the present invention  
 XX Sequence 17 BP; 4 A; 0 C; 9 G; 0 T; 4 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 56.2%; Pred. No. 5.2e+02;  
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1698 GGTCGAGCTTGGGTTA 1713  
 DB 2 GGAGGAGGUAGGUUA 17  
 RESULT 766  
 ACD55653/C  
 ID ACD55653 standard; RNA; 17 BP.  
 XX AC  
 XX ACD55653;  
 XX AC  
 DT 23-SEP-2003 (first entry)  
 XX  
 DE HBV amberzyme substrate sequence #163.  
 XX

KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX Hepatitis B virus.  
 OS WO200281494-A1.  
 PN 17-OCT-2002.  
 XX 26-MAR-2002; 2002WO-US009187.  
 XX 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORE/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX WPI; 2003-229207/22.  
 XX Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX Example 1; Page 206; 387pp; English.  
 XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HBV  
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences  
 CC disclosed in the present invention  
 XX Sequence 17 BP; 5 A; 0 C; 8 G; 0 T; 4 U; 0 Other;  
 SQ  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1741 AACTCTCTCCCTATCT 1756  
 DB 17 AACTCTCTCCCTATCT 2

XX	Result 767
SQ	Sequence 17 BP; 3 A; 6 C; 0 G; 0 T; 8 U; 0 Other;
ID	ACD51378 standard; RNA; 17 BP.
XX	
AC	ACD51378;
XX	
DT	23-SEP-2003 (first entry)
XX	
DE	HCV hammerhead ribozyme substrate sequence #538.
XX	
KW	Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW	RNA stability; RNA expression; RNA synthesis; antisense;
KW	enzymatic nucleic acid; hammerhead ribozyme; DNzyme; zinzyme;
KW	amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW	HBV reverse transcriptase; Enhancer I region; viral replication;
KW	degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW	liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX	virucide; antiinflammatory; substrate; ss.
OS	Hepatitis B virus.
XX	
PN	WO200281494-A1.
XX	
PD	17-OCT-2002.
XX	
Pf	26-MAR-2002; 2002WO-US009187.
XX	
PR	26-MAR-2001; 2001US-00817879.
PR	08-JUN-2001; 2001US-00877478.
PR	08-JUN-2001; 2001US-0296876P.
PR	24-OCT-2001; 2001US-0335059P.
PR	05-DEC-2001; 2001US-0337055P.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
PA	(BLAT/) BLATT L.
PA	(MACE/) MACEJAK D.
PA	(MCSW/) MCSWIGGEN J.
PA	(MORR/) MORRISSEY D.
PA	(PAVC/) PAVCO P.
PA	(LEEP/) LEE P.
PA	(DRAP/) DRAPER K.
PA	(ROBE/) ROBERTS E.
XX	
PI	Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI	Draper K, Roberts E;
XX	
DR	WPI; 2003-229207/22.
XX	
PT	Novel compound useful for treating cirrhosis, liver failure,
PT	hepatocellular carcinoma, or condition associated with hepatitis C virus
PT	infection.
PS	Example 1; Page 146; 387pp; English.
XX	
CC	The present invention relates to nucleic acid molecules which modulate
CC	the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC	Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC	and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,
CC	inozymes, zinzymes, amberzemes, and G-cleaver ribozymes. Also disclosed
CC	are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC	transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC	as oligonucleotides that specifically bind the Enhancer I region of HBV
CC	DNA. The nucleic acids may be used to modulate the expression of HBV
CC	genes and HBV viral replication. Also disclosed is a method for screening
CC	compounds and/or potential therapies directed against HBV, and compounds
CC	that modulate the expression and/or replication of HCV. The compounds and
CC	methods of the invention are useful for the treatment of degenerative and
CC	disease states related to HBV and HCV infection, replication and gene
CC	expression such as cirrhosis, liver failure, and hepatocellular
CC	carcinoma. The present sequence represents a substrate for one of the HBV
CC	ribozyme, inozyme, G-cleaver, zinzyme, DNzyme or amberzyme sequences
CC	disclosed in the present invention

as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HCV DNAzyme or minus strand DNAzyme sequences disclosed in the present invention

Sequence 17 BP: 4 A; 8 C; 4 G; 0 T; 1 U; 0 Other;

Query Match	8.1%;	Score 11.2;	DB 1;	Length 17;
Best Local Similarity	75.0%;	Pred. No. 5.2e+02;		
Matches	12:	Conservative	3:	Indels 0;
Gaps	0;	Mismatches	1:	

Qy 1660 CAGGCTCACAGCTGGA 1675  
pb 2 CAGGCUACCGCCGCA 17

RESULT 769  
ACD51053  
ID ACD51053 standard: RNA: 17 BP.

XX ACD51053;  
AC  
XX  
DT 23-SEP-2003 (first entry)

DE HBV hammerhead ribozyme substrate sequence #366.

Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
RNA stability; RNA expression; RNA synthesis; antisense;  
enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinczyme;  
ambrzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
HBV reverse transcriptase; Enhancer I region; viral replication;  
degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
virocide; antiinflammatory; substrate; ss.

OS Hepatitis B virus.

AA PN WO200281494-A1.

17-OCT-2002

XX  
PE  
26-MAR-2002. 2002WQ-IIS009187.XX  
PB 26-MAR-2001: 2001US-00817879

PR 08-JUN-2001; 2001US-0087747B.  
 PR 08-JUN-2001; 2001US-0386876P  
 PR 08-JUN-2001; 2001US-0386876P

PR 24-OCT-2001; 2001US-0335059P.

XX

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (PVC/) PAVCO P.

PA (DRAP/) DRAPER K.

XX  
XXXXX(0000)

FI Biall E, Macejak D, Roberts E:  
PI Draper K. Roberts E:

XX  
DR WPT- 2003-229207/22.

XX Naval compound useful for treating

PT hepatocellular carcinoma, or

infection.

Example 1; Page 143; 387pp; English.

The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes, inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HBV ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences disclosed in the present invention

Sequence 17 BP; 3 A; 4 C; 5 G; 0 T; 5 U; 0 Other;

Query Match	8.1%	Score 11.2;	DB 1;	Length 17;
Best Local Similarity	56.2%;	Pred. No. 5.2e+02;		
Matches	9;	Conservative	4;	Mismatches 3;
				Indels 0;
				Gaps 0;

QY 1680 TGGTGTCTCCTCCAGC 1695  
          :||:|:  
Db 1 UGGUGUUCACCAGC 16

RESULT 770

ACD64268  
ID ACD64268 standard; RNA; 17 BP.

XX  
AC  
ACD64268.XX  
DT 30-SEP-2003 (first entry)XX  
NE  
HCY minus strand DNAzyme substrate sequence #1459.

XX	Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW	RNA stability; RNA expression; RNA synthesis; antisense;
KW	enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinczyme;
KW	ambzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW	HBV reverse transcriptase; Enhancer I region; viral replication;
KW	degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW	liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW	virucide; antiinflammatory; substrate; ss.

XX  
NS  
Hepatitis C virus.

XX  
PN  
W0200281494-A1XX  
17-0000-2002XX  
DE  
36-MAR-2003. 2003WQ-IIS009187

XX  
BB  
CC MAP-2001, 2001US-00817879

PR 08-JUN-2001; 2001US-0087/478.  
 PR 08-JUN-2001; 2001US-0395876P  
 PR 08-JUN-2001; 2001US-0395876P

PR 24-OCT-2001; 2001US-0335059P.

[illegible]

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (PVC//) PAVCO P.

PA (LEBP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L, Macejak D, Meswigen J, Morrissey J, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX WPI; 2003-229207/22.  
 DR Novel compound useful for treating cirrhosis, liver failure,  
 XX hepatocellular carcinoma, or condition associated with hepatitis C virus  
 XX infection.  
 PS Claim 1; Page 301; 387pp; English.  
 XX  
 CC The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNazyme or minus strand DNazyme sequences disclosed in the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 0 A; 9 C; 5 G; 0 T; 3 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 5.2e+02;  
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1677 CCTGGTGTCCTCCCC 1692  
 DB |||..||:||||  
 2 CCGCGGUGUCUCCCC 17  
 RESULT 771  
 ACD64752/c  
 ID ACD64752 standard; RNA; 17 BP.  
 AC ACD64752;  
 XX  
 DT 30-SEP-2003 (first entry)  
 XX HCV minus strand DNazyme substrate sequence #1719.  
 DE  
 XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 XX WO200281494-A1.  
 PN  
 XX 17-OCT-2002.  
 PD  
 XX 26-MAR-2002; 2002WO-US0009187.  
 PF  
 XX 26-MAR-2001; 2001US-00817879.  
 PR

PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEBP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L, Macejak D, Meswigen J, Morrissey J, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX WPI; 2003-229207/22.  
 DR Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 PS Claim 1; Page 305; 387pp; English.  
 XX  
 CC The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNazyme or minus strand DNazyme sequences disclosed in the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 2 A; 4 C; 8 G; 0 T; 3 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1660 CAGGCTCACAGCTGGA 1675  
 DB |||||  
 17 CAGGCTCACGCGCA 2  
 RESULT 772  
 ACC67762/c  
 ID ACC67762 standard; DNA; 17 BP.  
 XX ACC67762;  
 AC  
 XX  
 DT 01-JUL-2003 (first entry)  
 XX  
 XX Murine oligonucleotide associated with tumour suppression, SEQ ID 5009.  
 DE  
 XX  
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrenia; ss.  
 XX  
 XX Mus musculus.  
 OS



Mon Aug 30 09:26:45 2004

```
PN WO2003025176-A2.
XX
PD
XX
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
XX 17-SEP-2001; 2001FR-00011979.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-333167/31.
DR
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; Page 616; 738pp; French.
PS
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCAGCTGGGAAAC 1677
Db 16 GCCTTACAGTGGATC 1
RESULT 773
ACC64522
ID ACC64522 standard; DNA; 17 BP.
XX
XX ACC64522;
XX
XX 01-JUL-2003 (first entry)
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 1769.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
XX viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; ss.
XX
XX Mus musculus.
XX
XX WO2003025176-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004210.
XX
XX 17-SEP-2001; 2001FR-00011979.
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-333167/31.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; Page 616; 738pp; French.
PS
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1662 GGCTCAGCTGGGAAAC 1677
Db 16 GCCTTACAGTGGATC 1
RESULT 774
ACC66061/c
ID ACC66061 standard; DNA; 17 BP.
XX
XX ACC66061;
XX
XX 01-JUL-2003 (first entry)
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 3308.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
XX viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; ss.
XX
XX Mus musculus.
XX
XX WO2003025176-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004210.
XX
XX 17-SEP-2001; 2001FR-00011979.
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-333167/31.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; Page 417; 738pp; French.
PS
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 6 A; 8 C; 1 G; 2 T; 0 U; 0 Other;
SQ
Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1752 ATCCTAAAGGCCCACT 1767
Db 2 ATCCCAACACCACT 17
RESULT 774
ACC66061/c
ID ACC66061 standard; DNA; 17 BP.
XX
XX ACC66061;
XX
XX 01-JUL-2003 (first entry)
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 3308.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
XX viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; ss.
XX
XX Mus musculus.
XX
XX WO2003025176-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004210.
XX
XX 17-SEP-2001; 2001FR-00011979.
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-333167/31.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; Page 417; 738pp; French.
PS
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 6 A; 8 C; 1 G; 2 T; 0 U; 0 Other;
SQ
```



XX WPI; 2003-333167/31.

XX DR

XX CC

XX PT New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.

XX PT

XX PT

XX PS Disclosure; Page 248; 738pp; French.

XX CC

XX CC The present invention relates to murine oligonucleotides (ACC62754-ACC6806), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistance. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, e.g. as one component of a gene chip; in vitro as (anti)sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia

XX CC

SQ Sequence 17 BP; 4 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0

QY 1717 GTACGGAGATGGAGAT 1732  
||| |||||  
17 GTCGGAATATGGAGAT 2

Db

RESULT 779

ACC64238/c

ID ACC64238 standard; DNA; 17 BP.

XX CC

XX AC ACC64238;

XX CC

XX DT 01-JUL-2003 (first entry)

XX DE Murine oligonucleotide associated with tumour suppression, SEQ ID 1485.

XX CC

XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance;

XX KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; ss.

XX CC

XX OS Mus musculus.

XX CS

XX PN WO2003025176-A2.

XX CC

XX PD 27-MAR-2003.

XX PF 17-SEP-2002; 2002WO-IB004210.

XX CC

XX PR 17-SEP-2001; 2001PR-00011979.

XX CC

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX CC

XX PI Telerman A, Amson R, Tuijnder M;

XX DR

XX DR WPI; 2003-333167/31.

XX CC

XX CC New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.

XX CC

XX PS Disclosure; Page 204; 738pp; French.

XX CC

XX CC The present invention relates to murine oligonucleotides (ACC62754-ACC6806), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistance. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, e.g. as one component of a

CC gene chip; in vitro as (anti)sense reagents; and (2) for production of  
 CC recombinant polypeptides. The oligonucleotides are useful for preparation  
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia  
 XX  
 SQ Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1697 TCGTCGAGTTCGGTT 1712  
 DB 17 TCGTAGAAGTTGGAT 2

RESULT 780  
 ACC83620  
 ID ACC83620 standard; DNA; 17 BP.  
 XX  
 AC ACC83620;  
 XX  
 DT 08-SEP-2003 (first entry)  
 XX  
 DE Escherichia coli dGTPase dgt gene PCR primer or probe.  
 XX  
 KW Deoxyguanosine triphosphate triphosphohydrolase; dGTPase; enzyme;  
 KW EC-3.1.5.1; enteric bacteria; biosensor; biochip; PCR; primer; probe; ss.  
 XX  
 OS Escherichia coli.  
 XX  
 PN WO2003046201-A2.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 01-OCT-2002; 2002WO-US031323.  
 XX  
 PR 21-NOV-2001; 2001US-00991552.  
 XX  
 PA (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.  
 XX  
 PI Quirk S;  
 XX  
 PS WPI; 2003-482523/45.  
 XX

PT Detecting enteric bacteria of the family Enterobacteriaceae such as  
 PT Escherichia in food or water sample, by hybridizing test sample with a  
 PT probe, and detecting hybridization between probe and a nucleic acid in  
 PT sample.  
 XX  
 PS Claim 3; Page 63; 90pp; English.

CC The present sequence is that of an oligonucleotide that can be used as a  
 CC hybridisation probe for detecting or identifying Escherichia coli  
 CC guanosine triphosphate triphosphohydrolase (dGTPase) dgt gene sequences,  
 CC or as a primer for DNA synthesis, DNA sequencing or DNA amplification of  
 CC dGTPase nucleic acids. dGTPase is found only in Enterobacteriaceae, such  
 CC as Escherichia coli, Salmonella and Klebsiella species. Detection of the  
 CC enzyme is therefore a specific indicator that Enterobacteriaceae  
 CC pathogens are present in a test sample. The invention relates to the  
 CC detection of Enterobacteriaceae and to the identification of the genus or  
 CC genera of Enterobacteriaceae present in a test sample. It is based on the  
 CC detection of dGTPase nucleic acids or dGTPase enzyme using e.g.  
 CC hybridisation probes comprising the present nucleic acid, DNA  
 CC amplification primers, or biosensor chips comprising the present nucleic  
 CC acid. The methods are useful for determining whether food, water or other  
 CC samples are contaminated with enteric bacteria

Sequence 17 BP; 2 A; 5 C; 8 G; 2 T; 0 U; 0 Other;  
 Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1699 CTCACAGCTGGTGGCA 1704  
 DB 2 CTCGACGCTGGCGGCA 17

RESULT 781  
 ADB40118/c  
 ID ADB40118 standard; DNA; 17 BP.  
 XX  
 AC ADB40118;  
 XX  
 DT 18-DEC-2003 (revised)  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Tumour suppression/reversion associated nucleotide #441.  
 XX  
 KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
 KW diagnosis.

OS Homo sapiens.  
 XX  
 XX WO2003040369-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB004219.  
 XX  
 PR 17-SEP-2001; 2001FR-000:1981.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX  
 XX WPI; 2003-441574/41.

New nucleic acid encoding human prostate membrane-specific antigen,  
 useful e.g. for treatment of tumors and viral infection, also related  
 polypeptide and antibodies.

Disclosure; Page 83; 771pp; French.

CC The invention relates to the isolation of 6327 nucleotide sequences,  
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
 CC sequence having at least 80% identity, after optimal alignment, with the  
 CC nucleotides, a sequence that hybridizes under stringent conditions with  
 CC the nucleotides, or the complement, or corresponding RNA, of the  
 CC nucleotides. The nucleotides are used as probes or primers for detecting,  
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
 CC sense and antisense sequences, of nucleotides involved in tumour  
 CC suppression or reversion, apoptosis and/or viral resistance, to produce  
 CC recombinant polypeptides, and to prepare transgenic animals, as  
 CC cells containing the vectors). The nucleotides (also vectors containing them and  
 CC (Ab) against the polypeptide are useful for prevention and/or treatment  
 CC of viral infections or diseases characterized by development of tumours  
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
 CC Analysis of the expression of the nucleotides can be used for diagnosis  
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
 CC also be used to screen for their specific interactive molecules,  
 CC potentially useful for treating diseases associated with abnormal  
 CC expression of the nucleotides.

Sequence 17 BP; 6 A; 6 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1711 TTAGGAGTACGGAGAT 1726

|||||  
17 TTAGGAGTATGCGAT 2

Db  
RESULT 782  
ADB40655  
ID ADB40655 standard; DNA; 17 BP.  
XX AC  
XX ADB40655;  
XX  
XX 18-DEC-2003 (revised)  
DT 04-DEC-2003 (first entry)  
DE  
DE Tumour suppression/reversion associated nucleotide #978.  
XX  
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
KW diagnosis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2003040369-A2.  
PN  
XX  
XX 15-MAY-2003.  
PD  
XX  
XX 17-SEP-2002; 2002WO-IB004219.  
PF  
XX  
XX 17-SEP-2001; 2001FR-00011981.  
PR  
XX  
XX (MOLE-) MOLECULAR ENGINES LAB.  
PA  
XX  
XX Telerman A, Amson R, Tuijnder M;  
PI  
XX  
XX WPI; 2003-441574/41.  
DR  
XX  
XX New nucleic acid encoding human prostate membrane-specific antigen,  
PT useful e.g. for treatment of tumors and viral infection, also related  
PT polypeptide and antibodies.  
XX  
XX Disclosure; Page 146; 771pp; French.  
XX  
XX The invention relates to the isolation of 6327 nucleotide sequences,  
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
CC sequence having at least 80% identity, after optimal alignment, with the  
CC nucleotides, a sequence that hybridizes under stringent conditions with  
CC the nucleotides, or the complement, or corresponding RNA, of the  
CC nucleotides. The nucleotides are used as probes or primers for detecting,  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
CC sense and antisense sequences, of nucleotides involved in tumour  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC (Ab) against the polypeptide are useful for prevention and/or treatment  
CC of viral infections or diseases characterized by development of tumours  
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
CC Analysis of the expression of the nucleotides can be used for diagnosis  
CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
CC also be used to screen for their specific interactive molecules,  
CC potentially useful for treating diseases associated with abnormal  
CC expression of the nucleotides.  
XX  
SQ Sequence 17 BP; 3 A; 10 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1735 GCTCCCACTCTCTCC 1750  
Db 1 GATCCCACTGCCCC 16

RESULT 783  
ADB40250  
ID ADB40250 standard; DNA; 17 BP.  
XX AC  
XX ADB40250;  
XX  
XX 18-DEC-2003 (revised)  
DT 04-DEC-2003 (first entry)  
DE  
DE Tumour suppression/reversion associated nucleotide #573.  
XX  
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
KW diagnosis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2003040369-A2.  
PN  
XX  
XX 15-MAY-2003.  
PD  
XX  
XX 17-SEP-2002; 2002WO-IB004219.  
PF  
XX  
XX 17-SEP-2001; 2001FR-00011981.  
PR  
XX  
XX (MOLE-) MOLECULAR ENGINES LAB.  
PA  
XX  
XX Telerman A, Amson R, Tuijnder M;  
PI  
XX  
XX WPI; 2003-441574/41.  
DR  
XX  
XX New nucleic acid encoding human prostate membrane-specific antigen,  
PT useful e.g. for treatment of tumors and viral infection, also related  
PT polypeptide and antibodies.  
XX  
XX Disclosure; Page 99; 771pp; French.  
XX  
XX The invention relates to the isolation of 6327 nucleotide sequences,  
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
CC sequence having at least 80% identity, after optimal alignment, with the  
CC nucleotides, a sequence that hybridizes under stringent conditions with  
CC the nucleotides, or the complement, or corresponding RNA, of the  
CC nucleotides. The nucleotides are used as probes or primers for detecting,  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
CC sense and antisense sequences, of nucleotides involved in tumour  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC (Ab) against the polypeptide are useful for prevention and/or treatment  
CC of viral infections or diseases characterized by development of tumours  
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
CC Analysis of the expression of the nucleotides can be used for diagnosis  
CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
CC also be used to screen for their specific interactive molecules,  
CC potentially useful for treating diseases associated with abnormal  
CC expression of the nucleotides.  
XX  
SQ Sequence 17 BP; 6 A; 8 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1735 GCTCCCACTCTCTCC 1750  
Db 1 GATCCCACTCTCTCC 16

RESULT 784  
ADB39772

```

ID ADB39772 standard; DNA; 17 BP.
XX AC
XX ADB39772;
XX DT
XX DE
XX DT 18-DEC-2003 (revised)
XX DT 04-DEC-2003 (first entry)
XX DE
XX DE Tumour suppression/reversion associated nucleotide #95.
XX KW
XX KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
XX KW primer; probe; tumour suppression; tumour reversion; apoptosis;
XX KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX KW diagnosis.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO2003040369-A2.
XX PD
XX PD 15-MAY-2003.
XX PF
XX PF 17-SEP-2002; 2002WO-IB004219.
XX PR
XX PR 17-SEP-2001; 2001PR-00011981.
XX PA
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI
XX PI Telerman A, Amson R, Tuijnder M;
XX DR
XX DR WPI; 2003-441574/41.
XX PT
XX PT New nucleic acid encoding human prostate membrane-specific antigen,
XX PT useful e.g. for treatment of tumors and viral infection, also related
XX PT polypeptide and antibodies.
XX PS
XX PS Disclosure; Page 43; 71pp; French.
XX CC
XX CC The invention relates to the isolation of 6327 nucleotide sequences,
XX CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX CC sequence having at least 80% identity, after optimal alignment, with the
XX CC nucleotides, a sequence that hybridizes under stringent conditions with
XX CC the nucleotides, or the complement, or corresponding RNA, of the
XX CC nucleotides. The nucleotides are used as probes or primers for detecting,
XX CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX CC sense and antisense sequences, of nucleotides involved in tumour
XX CC suppression or reversion, apoptosis and or viral resistance, to produce
XX CC recombinant polypeptides, and to prepare transgenic animals, as
XX CC experimental models. The nucleotides (also vectors containing them and
XX CC cells containing the vectors), the encoded polypeptides and antibodies
XX CC (Ab) against the polypeptide are useful for prevention and/or treatment
XX CC of viral infections or diseases characterized by development of tumours
XX CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX CC Analysis of the expression of the nucleotides can be used for diagnosis
XX CC and/or prognosis of these diseases. The nucleotides and polypeptides can
XX CC also be used to screen for their specific interactive molecules,
XX CC potentially useful for treating diseases associated with abnormal
XX CC expression of the nucleotides.
XX SQ
XX SQ Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Fred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1663 GCTCACAGCTGGACC 1678
Db 1 GATCACACCGGAAC 16

RESULT 785
ADC04842/c
ID ADC04842 standard; DNA; 17 BP.
XX AC
XX AC ADC04842;

```

```

XX 18-DEC-2003 (first entry)
XX Human Na/H exchanger-like protein 1 gene oligonucleotide #1289.
XX ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
XX NHEP1; passive replacement therapy; vaccine; diagnosis.
XX OS
XX OS Homo sapiens.
XX PN
XX PN EP1273660-A2.
XX PD
XX PD 08-JAN-2003.
XX PF
XX PF 25-JAN-2002; 2002EP-00001160.
XX PR
XX PR 30-JAN-2001; 2001WO-US0000666.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 21-DEC-2001; 2001US-0343331P.
XX PA
XX PA (AEOM-) AEOMICA INC.
XX PI
XX PI Gu Y;
XX DR
XX DR WPI; 2003-302724/30.
XX PT
XX PT New human sodium-hydrogen exchanger like protein 1 (NHEP1), useful as a
XX PT passive replacement therapy or as a vaccine for treating or preventing
XX PT disorders associated with aberrant expression or activity of human
XX PT NHEP1.
XX PS
XX PS Example 2; SEQ ID NO 1329; 468pp; English.
XX CC
XX CC The invention relates to a nucleic acid molecule which encodes a Na+/H+
XX CC exchanger like protein (NHEP1). The NHEP1 nucleic acid molecule, NHEP1
XX CC polypeptide, an antibody against the protein or its antigen-binding
XX CC fragment is useful in therapy. The NHEP1 nucleic acid molecule, NHEP1
XX CC polypeptide and an agonist are particularly useful for manufacturing a
XX CC medicament for treating or preventing a disorder associated with
XX CC decreased expression or activity of human NHEP1. The antibody or its
XX CC antigen-binding fragment, and an antagonist, are useful for manufacturing
XX CC a medicament for treating or preventing a disorder associated with
XX CC increased expression or activity of human NHEP1. The NHEP1 nucleic acid
XX CC or protein is useful as passive replacement therapy, as a vaccine, or in
XX CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
XX CC spanning the sequence of the human NHEP1 gene (ADC03514).
XX SQ
XX SQ Sequence 17 BP; 0 A; 11 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Fred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1713 AGGAGTACGAGATGG 1728
Db 17 AGGAGGAGGAGAGCG 2

RESULT 786
ADC04230
ID ADC04230 standard; DNA; 17 BP.
XX AC
XX AC ADC04230;
XX DT
XX DT 18-DEC-2003 (first entry)
XX DE
XX DE Human Na/H exchanger-like protein 1 gene oligonucleotide #677.
XX KW
XX KW ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
XX KW NHEP1; passive replacement therapy; vaccine; diagnosis.
XX OS
XX OS Homo sapiens.

```

```

PN EP1273660-A2.
XX
XX PD
XX
XX PF
XX 25-JAN-2002; 2002EP-00001160.
XX
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 21-DEC-2001; 2001US-0343331P.
XX
XX PA (AEOM-) AEOMICA INC.
XX
XX PI Gu Y;
XX
XX DR WPI; 2003-302724/30.
XX
XX PT New human sodium-hydrogen exchanger like protein 1 (NHEPL1), useful as a
XX PT passive replacement therapy or as a vaccine for treating or preventing
XX PT disorders associated with aberrant expression or activity of human
XX PT NHEPL1.
XX
XX PS Example 2; SEQ ID NO 717; 468pp; English.
XX
XX CC The invention relates to a nucleic acid molecule which encodes a Na+/H+
XX CC exchanger like protein (NHEPL1). The NHEPL1 nucleic acid molecule, NHEPL1
XX CC polypeptide, an antibody against the protein or its antigen-binding
XX CC fragment is useful in therapy. The NHEPL1 nucleic acid molecule, NHEPL1
XX CC polypeptide and an agonist are particularly useful for manufacturing a
XX CC medicament for treating or preventing a disorder associated with
XX CC decreased expression or activity of human NHEPL1. The antibody or its
XX CC antigen-binding fragment, and an antagonist, are useful for manufacturing
XX CC a medicament for treating or preventing a disorder associated with
XX CC increased expression or activity of human NHEPL1. The NHEPL1 nucleic acid
XX CC or protein is useful as passive replacement therapy, as a vaccine, or in
XX CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
XX CC spanning the sequence of the human NHEPL1 gene (ADC03514).
XX
XX SQ Sequence 17 BP; 4 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Qy 1679 CTGGTGTCTCTCCAG 1694
Db 1 CTGATGTCGTCTACAG 16

RESULT 787
ADC04229
ID ADC04229 standard; DNA; 17 BP.
XX
XX AC ADC04229;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Human Na/H exchanger-like protein 1 gene oligonucleotide #676.
XX
XX KW ss: gene therapy; vaccine; sodium/hydrogen exchanger like protein;
XX KW NHEPL1; passive replacement therapy; vaccine; diagnosis.
XX
XX OS Homo sapiens.
XX
XX PN EP1273660-A2.
XX
XX PD 08-JAN-2003.
XX
XX PF 25-JAN-2002; 2002EP-00001160.
XX
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 21-DEC-2001; 2001US-0343331P.
XX
XX PA (AEOM-) AEOMICA INC.
XX
XX PI Gu Y;
XX
XX DR WPI; 2003-302724/30.
XX
XX PT New human sodium-hydrogen exchanger like protein 1 (NHEPL1), useful as a
XX PT passive replacement therapy or as a vaccine for treating or preventing
XX PT disorders associated with aberrant expression or activity of human
XX PT NHEPL1.
XX
XX SQ Sequence 17 BP; 4 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 8.1%; Score 11.2; DB 1; Length 17;
XX Best Local Similarity 81.2%; Pred. No. 5.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Qy 1679 CTGGTGTCTCTCCAG 1694
Db 1 CTGATGTCGTCTACAG 16

RESULT 788
ADC04843/C
ID ADC04843 standard; DNA; 17 BP.
XX
XX AC ADC04843;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Human Na/H exchanger-like protein 1 gene oligonucleotide #1290.
XX
XX KW ss: gene therapy; vaccine; sodium/hydrogen exchanger like protein;
XX KW NHEPL1; passive replacement therapy; vaccine; diagnosis.
XX
XX OS Homo sapiens.
XX
XX PN EP1273660-A2.
XX
XX PD 08-JAN-2003.
XX
XX PF 25-JAN-2002; 2002EP-00001160.
XX
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 21-DEC-2001; 2001US-0343331P.
XX
XX PA (AEOM-) AEOMICA INC.
XX
XX PI Gu Y;
XX
XX DR WPI; 2003-302724/30.
XX
XX PT New human sodium-hydrogen exchanger like protein 1 (NHEPL1), useful as a
XX PT passive replacement therapy or as a vaccine for treating or preventing
XX PT disorders associated with aberrant expression or activity of human
XX PT NHEPL1.

```

XX PS Example 2; SEQ ID NO 1330; 468bp; English.

XX CC The invention relates to a nucleic acid molecule which encodes a Na+/H+ exchanger-like protein (NHEP1). The NHEP1 nucleic acid molecule, NHEP1 polypeptide, an antibody against the protein or its antigen-binding fragment is useful in therapy. The NHEP1 nucleic acid molecule, NHEP1 polypeptide and an agonist are particularly useful for manufacturing a medicament for treating or preventing a disorder associated with decreased expression or activity of human NHEP1. The antibody or its antigen-binding fragment, and an antagonist, are useful for manufacturing a medicament for treating or preventing a disorder associated with increased expression or activity of human NHEP1. The NHEP1 nucleic acid or protein is useful as passive replacement therapy, as a vaccine, or in diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide spanning the sequence of the human NHEP1 gene (ADC03514).

XX SQ Sequence 17 BP; 0 A; 10 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1713 AGGAGTACGGAGATGG 1728  
DB 16 AGGAGGAGGAGAGGG 1

RESULT 789  
ADB45742/c

ID ADB45742 standard; DNA; 17 BP.

XX AC ADB45742;

XX DT 18-DEC-2003 (first entry)

XX DE Tumour suppression/reversion associated nucleotide #6065.

XX KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
KW diagnosis.

XX OS Homo sapiens.

XX PN WO2003040369-A2.

XX PD 15-MAY-2003.

XX PF 17-SEP-2002; 2002WO-IB004219.

XX PR 17-SEP-2001; 2001FR-00011981.

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;

XX DR WPI; 2003-441574/41.

XX PT New nucleic acid encoding human prostate membrane-specific antigen,  
PT useful e.g. for treatment of tumors and viral infection, also related  
PT polypeptide and antibodies.

XX PS Disclosure; Page 741; 771pp; French.

XX CC The invention relates to the isolation of 6327 nucleotide sequences,  
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
CC sequence having at least 80% identity, after optimal alignment, with the  
CC nucleotides, a sequence that hybridizes under stringent conditions with  
CC the nucleotides, or the complement, or corresponding RNA, of the  
CC nucleotides. The nucleotides are used as probes or primers for detecting,  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
CC sense and antisense sequences, of nucleotides involved in tumour  
CC suppression or reversion, apoptosis and/or viral resistance, to produce  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC cells containing the vectors), the encoded polypeptides and antibodies

CC suppression or reversion, apoptosis and/or viral resistance, to produce  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC cells containing the vectors), the encoded polypeptides and antibodies

CC suppressor or reversion, apoptosis and/or viral resistance, to produce  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC cells containing the vectors), the encoded polypeptides and antibodies

CC (Ab) against the polypeptide are useful for prevention and/or treatment  
CC of viral infections or diseases characterized by development of tumours  
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

CC Analysis of the expression of the nucleotides can be used for diagnosis  
CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
CC also be used to screen for their specific interactive molecules,  
CC potentially useful for treating diseases associated with abnormal  
CC expression of the nucleotides.

XX SQ Sequence 17 BP; 3 A; 9 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1717 GTACGGAGATGGAGAT 1732  
DB 17 GGATGGGATGGAGAT 2

RESULT 790  
ADB45372

ID ADB45372 standard; DNA; 17 BP.

XX AC ADB45372;

XX DT 18-DEC-2003 (first entry)

XX DE Tumour suppression/reversion associated nucleotide #5695.

XX KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
KW diagnosis.

XX OS Homo sapiens.

XX PN WO2003040369-A2.

XX PD 15-MAY-2003.

XX PF 17-SEP-2002; 2002WO-IB034219.

XX PR 17-SEP-2001; 2001FR-00011981.

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;

XX DR WPI; 2003-441574/41.

XX PT New nucleic acid encoding human prostate membrane-specific antigen,  
PT useful e.g. for treatment of tumors and viral infection, also related  
PT polypeptide and antibodies.

XX PS Disclosure; Page 697; 771pp; French.

XX CC The invention relates to the isolation of 6327 nucleotide sequences,  
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
CC sequence having at least 80% identity, after optimal alignment, with the  
CC nucleotides, a sequence that hybridizes under stringent conditions with  
CC the nucleotides, or the complement, or corresponding RNA, of the  
CC nucleotides. The nucleotides are used as probes or primers for detecting,  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
CC sense and antisense sequences, of nucleotides involved in tumour  
CC suppression or reversion, apoptosis and/or viral resistance, to produce  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC cells containing the vectors), the encoded polypeptides and antibodies



CC (Ab) against the polypeptide are useful for prevention and/or treatment  
 CC of viral infections or diseases characterized by development of tumours  
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
 CC Analysis of the expression of the nucleotides can be used for diagnosis  
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
 CC also be used to screen for their specific interactive molecules,  
 CC potentially useful for treating diseases associated with abnormal  
 CC expression of the nucleotides.  
 XX Sequence 17 BP; 6 A; 4 C; 4 G; 3 T; 0 U; 0 Other;  
 SQ

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTACAG 1670  
 DB 2 ATCACAGGCTTACAG 17

RESULT 791  
 ADB4458/c  
 ID ADB4458 standard; DNA; 17 BP.  
 XX AC  
 XX ADB4458;  
 XX DT 18-DEC-2003 (first entry)  
 XX DE Tumour suppression/reversion associated nucleotide #5181.  
 XX cytotatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
 KW diagnosis.  
 XX OS Homo sapiens.  
 XX WO2003040369-A2.  
 XX PN 15-MAY-2003.  
 XX PD 17-SEP-2002; 2002WO-IB004219.  
 XX PF 17-SEP-2001; 2001FR-00011981.  
 XX PR (MOLE-) MOLECULAR ENGINES LAB.  
 XX PA Telerman A, Amson R, Tuijnder M;  
 XX WPI; 2003-441574/41.  
 XX New nucleic acid encoding human prostate membrane-specific antigen,  
 PT useful e.g. for treatment of tumors and viral infection, also related  
 PT polypeptide and antibodies.  
 XX PS Disclosure; Page 637; 771pp; French.  
 XX The invention relates to the isolation of 6327 nucleotide sequences,  
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
 CC sequence having at least 80% identity, after optimal alignment, with the  
 CC nucleotides, a sequence that hybridizes under stringent conditions with  
 CC the nucleotides, or the complement, or corresponding RNA, of the  
 CC nucleotides. The nucleotides are used as probes or primers for detecting,  
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
 CC sense and antisense sequences, of nucleotides involved in tumour  
 CC suppression or reversion, apoptosis and or viral resistance, to produce  
 CC recombinant polypeptides, and to prepare transgenic animals, as  
 CC experimental models. The nucleotides (also vectors containing them and  
 CC cells containing the vectors), the encoded polypeptides and antibodies  
 CC (Ab) against the polypeptide are useful for prevention and/or treatment  
 CC of viral infections or diseases characterized by development of tumours  
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
 CC Analysis of the expression of the nucleotides can be used for diagnosis

CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
 CC also be used to screen for their specific interactive molecules,  
 CC potentially useful for treating diseases associated with abnormal  
 CC expression of the nucleotides.  
 XX Sequence 17 BP; 4 A; 4 C; 1 G; 8 T; 0 U; 0 Other;  
 SQ

Query Match 8.1%; Score 11.2; DB 1; Length 17;  
 Best Local Similarity 81.2%; Pred. No. 5.2e+02;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1723 AGATGGAGATTGGTC 1738  
 DB 16 AATGGAAATTGGATC 1

RESULT 792  
 ADB4800/c  
 ID ADB4800 standard; DNA; 17 BP.  
 XX AC ADE48000;  
 XX DT 29-JAN-2004 (first entry)  
 XX DE Human NOVX reverse PCR primer SEQ ID NO:362.  
 XX human; cardiant; antiarteriosclerotic; hypotensive; immunosuppressive;  
 KW dermatological; anorectic; cytostatic; antidiabetic; haemostatic;  
 KW anti-HIV; antiasthmatic; antibacterial; virucide; neuroprotective;  
 KW nootropic; antiparkinsonian; antilipaemic; gene therapy; vaccine; PCR;  
 KW primer; ss.  
 XX OS Homo sapiens.  
 XX WO2003076642-A2.  
 XX PN 18-SEP-2003.  
 XX PD 02-AUG-2002; 2002WO-US024459.  
 XX PF 02-AUG-2001; 2001US-0309501P.  
 XX PR 03-AUG-2001; 2001US-0310291P.  
 XX PR 08-AUG-2001; 2001US-0310951P.  
 XX PR 09-AUG-2001; 2001US-0311322P.  
 XX PR 13-AUG-2001; 2001US-0311979P.  
 XX PR 14-AUG-2001; 2001US-0312203P.  
 XX PR 17-AUG-2001; 2001US-0313156P.  
 XX PR 17-AUG-2001; 2001US-0313201P.  
 XX PR 20-AUG-2001; 2001US-0313702P.  
 XX PR 21-AUG-2001; 2001US-0314031P.  
 XX PR 23-AUG-2001; 2001US-0314466P.  
 XX PR 28-AUG-2001; 2001US-0315403P.  
 XX PR 29-AUG-2001; 2001US-0315853P.  
 XX PR 31-AUG-2001; 2001US-0316508P.  
 XX PR 21-SEP-2001; 2001US-0323936P.  
 XX PR 03-DEC-2001; 2001US-0338078P.  
 XX PR 05-FEB-2002; 2002US-0354655P.  
 XX PR 05-MAR-2002; 2002US-0361764P.  
 XX PR 19-APR-2002; 2002US-0373825P.  
 XX PR 15-MAY-2002; 2002US-0380971P.  
 XX PR 15-MAY-2002; 2002US-0380980P.  
 XX PR 16-MAY-2002; 2002US-0381039P.  
 XX PR 28-MAY-2002; 2002US-0383761P.  
 XX PR 29-MAY-2002; 2002US-0383877P.  
 XX PR 01-AUG-2002; 2002US-00210130.  
 XX (CURA-) CURAGEN CORP.  
 XX Zerhusen BD, Patturajan M, Kekuda R, Miller CE, Rieger DK;  
 PI Pena CPA, Shimkets RA, Li L, Berghs C, Zhong M, Casman SJ, Voss EZ;  
 PI Boldog FL, Padigaru M, Smithson G, Shenoy SG, Ji W, Gorman L;  
 PI Vernet CAM, Leite MW, Guo X, Anderson DW, Spytek KA, Gerlach VL;  
 PI Burgess CE, Khramtsov NV, Ort T, Ellerman K, Rastelli L, Agee ML;

PI Chaudhuri A, Chant JS, Dipippo VA, Edinger SR, Eisen A, Gangolli EA;  
PI Giot L, Ooi CE, Rothenberg ME, Spaderna SK, Hjalte T, Liu X;  
PI Taupier RJ, Catterton E;  
XX  
DR WPI; 2003-779062/73.  
XX  
XX New NOVX polypeptides and nucleic acids, useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, diabetes,  
PT atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing  
PT or pharmacogenomics.  
XX  
PS Example 49; SEQ ID NO 362; 562pp; English.  
XX  
XX The invention relates to a novel (NOVX) human polypeptide. A polypeptide  
CC of the invention has cardiant, antiarteriosclerotic, hypotensive,  
CC immunosuppressive, dermatological, anorectic, cytostatic, antidiabetic,  
CC haemostatic, anti-HIV, antiasthmatic, antibacterial, virucide,  
CC neuroprotective, nootropic, antiparkinsonian, and antilipaeamic activity.  
CC A polynucleotide encoding a polypeptide of the invention may have a use  
CC in gene therapy, and as a vaccine. A polypeptide of the invention is  
CC useful in the manufacture of a medicament for treating a syndrome  
CC associated with a human disease, the disease selected from a pathology  
CC associated with the polypeptide. These may also be used in diagnosing,  
CC treating or preventing NOVX-associated disorders such as cardiomyopathy,  
CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,  
CC haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease,  
CC multiple sclerosis, infections, anorexia, cancer-associated cachexia,  
CC neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's  
CC disease), haematopoietic disorders, dyslipidaemias and other wasting  
CC disorders associated with chronic diseases. The nucleic acids are also  
CC used as hybridisation probes, in chromosome mapping, tissue typing,  
CC preventive medicine, and pharmacogenomics. The polypeptides are also  
CC useful as vaccines. The present sequence represents a PCR primer used in  
CC the invention.  
XX  
SQ Sequence 17 BP; 2 A; 9 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 8.1%; Score 11.2; DB 1; Length 17;  
Best Local Similarity 81.2%; Pred. NO. 5.2e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1719 ACCGAGTGGAGTGG 1734  
DB 16 ACCGAGTGGAGTGG 1  
RESULT 793  
AAA92575/c  
ID AAA92575 standard; DNA; 18 BP.  
XX  
AC AAA92575;  
XX  
DT 04-JAN-2001 (first entry)  
XX  
DE Antisense oligonucleotide ISIS# 30285.  
XX  
XX Human, SRA; steroid receptor RNA activator; cytostatic; antiinflammatory;  
KW SRA inhibitor; cancer; infection; antisense oligonucleotide; ss.  
XX  
OS Synthetic.  
XX  
XX US6107092-A.  
PN  
XX 22-AUG-2000.  
PD  
XX 29-MAR-1999; 99US-00280409.  
PF  
XX 29-MAR-1999; 99US-00280409.  
PR  
XX (ISIS-) ISIS PHARM INC.  
PA (BAYU) BAYLOR COLLEGE MEDICINE.  
XX  
XX Cowsett LM, Bennett CF, O'malley BW;  
PI

XX  
DR WPI; 2000-586211/55.  
XX  
PT Antisense compounds targeted to steroid receptor RNA activator useful for  
PT diagnosis, prophylaxis and treatment of diseases associated with the  
PT steroid activator, such as infection, inflammation or tumor formation.  
XX  
PS Claim 3; Col 41; 47pp; English.  
XX  
CC The present sequence is one of a large number of antisense  
CC oligonucleotides which is directed against one of four human steroid  
CC receptor RNA activator (SRA) nucleic acid sequences. Two series of  
CC antisense oligonucleotides were synthesised. The first series comprised 8  
CC -30 oligodeoxynucleotides with a phosphorothioate backbone. The second  
CC series comprised chimeric oligonucleotides composed of a central gap  
CC region, consisting of ten 2'-deoxynucleotides, which was flanked on both  
CC sides by four-nucleotide wings. The wings were composed of 2'-  
CC methoxyethyl (2'-MOE) nucleotides. Both series contained the same  
CC nucleotide sequences. The antisense compounds are useful for research,  
CC diagnosis, treatment and prophylaxis to prevent or delay infection,  
CC inflammation or tumour formation. Therapeutically the oligonucleotides  
CC are highly safe and are effectively administered to humans  
XX  
SQ Sequence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 U; 0 Other;  
Query Match 8.1%; Score 11.2; DB 1; Length 18;  
Best Local Similarity 81.2%; Pred. NO. 5.6e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1658 ACCAGGCTTCAGCAG 1673  
DB 16 ACCAGGCTTCAGCAG 1  
RESULT 794  
AAC58274/c  
ID AAC58274 standard; DNA; 19 BP.  
XX  
AC AAC58274;  
XX  
DT 29-JAN-2001 (first entry)  
XX  
DE Human PRO212 reverse PCR primer SEQ ID NO:93.  
XX  
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
KW proliferation; tumorigenesis; identification; cancer; PCR primer;  
KW hybridisation; probe; cytostatic; nootropic; neuroprotective;  
KW antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic;  
KW leukaemia; lymphoid malignancy; neuronal disorder; glial disorder;  
KW astrocytal disorder; hypothalamic disorder; glandular disorder;  
KW macrophagal disorder; epithelial disorder; stromal disorder;  
KW blastocoele disorder; inflammatory disorder; angiogenic;  
KW immunologic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200053755-A2.  
PN  
XX 14-SEP-2000.  
PD  
XX 06-JAN-2000; 2000WO-US000376.  
PF  
XX 08-MAR-1999; 99WO-US005028.  
PR  
XX 02-JUN-1999; 99WO-US012252.  
PR  
XX 23-JUN-1999; 99US-0141037P.  
PR  
XX 07-JUL-1999; 99US-0143048P.  
PR  
XX 26-JUL-1999; 99US-0145698P.  
PR  
XX 30-NOV-1999; 99WO-US028313.  
PR  
XX 20-DEC-1999; 99WO-US033911.  
PR  
XX 05-JAN-2000; 2000WO-US000219.  
XX  
XX (GETH) GENENTECH INC.  
XX

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
PI Watanabe CK, Wood WI;  
XX WPI; 2000-572270/53.  
XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
PT treatment, diagnosis and prevention of cancer.  
XX  
XX Example 23; Page 133; 286pp; English.  
XX  
XX The present invention describes an isolated antibody that binds to one of  
CC the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,  
CC PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,  
CC PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,  
CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR  
CC PRO2199. PRO antagonists can be used to inhibit tumour cell growth. The  
CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis  
CC and prevention of cancer. The antibodies and other anti-tumour compounds  
CC maybe used to treat various conditions, including those characterised by  
CC overexpression and/or activation of the amplified PRO genes. Exemplary  
CC conditions or disorders to be treated with such antibodies and other  
CC compounds include benign or malignant tumours (e.g., renal, liver,  
CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,  
CC pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,  
CC glioblastomas, and various head and neck tumours), leukaemias and  
CC lymphoid malignancies, other disorders such as neuronal, glial,  
CC astrocytal, hypothalamic and other glandular, macrophagal, epithelial,  
CC stromal and blastocoele disorders, and inflammatory, angiogenic and  
CC immunologic disorders. AAC58242 to AAC58366 represent PCR primers and  
CC hybridisation probes used in the isolation of the human PRO sequences.  
CC AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO  
CC polynucleotide and protein sequences given in the exemplification of the  
CC present invention  
XX  
XX Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 8.1%; Score 11.2; DB 1; Length 19;  
Best Local Similarity 81.2%; Pred. No. 5.9e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1655 AGCACACAGGCTACAG 1670  
Db 17 AGCACACAGGCTACAG 2  
  
RESULT 795  
ADB66783/C  
ID ADB66783 standard; DNA; 20 BP.  
XX  
XX ADB66783;  
XX  
XX 04-DEC-2003 (first entry)  
XX  
XX Human E2A-Pbx1 antisense phosphorothioate oligonucleotide ISIS No. 16123.  
DE  
DE Human; E2A-Pbx1; antisense; phosphorothioate;  
KW pre-B-cell acute lymphocytic leukaemia; sarcomatous cancer; E2A-HLA;  
KW E2A-HLF; cytostatic; ss.  
XX  
XX Synthetic.  
OS  
OS Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
PH modified\_base 1..20  
FT /\*tag= a  
FT /mod base= OTHER  
FT /note= "phosphorothioate internucleotide linkages"  
XX  
XX US6607915-B1.  
XX  
XX 19-AUG-2003.  
XX  
XX 25-JUL-2000; 2000US-00624945.

XX 30-SEP-1999; 99US-0156836P.  
DR  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Monia BP, Wancewicz E;  
XX  
XX WPI; 2003-707866/67.  
DR  
XX  
XX New antisense compounds targeted to nucleic acids encoding E2A-Pbx1,  
PT useful for inhibiting the expression of E2A-Pbx1, and for treating or  
PT diagnosing a disease associated with overexpression of E2A-Pbx1, e.g.  
PT sarcomatous cancer.  
XX  
XX Example 2; Col 24; 20pp; English.  
PS  
XX The present invention relates to antisense compounds targeted to  
CC polynucleotide sequences encoding human E2A-Pbx1. The antisense compounds  
CC comprise antisense phosphorothioate oligonucleotides. The antisense  
CC compounds are useful for inhibiting the expression of E2A-Pbx1, and for  
CC treating or diagnosing a disease or condition associated with the  
CC overexpression or constitutive activation of E2A-Pbx1, e.g. pre-B-cell  
CC acute lymphocytic leukaemia or sarcomatous cancer. The compounds are also  
CC useful as research reagents and tools, e.g. for detecting and determining  
CC the role of E2-Pbx1 in various cell functions and physiological  
CC processes. The present sequence represents a human E2A-Pbx1 antisense  
CC phosphorothioate oligonucleotide.  
XX  
XX Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 U; 0 Other;  
SQ  
Query Match 8.1%; Score 11.2; DB 1; Length 20;  
Best Local Similarity 81.2%; Pred. No. 6.3e+02;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1668 CAGCTGGAAACCTGGT 1683  
Db 16 CAGCTGTCAGCCTGGT 1  
  
RESULT 796  
ABV69782  
ID ABV69782 standard; cDNA; 11 BP.  
XX  
XX ABV69782;  
AC  
XX  
XX 21-OCT-2002 (first entry)  
DT  
XX  
XX Human skin EST 7568.  
DE  
XX  
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
XX Homo sapiens.  
OS  
OS  
XX WO200253774-A2.  
XX  
XX 11-JUL-2002.  
PD  
XX  
XX 20-DEC-2001; 2001WO-EP015179.  
XX  
XX 03-JAN-2001; 2001DE-01000127.  
XX  
XX (HENK ) HENKEL KGAA.  
XX  
XX Petersohn D, Conradt M, Hofmann K;  
XX  
XX WPI; 2002-590638/63.  
XX  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX

PS Claim 24; Page 239; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 0 A; 4 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 7.9%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1681 GGTCGTCTCTC 1691  
DB 1 GGTCGTCTCTC 11  
RESULT 797  
ABV62361  
ID ABV62361 standard; cDNA; 11 BP.  
XX  
AC ABV62361;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 147.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
WPI; 2002-590638/63.  
XX  
DR In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 30; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag

CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 0 A; 4 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 7.9%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1681 GGTCGTCTCTC 1691  
DB 1 GGTCGTCTCTC 11  
RESULT 798  
ABI08693  
ID ABI08693 standard; DNA; 12 BP.  
XX  
AC ABI08693;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 308666 for detecting SNP TSC0023148.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB00713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 308666; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 1 A; 7 C; 0 G; 4 T; 0 U; 0 Other;  
Query Match 7.9%; Score 11; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1746 CTCCTATCTCT 1756  
DB 1 CTCCTATCTCT 11

```

RESULT 799
ABI58915/C
ID ABI58915 standard; DNA; 12 BP.
XX
XX AC ABI58915;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 358888 for detecting SNP TSC0051363.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX FN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 358888; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 4 A; 0 C; 7 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1746 CTCCTATCTCT 1756
XX |||||||
XX 12 CTCCTATCTCT 2
XX
XX RESULT 800
ABI01113
ID ABI01113 standard; DNA; 12 BP.
XX
XX AC ABI01113;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 301086 for detecting SNP TSC0019345.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

```

```

XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 301086; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1737 TCCCACTCTCT 1747
XX |||||||
XX 2 TCCCACTCTCT 12
XX
XX Db
XX
XX RESULT 801
ABI53626
ID ABI53626 standard; DNA; 12 BP.
XX
XX AC ABI53626;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 353599 for detecting SNP TSC0048610.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX FN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX

```



```

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

QY 1747 TCCTATCCTA 1757
Db 12 TCCTATCCTA 2
|||||

RESULT 804
ABI81002/c
ID ABI81002 standard; DNA; 12 BP.
XX
AC ABI81002;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 380975 for detecting SNP TSC0064086.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 380975; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
XX
Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1724 GATGGAGATTG 1734
Db 12 GATGGAGATTG 2
|||||

RESULT 805
ABI68036
ID ABI68036 standard; DNA; 12 BP.
XX
XX ABI68036;
AC

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

QY 1724 GATGGAGATTG 1734
Db 12 GATGGAGATTG 2
|||||

RESULT 806
ABI59814
ID ABI59814 standard; DNA; 12 BP.
XX
XX ABI59814;
AC

Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1724 GATGGAGATTG 1734
Db 1 GATGGAGATTG 11
|||||

RESULT 806
ABI59814
ID ABI59814 standard; DNA; 12 BP.
XX
XX ABI59814;
AC

Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1724 GATGGAGATTG 1734
Db 12 GATGGAGATTG 2
|||||

RESULT 805
ABI68036
ID ABI68036 standard; DNA; 12 BP.
XX
XX ABI68036;
AC

Oligonucleotide primer SEQ ID NO 359787 for detecting SNP TSC0051760.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.

```

```

PD XX 18-OCT-2001.
PF XX
PR XX 06-APR-2001; 2001WO-IB000713.
PR XX
PR XX 07-APR-2000; 2000DE-01019173.
PR XX
PR XX (EPIG-) EPIGENOMICS AG.
PR XX
PI XX Olek A, Piepenbrock C, Berlin K;
PI XX
DR XX WPI; 2001-657177/75.
DR XX
PT XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT XX designed to detect single-nucleotide polymorphisms and cytosine
PT XX methylation status.
XX XX
PS Claim 1; SEQ ID NO 359787; 29pp + Sequence Listing; German.
XX XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX XX
SQ Sequence 12 BP; 4 A; 0 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1721 GGAGATGGAGA 1731
DB 1 GGAGATGGAGA 11
RESULT 807
ABI77791/c
ID ABI77791 standard; DNA; 12 BP.
XX
AC ABI77791;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 377764 for detecting SNP TSC0007286.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF Oligonucleotide primer SEQ ID NO 377764 for detecting SNP TSC0007286.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
PR 07-APR-2000; 2000DE-01019173.
PR XX
PA (EPIG-) EPIGENOMICS AG.
PI XX Olek A, Piepenbrock C, Berlin K;
PI XX
DR WPI; 2001-657177/75.
DR XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX XX
PS Claim 1; SEQ ID NO 377764; 29pp + Sequence Listing; German.
XX XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX XX
SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1704 AGTTCGGTTAG 1714
DB 11 AGTTCGGTTAG 11
RESULT 808
ABH98049
ID ABH98049 standard; DNA; 12 BP.
XX
AC ABH98049;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 298042 for detecting SNP TSC0017887.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
PR 07-APR-2000; 2000DE-01019173.
PR XX
PA (EPIG-) EPIGENOMICS AG.
PI XX Olek A, Piepenbrock C, Berlin K;
PI XX
DR WPI; 2001-657177/75.
DR XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX XX
PS Claim 1; SEQ ID NO 298042; 29pp + Sequence Listing; German.
XX XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX XX

```



DB	2	AGTTCGGTTAG	12
RESULT 810			
ABI40118			
ABI40118	standard; DNA; 12 BP.		
XX			
AC	ABI40118;		
XX			
XX			
XX	22-FEB-2002 (first entry)		
DE			
XX	Oligonucleotide primer SEQ ID NO 340091 for detecting SNP TSC0041342.		
XX			
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;		
XX	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;		
XX	central nervous system; gastrointestinal; respiratory; immune; metabolic.		
OS	Homo sapiens.		
XX			
WO	200177384-A2.		
PN			
XX	18-OCT-2001.		
PD			
XX			
XX	06-APR-2001; 2001WO-IB000713.		
XX			
XX	07-APR-2000; 2000DE-01019173.		
PR			
XX	(EPIG-) EPIGENOMICS AG.		
XX			
PA	Olek A, Piepenbrock C, Berlin K;		
XX			
PI			
XX	WPI; 2001-657177/75.		
DR			
XX			
XX	Set of oligonucleotides, useful for diagnosis and cell typing, is		
PT	designed to detect single-nucleotide polymorphisms and cytosine		
PT	methylation status.		
PT			
XX			
PS	Claim 1; SEQ ID NO 340091; 29pp + Sequence Listing; German.		
XX			
CC	This invention describes novel oligonucleotide primers or peptide nucleic		
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)		
CC	and cytosine methylation status in chemically pretreated genomic DNA. The		
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a		
CC	range of diseases including immune system, gastrointestinal, respiratory,		
CC	central nervous system, cardiovascular and metabolic disorders. The		
CC	oligomers are also used for detecting cell type differentiation. ABC00010		
CC	-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073		
CC	represent the oligomers described in the invention. NOTE: The sequence		
CC	data for this patent did not form part of the printed specification, but		
CC	was obtained in electronic format from WIPO at		
CC	ftp.wipo.int/pub/published_pct_sequences		
XX			
XX	Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;		
Query Match	7.9%; Score 11; DB 1; Length 12;		
Best Local Similarity	100.0%; Pred. No. 3.6e+02;		
Matches	11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1708 GGGTTAGGAGT 1718		
Db	1 GGGTTAGGAGT 11		
RESULT 811			
ABC37623			
ID	ABC37623 standard; DNA; 13 BP.		
XX			
AC	ABC37623;		
XX			
XX	20-FEB-2002 (first entry)		
XX			
XX	Oligonucleotide SEQ ID NO 37640 for detecting SNP TSC0011712.		
XX			

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 37640; 29pp + Sequence Listing; German.  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC000010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 1 A; 8 C; 0 G; 3 T; 0 U; 1 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1745 CCTCCCTATCC 1755  
 DB |||||  
 2 CCTCCCTATCC 12  
 RESULT 812  
 ABF99563  
 ID ABF99563 standard; DNA; 13 BP.  
 AC ABF99563;  
 XX 22-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 198560 for detecting SNP TSC0048863.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 198560; 29pp + Sequence Listing; German.  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC000010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1749 CCTATCCTAAA 1759  
 DB |||||  
 1 CCTATCCTAAA 11  
 RESULT 813  
 ABH01585  
 ID ABH01585 standard; DNA; 13 BP.  
 AC ABH01585;  
 XX 22-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 201562 for detecting SNP TSC0049571.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 201562; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 2 A; 8 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1736 CTCCCAACTCC 1746  
 Db 3 CTCCCAACTCC 13  
 RESULT 814  
 ABH30529/c  
 ID ABH30529 standard; DNA; 13 BP.  
 AC ABH30529;  
 XX  
 DT 22-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 230506 for detecting SNP TSC0056222.  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 PR 07-APR-2000; 2000DE-01019173.  
 PA (EPIG-) EPIGENOMICS AG.  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PS Claim 1; SEQ ID NO 230506; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 13 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 1 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 84.6%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1724 GATGGAGATTGCC 1736  
 Db 13 GATGGAGATTGGY 1  
 RESULT 815  
 ABC21702  
 ID ABC21702 standard; DNA; 13 BP.  
 XX  
 AC ABC21702;  
 XX  
 DT 20-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 21719 for detecting SNP TSC0004349.  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 PR 07-APR-2000; 2000DE-01019173.  
 PA (EPIG-) EPIGENOMICS AG.  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PS Claim 1; SEQ ID NO 21719; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 1 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 84.6%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1721 GGAGATGGAGATT 1733  
 Db 1 GGAGTTGGAGATY 13  
 RESULT 816  
 ABF22699

```

ID ABF22699 standard; DNA; 13 BP.
XX AC ABF22699;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 122696 for detecting SNP TSC0030668.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 122696; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 0 A; 8 C; 0 G; 4 T; 0 U; 1 Other;
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 84.6%; Pred. No. 4.1e+02;
XX Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX QY 1742 ACTCTCTCCCTATC 1754
XX Db :|||||||
XX 1 RCTCTCCCTCTC 13
XX RESULT 817
XX ABF28976/c
XX ID ABF28976 standard; DNA; 13 BP.
XX AC ABF28976;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 128973 for detecting SNP TSC0032287.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 122696; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 84.6%; Pred. No. 4.1e+02;
XX Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX QY 1742 ACTCTCTCCCTATC 1754
XX Db :|||||||
XX 1 RCTCTCCCTCTC 13
XX RESULT 817
XX ABF28976/c
XX ID ABF28976 standard; DNA; 13 BP.
XX AC ABF28976;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 128973 for detecting SNP TSC0032287.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 128973; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 107.0%; Pred. No. 4.1e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1735 GCTCCCACTC 1745
XX Db |||||
XX 12 GCTCCCACTC 2
XX RESULT 818
XX ABH01584/c
XX ID ABH01584 standard; DNA; 13 BP.
XX AC ABH01584;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 201561 for detecting SNP TSC0049571.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 128973; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 2 A; 1 C; 7 G; 3 T; 0 U; 0 Other;
```

DR WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 FT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 201561; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 0 C; 8 G; 2 T; 0 U; 0 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 CTCCTCAACTCC 1746  
 Db 11 CTCCTCAACTCC 1  
 |||||

RESULT 819  
 ABH31314/c  
 ID ABH31314 standard; DNA; 13 BP.  
 AC ABH31314;  
 XX  
 XX 22-FEB-2002 (first entry)  
 DT  
 DE Oligonucleotide SEQ ID NO 231291 for detecting SNP TSC0056398.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 PN  
 PD 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 FR  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 FT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 231291; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 1 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1748 CCTATCCTAA 1758  
 Db 12 CCTATCCTAA 2  
 |||||

RESULT 820  
 ABH08492  
 ID ABH08492 standard; DNA; 13 BP.  
 XX  
 AC ABH08492;  
 XX  
 XX 22-FEB-2002 (first entry)  
 DT  
 DE Oligonucleotide SEQ ID NO 208469 for detecting SNP TSC0050942.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 PN  
 PD 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 FR  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 FT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 208469; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1698 GGTGGAAGTTG 1708  
 Db 1 GGTGGAAGTTG 11  
 RESULT 821  
 ABH22016  
 ID ABH22016 standard; DNA; 13 BP.  
 AC ABH22016;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 221993 for detecting SNP TSC0054021.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 AC 18-OCT-2001.  
 XX  
 DT 06-APR-2001; 2001WO-IB000713.  
 XX  
 DE 07-APR-2000; 2000DE-01019173.  
 XX  
 KW (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 221993; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 1 Other;  
 XX  
 CC Query Match 7.9%; Score 11; DB 1; Length 13;  
 CC Best Local Similarity 84.6%; Pred. No. 4.1e+02;  
 CC Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 1700 TGGAAAGTTGGTT 1712  
 Db 1 TGGAAAGTTGGTT 13  
 RESULT 822  
 ABH35639/c  
 ID ABH35639 standard; DNA; 13 BP.  
 XX  
 AC ABH35639;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX

XX  
 DE Oligonucleotide SEQ ID NO 235616 for detecting SNP TSC0057525.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 AC 18-OCT-2001.  
 XX  
 DT 06-APR-2001; 2001WO-IB000713.  
 XX  
 DE 07-APR-2000; 2000DE-01019173.  
 XX  
 KW (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 235616; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;  
 XX  
 CC Query Match 7.9%; Score 11; DB 1; Length 13;  
 CC Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1707 TGGGTTAGGAG 1717  
 Db 13 TGGGTTAGGAG 3  
 RESULT 823  
 ABF86040  
 ID ABF86040 standard; DNA; 13 BP.  
 XX  
 AC ABF86040;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 186037 for detecting SNP TSC0045841.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 AC 18-OCT-2001.  
 XX

PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 186037; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 1 C; 7 G; 1 T; 0 U; 1 Other;  
  
Query Match 7.9%; Score 11; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred.No. 4.1e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1714 GGAGTACGGAG 1724  
Db 13 GGAGTACGGAG 3  
  
RESULT 824  
ABC82521  
ID ABC82521 standard; DNA; 13 BP.  
XX  
AC ABC82521;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 82538 for detecting SNP TSC0020824.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 82538; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 1 C; 7 G; 1 T; 0 U; 1 Other;  
  
Query Match 7.9%; Score 11; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred.No. 4.1e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1714 GGAGTACGGAG 1724  
Db 1 GGAGTACGGAG 11  
  
RESULT 824  
ABF86041/C  
ID ABF86041 standard; DNA; 13 BP.  
XX  
AC ABF86041;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 186038 for detecting SNP TSC0045841.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

```
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 1 Other;

  Query Match      7.9%; Score 11; DB 1; Length 13;
  Best Local Similarity 84.6%; Pred. No. 4.1e+02;
  Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1741 AACTCTCTCCCTAT 1753
Db :|||||
1 RACTCTCTACCTAT 13

RESULT 826
ABF35842
ID ABF35842 standard; DNA; 13 BP.
XX
AC ABF35842;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 135839 for detecting SNP TSC0033923.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WO200177384-A2.
XX
PT 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WO200177384-A2.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 135839; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABF35842, ABF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 1 Other;

  Query Match      7.9%; Score 11; DB 1; Length 13;
  Best Local Similarity 84.6%; Pred. No. 4.1e+02;
  Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1721 GGAGATCGAGATT 1733
Db :|||||
1 GGAGATCGAGATY 13

RESULT 828
ABH31315
ID ABH31315 standard; DNA; 13 BP.
XX
AC ABH31315;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 231292 for detecting SNP TSC0056398.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
```



KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 231292; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;  
 SQ Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1748 CCCTATCCTAA 1758  
 Db 2 CCCTATCCTAA 12  
 RESULT 829  
 ABC82520/c  
 ID ABC82520 standard; DNA; 13 BP.  
 XX ABC82520;  
 AC ABC82520;  
 XX 21-FEB-2002 (first entry)  
 DT Oligonucleotide SEQ ID NO 82537 for detecting SNP TSC0020824.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 KW Homo sapiens.  
 OS WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 82537; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 1 Other;  
 SQ Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 84.6%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1741 AACTCTCTCCCTAT 1753  
 Db 13 RACTCTTACCTAT 1  
 RESULT 830  
 ABF15181/c  
 ID ABF15181 standard; DNA; 13 BP.  
 XX ABF15181;  
 AC ABF15181;  
 XX 21-FEB-2002 (first entry)  
 DT Oligonucleotide SEQ ID NO 115178 for detecting SNP TSC0028862.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 KW Homo sapiens.  
 OS WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 115178; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1697 TGGTGGAGATT 1707

Db 11 TGGTGGAGATT 1

RESULT 831

ABC33136  
 ID ABC33136 standard; DNA; 13 BP.

XX AC ABC33136;

XX DT 20-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 33153 for detecting SNP TSC0010569.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 33153; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 6 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

RESULT 832

ABF35843/C

ID ABF35843 standard; DNA; 13 BP.

XX

Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1722 GAGATGGAGAT 1732

Db 2 GAGATGGAGAT 12

RESULT 832

ABF15180

ID ABF15180 standard; DNA; 13 BP.

XX AC ABF15180;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 115177 for detecting SNP TSC0028862.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 115177; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1697 TGGTGGAGATT 1707

Db 3 TGGTGGAGATT 13

RESULT 833

ABF35843/C

ID ABF35843 standard; DNA; 13 BP.

XX

AC ABF35843;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 135840 for detecting SNP TSC0033923.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 135840; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 2 A; 5 C; 1 G; 4 T; 0 U; 1 Other;  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 2 A; 5 C; 1 G; 4 T; 0 U; 1 Other;  
 XX  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 84.6%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 1721 GGAGATGGAGATT 1733  
 Db 13 GGAGATCGAGATY 1  
 ||||| |||||  
 RESULT 834  
 ABF46427/c  
 ID ABF46427 standard; DNA; 13 BP.  
 XX  
 AC ABF46427;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 146424 for detecting SNP TSC0036912.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX

XX 18-OCT-2001.  
 XX  
 PD 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 146424; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 2 A; 6 C; 0 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1722 GAGATGGAGAT 1732  
 Db 12 GAGATGGAGAT 2  
 ||||| |||||  
 RESULT 835  
 ABH05407/c  
 ID ABH05407 standard; DNA; 13 BP.  
 XX  
 AC ABH05407;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 205384 for detecting SNP TSC0050352.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX





```
PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 135837; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 1 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 4.1e+02;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1721 GGAGATGGAGATT 1733
DB 1 GGAGATTGAGATY 13
RESULT 841
ABH08493/c
ID ABH08493 standard; DNA; 13 BP.
XX AC ABH08493;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 208470 for detecting SNP TSC0050942.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 208470; 29pp + Sequence Listing; German.
PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms (SNP)
PT and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1698 GGTGGAGTTG 1708
DB 13 GGTGGAGTTG 3
RESULT 842
ABC61029/c
ID ABC61029 standard; DNA; 13 BP.
XX AC ABC61029;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 61046 for detecting SNP TSC0016265.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 61046; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
```

```
XX SQ Sequence 13 BP; 1 A; 7 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGA 1731
|||||
Db 13 GGAGATGGAGA 3

RESULT 843
ABH19250
ID ABH19250 standard; DNA; 13 BP.
AC ABH19250;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 219227 for detecting SNP TSC0053301.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPITG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PN WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 219227; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1715 GAGTACGGAGA 1725
|||||
Db 2 GAGTACGGAGA 12

RESULT 844
ABH21128/c
ID ABH21128 standard; DNA; 13 BP.
XX
AC ABH21128;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 221105 for detecting SNP TSC0053805.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (BPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PN WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 221105; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 1 Other;
Query Match 7.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1737 TCCCAACTCCT 1747
|||||
Db 11 TCCCAACTCCT 1

RESULT 845
ABF98562/c
ID ABF98562 standard; DNA; 13 BP.
XX
AC ABF98562;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 198559 for detecting SNP TSC0048863.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
```

```
OS Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 198559; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 1749 CCTATCCTAAA 1759
Db 13 CCTATCCTAAA 3
RESULT 846
ABF84271/C
ID ABF84271 standard; DNA; 13 BP.
AC ABF84271;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 184268 for detecting SNP TSC0006682.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
PI
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 130.0%; Pred. No. 4.1e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 1723 AGATGGAGATT 1733
Db 11 AGATGGAGATT 1
RESULT 847
ABF46426
ID ABF46426 standard; DNA; 13 BP.
AC ABF46426;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 146423 for detecting SNP TSC0036912.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 146423; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
```



CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1722 GAGATGGAGAT 1732  
 DB 2 GAGATGGAGAT 12  
 |||||  
 RESULT 848  
 ABF15421/c  
 ID ABF15421 standard; DNA; 13 BP.  
 XX  
 AC ABF15421;  
 XX  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 115418 for detecting SNP TSC0028927.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB0000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 115418; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 2 A; 6 C; 1 G; 3 T; 0 U; 1 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1722 GAGATGGAGAT 1732  
 DB 2 GAGATGGAGAT 12  
 |||||  
 RESULT 848  
 ABF15421/c  
 ID ABF15421 standard; DNA; 13 BP.  
 XX  
 AC ABF15421;  
 XX  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 115418 for detecting SNP TSC0028927.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB0000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 115418; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 2 A; 6 C; 1 G; 3 T; 0 U; 1 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1694 GCCTGGTGGAA 1704  
 DB 13 GCCTGGTGGAA 3  
 |||||  
 RESULT 849  
 ABH21129  
 ID ABH21129 standard; DNA; 13 BP.  
 XX  
 AC ABH21129;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 221106 for detecting SNP TSC0053805.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB0000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 221106; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1737 TCCCAACTCCT 1747  
 DB 3 TCCCAACTCCT 13  
 |||||  
 RESULT 850  
 ABH05406  
 ID ABH05406 standard; DNA; 13 BP.  
 XX  
 AC ABH05406;  
 XX

DT	22-FEB-2002	(first entry)
XX	Oligonucleotide SEQ ID NO 205383 for detecting SNP TSC0050352.	
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;	
XX	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;	
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.	
KW	Homo sapiens.	
OS	WO200177384-A2.	
PN	18-OCT-2001.	
PD	XX	
PX	XX	
PF	06-APR-2001; 2001WO-IB000713.	
PR	XX	
PS	07-APR-2000; 2000DE-01019173.	
PT	XX	
PP	(EPIG-) EPIGENOMICS AG.	
PA	Olek A, Piepenbrock C, Berlin K;	
PI	WIPI; 2001-657177/75.	
PL	Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.	
PT	Claim 1; SEQ ID NO 33154; 29pp + Sequence Listing; German.	
PS	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences	
CC	Query Match 7.9%; Score 11; DB 1; Length 13;	
CC	Best Local Similarity 84.6%; Pred. No. 4.1e+02;	
CC	Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
CC	Sequence 13 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 1 Other;	
CC	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences	
CC	Query Match 7.9%; Score 11; DB 1; Length 13;	
CC	Best Local Similarity 84.6%; Pred. No. 4.1e+02;	
CC	Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
CC	Sequence 13 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 1 Other;	
CC	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences	
CC	Query Match 7.9%; Score 11; DB 1; Length 13;	
CC	Best Local Similarity 84.6%; Pred. No. 4.1e+02;	
CC	Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
CC	Sequence 13 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 1 Other;	
CC	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences	
CC	Query Match 7.9%; Score 11; DB 1; Length 13;	
CC	Best Local Similarity 84.6%; Pred. No. 4.1e+02;	
CC	Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
CC	Sequence 13 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 1 Other;	
CC	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences	
CC	Query Match 7.9%; Score 11; DB 1; Length 13;	
CC	Best Local Similarity 84.6%; Pred. No. 4.1e+02;	
CC	Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
CC	Sequence 13 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 1 Other;	
CC	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences	
CC	Query Match 7.9%; Score 11; DB 1; Length 13;	
CC	Best Local Similarity 84.6%; Pred. No. 4.1e+02;	
CC	Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
CC	Sequence 13 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 1 Other;	
CC	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences	
CC	Query Match 7.9%; Score 11; DB 1; Length 13;	
CC	Best Local Similarity 84.6%; Pred. No. 4.1e+02;	
CC	Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
CC	Sequence 13 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 1 Other;	
CC	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences	
CC	Query Match 7.9%; Score 11; DB 1; Length 13;	
CC	Best Local Similarity 84.6%; Pred. No. 4.1e+02;	
CC	Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
CC	Sequence 13 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 1 Other;	
CC	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences	
CC	Query Match 7.9%; Score 11; DB 1; Length 13;	
CC	Best Local Similarity 84.6%; Pred. No. 4.1e+02;	
CC	Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
CC	Sequence 13 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 1 Other;	
CC	This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00	

PT methylation status.  
PS Claim 1; SEQ ID NO 184267; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 7.9%; Score 11; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1723 AGATGGAGATT 1733  
Db 3 AGATGGAGATT 13  
RESULT 853  
ABC61028  
ID ABC61028 standard; DNA; 13 BP.  
XX  
AC ABC61028;  
XX  
XX 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 61045 for detecting SNP TSC0016265.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 61045; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 5 A; 0 C; 7 G; 1 T; 0 U; 0 Other;  
Query Match 7.9%; Score 11; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1721 GGAGATGGAGA 1731  
Db 1 GGAGATGGAGA 11  
RESULT 854  
ABF22698/C  
ID ABF22698 standard; DNA; 13 BP.  
XX  
AC ABF22698;  
XX  
XX 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 122695 for detecting SNP TSC0030668.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 122695; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 0 C; 8 G; 0 T; 0 U; 1 Other;  
Query Match 7.9%; Score 11; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 4.1e+02;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1742 ACTCCTCCCTATC 1754  
Db 13 RCTCCTCCCTCTC 1

```

RESULT 855
ABF35841/C
ID ABF35841 standard; DNA; 13 BP.
XX
XX AC ABF35841;
XX
DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 135838 for detecting SNP TSC0033923.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 135838; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC0001
XX -ABF0010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 1 Other;
XX
XX Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 84.6%; Pred. No. 4.1e+02;
XX Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps
XX
XX QY 1721 GGAGATGGAGATT 1733
XX
XX Db 13 GGAGATTGAGATY 1
XX
XX
XX RESULT 856
XX ABC46635
XX ID ABC46635 standard; DNA; 13 BP.
XX
XX AC ABC46635;
XX
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 46652 for detecting SNP TSC0013461.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW
XX KW

```

PA (EPIG-) EPIGENOMICS AG.  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 DR  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 128974; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 7 C; 1 G; 2 T; 0 U; 0 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1735 GCTCCCAATC 1745  
 DB 2 GCTCCCAATC 12  
 RESULT 858  
 ABF15420  
 ID ABF15420 standard; DNA; 13 BP.  
 AC  
 AC ABF15420;  
 XX  
 XX 21-FEB-2002 (first entry)  
 DT  
 XX  
 DE Oligonucleotide SEQ ID NO 115417 for detecting SNP TSC0028927.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 PR  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 115417; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 3 A; 1 C; 6 G; 2 T; 0 U; 1 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1694 GCGTGGTGGA 1704  
 DB 1 GCGTGGTGGA 11  
 RESULT 859  
 ABH19251/C  
 ID ABH19251 standard; DNA; 13 BP.  
 AC  
 AC ABH19251;  
 XX  
 XX 22-FEB-2002 (first entry)  
 DT  
 XX  
 DE Oligonucleotide SEQ ID NO 219228 for detecting SNP TSC0053301.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 PR  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 219228; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 2 A; 6 C; 1 G; 4 T; 0 U; 0 Other;

Mon Aug 30 09:26:45 2004

schultz139-3.rng

```

XX AC AAF29395;
XX DT 27-APR-2001 (first entry)
XX DE Oligonucleotide primer 2 DNA sequence.
XX KW Selective base pair; steric hindrance; static repulsion; ss.
XX OS Synthetic.
XX PN WO200105801-A1.
XX PD 25-JAN-2001.
XX PF 14-JUL-2000; 2000WO-JP04720.
XX PR 15-JUL-1999; 99JP-00201450.
XX PR 02-MAY-2000; 2000JP-00133519.
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX PI Hirao I, Ishikawa M, Fujiwara T, Yokoyama S;
XX DR WPI; 2001-147320/15.
XX XX Non-natural nucleic acid base pair recognised by polymerases for
PT production of artificial genes for treatment of genetic disorders.
XX PS Disclosure; Page 14; 64pp; Japanese.
XX CC This invention relates to a non-natural selective base pair for nucleic
CC acids produced by introducing to a nucleic acid base a group imparting
CC steric hindrance to pairing with the counter-base, static repulsion and a
CC stacking effect. The non-natural selective base pair can be used in the
CC production of non-natural genes and their use in the production of nucleic
CC proteins containing non-natural amino acids. The production of nucleic
CC acids for treatment of genetic disorders. Oligonucleotides AAF29385 -
CC AAF29398 represent template and primer sequences used in an example
CC illustrating the invention
XX SQ Sequence 14 BP; 5 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
XX Query Match 7.9%; Score 11; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1743 CTCCTCCCTAT 1753
DB 13 CTCCTCCCTAT 3
RESULT 862
AAV31919
ID AAV31919 standard; DNA; 15 BP.
XX AC AAV31919;
XX DT 21-AUG-1998 (first entry)
XX DE Peptide nucleic acid probe 62.
XX KW Peptide nucleic acid; PNA; probe; hybridisation; mycobacteria;
XX KW ribosomal nucleic acid; rRNA; drug-resistant strain; mutation; ss.
XX OS Synthetic.
XX OS Mycobacterium sp.
XX FH Key Location/Qualifiers
XX modified_base 1..15
XX FT /*tag= a
XX FT /note= "This sequence contains a polyamide backbone
XX FT instead of a deoxyribose backbone"

```

```

XX AC AAF29395;
XX DT 27-APR-2001 (first entry)
XX DE Oligonucleotide primer 2 DNA sequence.
XX KW Selective base pair; steric hindrance; static repulsion; ss.
XX OS Synthetic.
XX PN WO200105801-A1.
XX PD 25-JAN-2001.
XX PF 14-JUL-2000; 2000WO-JP04720.
XX PR 15-JUL-1999; 99JP-00201450.
XX PR 02-MAY-2000; 2000JP-00133519.
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX PI Hirao I, Ishikawa M, Fujiwara T, Yokoyama S;
XX DR WPI; 2001-147320/15.
XX XX Non-natural nucleic acid base pair recognised by polymerases for
PT production of artificial genes for treatment of genetic disorders.
XX PS Disclosure; Page 14; 64pp; Japanese.
XX CC This invention relates to a non-natural selective base pair for nucleic
CC acids produced by introducing to a nucleic acid base a group imparting
CC steric hindrance to pairing with the counter-base, static repulsion and a
CC stacking effect. The non-natural selective base pair can be used in the
CC production of non-natural genes and their use in the production of nucleic
CC proteins containing non-natural amino acids. The production of nucleic
CC acids for treatment of genetic disorders. Oligonucleotides AAF29385 -
CC AAF29398 represent template and primer sequences used in an example
CC illustrating the invention
XX SQ Sequence 14 BP; 5 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
XX Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1715 GAGTACGGAGA 1725
DB 12 GAGTACGGAGA 2
RESULT 860
ABH22017/c
ID ABH22017 standard; DNA; 13 BP.
XX AC ABH22017;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 221994 for detecting SNP TSC0054021.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 221994; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI02073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;
XX Query Match 7.9%; Score 11; DB 1; Length 13;
XX Best Local Similarity 84.6%; Pred. No. 4.1e+02;
XX Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1700 TGGAGTGGGTT 1712
DB 13 TGGAGTGGGTT 1
RESULT 861
AAF29395/c
ID AAF29395 standard; DNA; 14 BP.

```

```

XX PN WO9815648-A1.
XX PD 16-APR-1998.
XX PF 03-OCT-1997; 97WO-DK000425.
XX PR 04-OCT-1996; 96DK-00001096.
XX PR 18-OCT-1996; 96DK-00001156.
XX PR 05-MAY-1997; 97DK-00000512.
XX PA (DAKO-) DAKO AS.
XX PI Stender H, Lund K, Mollerup TA;
XX DR WPI; 1998-240831/21.
XX PT Peptide nucleic acid probes for detection of ribosomal nucleic acid of
XX PT mycobacteria - allow differentiation between species of tuberculosis
XX PT complex and others and can penetrate cell membranes without pretreatment.
XX PS Claim 22; Page 66; 106pp; English.
XX CC This is the nucleotide sequence of the peptide nucleic acid (PNA) probe
XX CC used in the method of the invention, to detect ribosomal nucleic acid of
XX CC mycobacteria. The probes are used, in situ or in vitro, for detection of
XX CC the Mycobacterium tuberculosis complex (MTC), specifically M.
XX CC tuberculosis, and especially in sputum samples, but also in other body
XX CC fluids, biopsy specimens, foods, soil, air and water. Particularly, they
XX CC are used to diagnose, stage or monitor infection, or for identification
XX CC of drug-resistant strains (which generally have mutations in rRNA)
XX SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1759 AGGCCCACTGG 1769
Db 4 AGGCCCACTGG 14

RESULT 863
AAAX31800
ID AAAX31800 standard; DNA; 15 BP.
AC AAAX31800;
XX
XX 21-MAY-1999 (first entry)
XX Transcript tag sequence increased in pancreatic and colorectal cancer.
DE Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
XX diagnosis; prognosis; treatment; ss.
XX Homo sapiens.
XX WO9853319-A2.
XX 26-NOV-1998.
XX 20-MAY-1998.
XX 20-MAY-1998; 98WO-US010277.
XX 21-MAY-1997; 97US-0047352P.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Vogelstein B, Kinzler KW;
XX WPI; 1999-070161/06.
XX Use of isolated gene transcripts - useful for developing products for the
XX level of at least one transcript in a first sample of a tissue to a

```

```

PT diagnosis, prognosis and treatment of cancers, particularly colon and
PT pancreatic cancer.
XX Disclosure; Page 79; 120pp; English.
XX
XX AAAX30947-31815 represent tag sequences of transcripts that are
XX differentially expressed in colorectal cancer, in pancreatic cancer, or
XX in both. The tag sequences can be used to identify genes by matching the
XX tag to a gen data base member, or by using the tag sequences as probes to
XX isolate unidentified genes from cDNA libraries. The tag sequences can
XX also be used in a method for diagnosing colon or pancreatic cancer in a
XX sample suspected of being neoplastic. The method comprises comparing the
XX level of at least one transcript in a first sample of a tissue to a
XX second sample, where the first sample is a colonic tissue suspected of
XX being neoplastic and the second sample is a normal human colonic tissue.
XX The transcript is identified by a tag selected from AAAX30947-31815. The
XX methods of the invention can be used in the diagnosis, prognosis and
XX treatment of cancer
XX SQ Sequence 15 BP; 4 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1672 TGAACCCCTGG 1682
Db 3 TGAACCCCTGG 13

RESULT 864
AAAX31164
ID AAAX31164 standard; DNA; 15 BP.
AC AAAX31164;
XX
XX 21-MAY-1999 (first entry)
XX Tag sequence of a transcript increased in colorectal cancer.
DE Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
XX diagnosis; prognosis; treatment; ss.
XX Homo sapiens.
XX WO9853319-A2.
XX 26-NOV-1998.
XX 20-MAY-1998; 98WO-US010277.
XX 21-MAY-1997; 97US-0047352P.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Vogelstein B, Kinzler KW;
XX WPI; 1999-070161/06.
XX Use of isolated gene transcripts - useful for developing products for the
XX diagnosis, prognosis and treatment of cancers, particularly colon and
XX pancreatic cancer.
XX Claim 2; Page 33; 120pp; English.
XX
XX AAAX30947-31815 represent tag sequences of transcripts that are
XX differentially expressed in colorectal cancer, in pancreatic cancer, or
XX in both. The tag sequences can be used to identify genes by matching the
XX tag to a gen data base member, or by using the tag sequences as probes to
XX isolate unidentified genes from cDNA libraries. The tag sequences can
XX also be used in a method for diagnosing colon or pancreatic cancer in a
XX sample suspected of being neoplastic. The method comprises comparing the
XX level of at least one transcript in a first sample of a tissue to a

```

second sample, where the first sample is a colonic tissue suspected of being neoplastic and the second sample is a normal human colonic tissue. The transcript is identified by a tag selected from AAX30947-31815. The methods of the invention can be used in the diagnosis, prognosis and treatment of cancer

Sequence 15 BP; 4 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1672 TGGAAACCTGG 1682  
Db 3 TGGAAACCTGG 13

RESULT 865  
AAI67293/c  
ID AAI67293 standard; DNA; 15 BP.  
XX AC AAI67293;  
XX DT 11-FEB-2002 (first entry)  
XX DE Human FKBP8 allele-specific oligonucleotide (ASO) probe.  
XX KW FKBP8-binding protein 8; FKBP8; haplotyping; polymorphism; cancer; ss;  
XX KW immunosuppression; human; allele-specific oligonucleotide; ASO; probe.  
XX OS Homo sapiens.  
XX PN WO200172965-A2.  
XX PD 04-OCT-2001.  
XX PF 26-MAR-2001; 2001WO-US009718.  
XX PR 24-MAR-2000; 2000US-0192125P.  
XX PA (GENA-) GENAISSANCE PHARM INC.  
XX PI Anastasio AE, Bentivegna SC, Choi JY, Klien SE, Koshy B;  
XX PI Stephens JC;  
XX WPI; 2001-626261/72.  
XX New haplotypes of the FKBP8-binding protein 8 gene, useful for genotyping that gene in individual and to design new therapy for associated disease such as immunosuppression and cancer.  
XX Claim 15; Page 13; 98pp; English.  
XX The invention relates to haplotyping the FKBP8-binding protein 8 (38kD) (FKBP8) gene in an individual. The method involves determining the identity of the nucleotide pair at one or more polymorphic sites, selected from P1 to P26 (described in the specification). The invention is useful to improve the efficiency and reliability of several steps in the discovery and development of drugs for treating diseases associated with FKBP8 activity, for example immunosuppression and cancer. Sequences AAI67274-299 represent allele-specific oligonucleotide (ASO) probes for detecting FKBP8 gene polymorphisms

Sequence 15 BP; 2 A; 7 C; 4 G; 1 T; 0 U; 1 Other;

Query Match 7.9%; Score 11; DB 1; Length 15;  
Best Local Similarity 84.6%; Pred. No. 4.9e+02;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1673 GGAACCTGGTGT 1685  
Db 15 GGCACCCGGTGT 3

RESULT 866  
AAFS0722  
ID AAF50722 standard; DNA; 15 BP.  
XX AC AAF50722;  
XX DT 30-MAR-2001 (first entry)  
XX DE IGF-I oligonucleotide #1692.  
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiac; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.  
XX OS Homo sapiens.  
XX PN WO200078341-A1.  
XX PD 28-DEC-2000.  
XX PF 21-JUN-2000; 2000WO-AU000693.  
XX PR 21-JUN-1999; 99US-0140345P.  
XX PA (MURD-) MURDOCH CHILDRENS RES INST.  
XX PI Wright CJ, Werther GA, Edmondson SR;  
XX WPI; 2001-041421/05.  
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.  
XX Example 8; Page 71; 201pp; English.  
XX The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

Sequence 15 BP; 6 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 7.9%; Score 11; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1667 ACAGCTGGAC 1677  
Db 4 ACAGCTGGAC 14

RESULT 867  
AAFS0724  
ID AAF50724 standard; DNA; 15 BP.



```

XX AC AAF50724;
XX XX
XX DT 30-MAR-2001 (first entry)
XX XX
XX DE IGF-I oligonucleotide #1684.
XX XX
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.
XX OS Homo sapiens.
XX XX
XX PN WO200078341-A1.
XX XX
XX PD 28-DEC-2000.
XX XX
XX PF 21-JUN-2000; 2000WO-AU000693.
XX XX
XX PR 21-JUN-1999; 99US-0140345P.
XX XX
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX XX
XX PI Wraight CJ, Werther GA, Edmondson SR;
XX XX WPI; 2001-041421/05.
XX DR
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX PT inhibits or reduces growth factor mediated cell proliferation and/or
XX PT inflammation.
XX PS Example 8; Page 71; 201pp; English.
XX XX
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX XX
XX SQ Sequence 15 BP; 6 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
XX XX
XX Query Match 7.9%; Score 11; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 4.9e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1667 ACAGCTGGGAAC 1677
XX Db |||||
XX 2 ACAGCTGGGAAC 12
XX
XX RESULT 868
XX AAF50721
XX ID AAF50721 standard; DNA; 15 BP.
XX XX
XX AC AAF50721;
XX XX
XX DT 30-MAR-2001 (first entry)
XX XX
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

```

```

XX DE IGF-I oligonucleotide #1681.
XX XX
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.
XX OS Homo sapiens.
XX XX
XX PN WO200078341-A1.
XX XX
XX PD 28-DEC-2000.
XX XX
XX PF 21-JUN-2000; 2000WO-AU000693.
XX XX
XX PR 21-JUN-1999; 99US-0140345P.
XX XX
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX XX
XX PI Wraight CJ, Werther GA, Edmondson SR;
XX XX WPI; 2001-041421/05.
XX DR
XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX PT inhibits or reduces growth factor mediated cell proliferation and/or
XX PT inflammation.
XX PS Example 8; Page 71; 201pp; English.
XX XX
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX XX
XX SQ Sequence 15 BP; 5 A; 5 C; 3 G; 2 T; 0 U; 0 Other;
XX XX
XX Query Match 7.9%; Score 11; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 4.9e+02;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1667 ACAGCTGGGAAC 1677
XX Db |||||
XX 5 ACAGCTGGGAAC 15
XX
XX RESULT 869
XX AAF50725
XX ID AAF50725 standard; DNA; 15 BP.
XX XX
XX AC AAF50725;
XX XX
XX DT 30-MAR-2001 (first entry)
XX XX
XX DE IGF-I oligonucleotide #1685.
XX XX
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

```

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.

XX Homo sapiens.  
 XX WO2000078341-A1.  
 XX 28-DEC-2000.  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX 21-JUN-1999; 99US-0140345P.  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 XX Wraight CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 XX inhibits or reduces growth factor mediated cell proliferation and/or  
 XX inflammation.

XX Example 8; Page 71; 201pp; English.  
 XX The present invention relates to a method for ameliorating the effects of  
 XX skin disorders. The method comprises contacting the skin with an  
 XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 XX inhibiting or reducing growth factor mediated cell proliferation,  
 XX inflammation and/or other disorders. The present sequence is an  
 XX oligonucleotide which can be used to design the antisense  
 XX oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 XX F45161). The method is useful for ameliorating the effects of psoriasis,  
 XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 XX hyperneovascular condition such as a neovascular condition of the retina,  
 XX brain or skin, growth factor-mediated malignancies, other sclerotic  
 XX disease, kidney disease, hyperproliferation of the inside of blood  
 XX vessels or any other hyperplasia

XX Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1667 ACAGCTGGAAC 1677  
 DB 1 ACAGCTGGAAC 11

RESULT 870  
 AAF50723  
 ID AAF50723 standard; DNA; 15 BP.  
 XX AC AAF50723;  
 XX 30-MAR-2001 (first entry)  
 XX IGF-I oligonucleotide #1683.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.

XX Homo sapiens.  
 XX WO2000078341-A1.  
 XX 28-DEC-2000.  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX 21-JUN-1999; 99US-0140345P.  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 XX Wraight CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 XX inhibits or reduces growth factor mediated cell proliferation and/or  
 XX inflammation.

XX Example 8; Page 71; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of  
 XX skin disorders. The method comprises contacting the skin with an  
 XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 XX inhibiting or reducing growth factor mediated cell proliferation,  
 XX inflammation and/or other disorders. The present sequence is an  
 XX oligonucleotide which can be used to design the antisense  
 XX oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 XX F45161). The method is useful for ameliorating the effects of psoriasis,  
 XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 XX hyperneovascular condition such as a neovascular condition of the retina,  
 XX brain or skin, growth factor-mediated malignancies, other sclerotic  
 XX disease, kidney disease, hyperproliferation of the inside of blood  
 XX vessels or any other hyperplasia

XX Sequence 15 BP; 6 A; 4 C; 3 G; 2 T; 0 U; 0 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1667 ACAGCTGGAAC 1677  
 DB 3 ACAGCTGGAAC 13

RESULT 871  
 AAS98658/c  
 ID AAS98658 standard; DNA; 15 BP.  
 XX AC AAS98658;  
 XX 26-MAR-2002 (first entry)  
 XX Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #24.  
 XX Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;  
 KW cytostatic; gene therapy; malignant histiocytosis; isogene;  
 KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;  
 KW genotype; human; allele specific oligonucleotide; ASO; probe; ss.

XX Homo sapiens.  
 XX WO200179225-A2.

PD 25-OCT-2001.  
 XX  
 PF 12-APR-2001; 2001WO-US012044.  
 XX  
 PR 12-APR-2000; 2000US-0196411P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Chew A, Choi JY, Koshy B;  
 XX  
 DR WPI; 2002-075058/10.  
 XX  
 XX  
 PT Novel polymorphic variants of colony stimulating factor 1 receptor useful  
 PT in studying expression and function of the protein, useful for screening  
 PT candidate drugs to treat diseases e.g. inflammatory disorders.  
 XX  
 PS Claim 15; Page 15; 164pp; English.  
 XX  
 CC The invention describes a novel isolated polynucleotide (I) comprising a  
 CC sequence which is a polymorphic variant (PV) of a reference sequence for  
 CC colony stimulating factor 1 receptor (CSF1R) gene, found on the  
 CC polypeptide are useful for improving the discovery and development of  
 CC drugs for treating diseases associated with CSF1R activity, e.g.,  
 CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders  
 CC and the haplotypes can be used to validate CSF1R as a candidate target  
 CC for treating a specific condition or disease predicted to be associated  
 CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also  
 CC be used in developing diagnostic tests and therapeutic treatments. (I) is  
 CC useful in studying the expression and function of CSF1R, and in  
 CC expressing CSF1R protein for use in screening for candidate drugs to  
 CC treat diseases related to CSF1R activity and in studying the effect of  
 CC the variation on the biological activity of CSF1R as well as on the  
 CC binding affinity of candidate drugs targeting CSF1R. Antibodies are  
 CC useful in a variety of diagnostic and prognostic formats and therapeutic  
 CC methods. A transgenic animal is useful in studying expression of the  
 CC CSF1R isogenes in vivo, for in vivo screening and testing of drugs  
 CC targeted against CSF1R protein, and for testing the efficacy of  
 CC therapeutic agents and compounds. Allele specific oligonucleotides (ASO)  
 CC are useful as probes and primers, and for assaying a polymorphism in the  
 CC target region. Without requiring any a priori knowledge of the phenotypic  
 CC effect of any particular CSF1R or haplotype the invention provides a  
 CC method for identifying lead compounds that are more likely to show  
 CC efficacy in clinical trials. This sequence is an allele specific  
 CC oligonucleotide probe used for detecting CSF1R gene polymorphisms,  
 CC described in the method of the invention  
 XX  
 SQ Sequence 15 BP; 3 A; 7 C; 1 G; 3 T; 0 U; 1 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 15;  
 Best Local Similarity 84.6%; Pred. No. 4.9e+02;  
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1673 GGAACCCCTGGTGT 1685  
 Db |||||  
 14 GGAACCTGGTGT 2  
 RESULT 872  
 ABK92567  
 ID ABK92567 standard; DNA; 15 BP.  
 XX  
 AC ABK92567;  
 XX  
 XX 20-AUG-2002 (first entry)  
 DE ASO primer #4 to detect human CHRM4 gene polymorphisms.  
 XX  
 KW Human; single nucleotide polymorphism; SNP; CHRM4; haplotyping;  
 KW chromosome 1p12-p11.2; cholinergic receptor muscarinic 4; genotyping;  
 KW Alzheimer's disease; neurological disorder;  
 KW allele-specific oligonucleotide; ASO; primer; ss.  
 XX  
 OS Homo sapiens.

XX  
 PN WO200236609-A2.  
 XX  
 PD 10-MAY-2002.  
 XX  
 PF 31-OCT-2001; 2001WO-US045709.  
 XX  
 PR 31-OCT-2000; 2000US-0244627P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 PA (PETE/) PETERSON N.  
 PA (ROUN/) ROUNDS E.  
 XX  
 PI Denton RR, Duda A, Gilson CR, Kazemi A, Nandabalan K, Tirrell C;  
 XX  
 DR WPI; 2002-489997/52.  
 XX  
 XX  
 PT Novel genetic variants of cholinergic receptor muscarinic 4 useful in  
 PT studying expression and function of protein, and for screening drugs to  
 PT treat diseases e.g. Alzheimer's disease and other neurological disorders.  
 XX  
 PS Claim 14; Page 13; 63pp; English.  
 XX  
 CC The present invention relates to novel single nucleotide polymorphisms  
 CC (SNPs) in the human cholinergic receptor, muscarinic 4 (CHRM4) gene  
 CC located on chromosome 1p12-p11.2, and methods for haplotyping and/or  
 CC genotyping the CHRM4 gene. The methods of the invention make use of  
 CC allele-specific oligonucleotides (ASOs) as probes and primers and/or  
 CC primer-extension oligonucleotides for detecting the CHRM4 gene  
 CC polymorphisms. The polynucleotides and screened compounds are useful for  
 CC the treatment of diseases associated with CHRM4 activity, such as  
 CC Alzheimer's disease and other neurological disorders. ASK92564-ABK92575  
 CC represent ASO primers for detecting human CHRM4 gene polymorphisms  
 XX  
 SQ Sequence 15 BP; 3 A; 5 C; 5 G; 1 T; 0 U; 1 Other;  
 Query Match 7.9%; Score 11; DB 1; Length 15;  
 Best Local Similarity 84.6%; Pred. No. 4.9e+02;  
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1658 ACCAGGCTCACAG 1670  
 Db |||||  
 3 ACCAGGCGCACRG 15  
 RESULT 873  
 ABK92619  
 ID ABK92619 standard; DNA; 15 BP.  
 XX  
 AC ABK92619;  
 XX  
 XX 20-AUG-2002 (first entry)  
 DE ASO primer #17 to detect human ADORA3 gene polymorphisms.  
 XX  
 KW Human; single nucleotide polymorphism; SNP; ADORA3; haplotyping;  
 KW chromosome 1p21-p13; adenosine A3 receptor; genotyping;  
 KW pathophysiological heart condition; myocardial ischaemia;  
 KW chronic heart failure; allele-specific oligonucleotide; ASO; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200236610-A2.  
 XX  
 PD 10-MAY-2002.  
 XX  
 PF 31-OCT-2001; 2001WO-US045718.  
 XX  
 PR 31-OCT-2000; 2000US-0244626P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Gilson CR, Kazemi A, Koshy B, Monroe G;

XX	WPI; 2002-489998/52.
DR	
XX	
PT	Novel genetic variants of the adenosine A3 receptor, useful therapeutically and in screening for drugs to treat diseases related to ADORA3 activity e.g., myocardial ischemia and chronic heart failure.
PT	
XX	
PS	Claim 15; Page 14; 82pp; English.
XX	
CC	The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human adenosine A3 receptor (ADORA3) gene located on chromosome 1p21-p13, and methods for haplotyping and/or genotyping the ADORA3 gene. The methods of the invention make use of allele-specific oligonucleotides (ASOs) as probes and primers and/or primer-extension oligonucleotides for detecting the ADORA3 gene polymorphisms. The polynucleotides and screened compounds are useful for the treatment of diseases associated with ADORA3 activity, such as pathophysiological conditions of the heart e.g. myocardial ischemia and chronic heart failure. ABK32603-ABK32628 represent ASO primers for detecting human ADORA3 gene polymorphisms
XX	
XX	Sequence 15 BP; 2 A; 6 C; 4 G; 2 T; 0 U; 1 Other;
SQ	
	Query Match 7.9%; Score 11; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 4.9e+02; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1759 AGGCCCACTGG 1769 
Db	2 AGGCCCACTGG 12
RESULT 874	
ID	ABK32117 standard; DNA; 15 BP.
XX	
AC	ABK32117;
XX	
DT	23-APR-2002 (first entry)
XX	
DE	Human colon cancer SAGE tag #218.
XX	
KW	Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW	serial analysis of gene expression; diagnostic; prognostic; probe;
KW	cancer marker; ss.
OS	Homo sapiens.
XX	
PN	US6333152-B1.
XX	
PD	25-DEC-2001.
XX	
PF	20-MAY-1998; 98US-00081646.
XX	
PR	20-MAY-1998; 98US-00081646.
XX	
PA	(UYJO ) UNIV JOHNS HOPKINS.
XX	
PI	Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX	
DR	WPI; 2002-153821/20.
XX	
PT	New human nucleic acid containing specific SAGE tags, useful as diagnostic markers for cancer, also derived probes.
PT	
XX	
PS	Disclosure; Col 93; 161pp; English.
XX	
CC	The invention relates to an isolated, purified human nucleic acid (I) that has the same sequence as a mRNA found in humans and is a SAGE (serial analysis of gene expression) tag comprising a single stranded probe containing at least 10 consecutive nucleotides. SAGE tags, are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer SAGE tags of the invention
XX	
XX	
SQ	Sequence 15 BP; 4 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
	Query Match 7.9%; Score 11; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 4.9e+02; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1672 TGAACCCCTGG 1682 
Db	3 TGAACCCCTGG 13
RESULT 876	
ID	AAL39485/c
XX	
AC	AAL39485 standard; DNA; 15 BP.
XX	
AC	AAL39485;
XX	

XX	WPI; 2002-489998/52.
DR	
XX	
PT	Novel genetic variants of the adenosine A3 receptor, useful therapeutically and in screening for drugs to treat diseases related to ADORA3 activity e.g., myocardial ischemia and chronic heart failure.
PT	
XX	
PS	Claim 15; Page 14; 82pp; English.
XX	
CC	The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human adenosine A3 receptor (ADORA3) gene located on chromosome 1p21-p13, and methods for haplotyping and/or genotyping the ADORA3 gene. The methods of the invention make use of allele-specific oligonucleotides (ASOs) as probes and primers and/or primer-extension oligonucleotides for detecting the ADORA3 gene polymorphisms. The polynucleotides and screened compounds are useful for the treatment of diseases associated with ADORA3 activity, such as pathophysiological conditions of the heart e.g. myocardial ischemia and chronic heart failure. ABK32603-ABK32628 represent ASO primers for detecting human ADORA3 gene polymorphisms
XX	
XX	Sequence 15 BP; 2 A; 6 C; 4 G; 2 T; 0 U; 1 Other;
SQ	
	Query Match 7.9%; Score 11; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 4.9e+02; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1759 AGGCCCACTGG 1769 
Db	2 AGGCCCACTGG 12
RESULT 874	
ABK32117	
ID	ABK32117 standard; DNA; 15 BP.
XX	
AC	ABK32117;
XX	
DT	23-APR-2002 (first entry)
XX	
DE	Human colon cancer SAGE tag #218.
XX	
KW	Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW	serial analysis of gene expression; diagnostic; prognostic; probe;
KW	cancer marker; ss.
XX	
OS	Homo sapiens.
XX	
PN	US6333152-B1.
XX	
PD	25-DEC-2001.
XX	
PF	20-MAY-1998; 98US-00081646.
XX	
PR	20-MAY-1998; 98US-00081646.
XX	
PA	(UYJO ) UNIV JOHNS HOPKINS.
XX	
PI	Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX	
DR	WPI; 2002-153821/20.
XX	
PT	New human nucleic acid containing specific SAGE tags, useful as diagnostic markers for cancer, also derived probes.
PT	
XX	
PS	Disclosure; Col 93; 161pp; English.
XX	
CC	The invention relates to an isolated, purified human nucleic acid (I) that has the same sequence as a mRNA found in humans and is a SAGE (serial analysis of gene expression) tag comprising a single stranded probe containing at least 10 consecutive nucleotides. SAGE tags, are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer SAGE tags of the invention
XX	
XX	
SQ	Sequence 15 BP; 4 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
	Query Match 7.9%; Score 11; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 4.9e+02; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1672 TGAACCCCTGG 1682 
Db	3 TGAACCCCTGG 13
RESULT 876	
AAL39485/c	
ID	AAL39485 standard; DNA; 15 BP.
XX	
AC	AAL39485;
XX	

```

DT XX 05-SEP-2002 (first entry)
DE XX CCBP2 detecting ASO probe SEQ ID No 12.
KW XX Chemokine binding protein 2; CCBP2; CCBP2 protein isoform; gene therapy;
KW XX polymorphic gene variant; single nucleotide polymorphism; human; probe;
XX ss.
XX Homo sapiens.
OS WO200232926-A2.
PN 25-APR-2002.
XX 12-OCT-2001; 2001WO-US042685.
XX 12-OCT-2000; 2000US-0239638P.
XX (GENA-) GENAISSANCE PHARM INC.
PA Armstrong B, Kazemi A, Koshy B;
PI WPI; 2002-435524/46.
DR XX
XX New genetic variants having polymorphisms in the chemokine binding
PT protein 2 (CCBP2) gene, useful for studying CCBP2 functions, and for
PT treating disorders affected by expression or function of the CCBP2
PT isogene.
XX Claim 14; Page 13; 84pp; English.
XX The invention relates to an isolated polynucleotide comprising genes and
CC haplotypes of the chemokine binding protein 2 (CCBP2) gene. Polymorphic
CC variants of the CCBP2 gene are useful in studying the expression and
CC function of CCBP2, and in expressing CCBP2 proteins for use in screening
CC candidate drugs for treating diseases associated with CCBP2 activity.
CC Polynucleotides comprising a polymorphic gene variant or fragment may be
CC used for therapeutic purposes, where a patient could benefit from
CC expression or increased expression of a particular CCBP2 protein isoform,
CC or an expression vector encoding the isoform may be administered to the
CC patient. Haplotype information is useful in improving the efficiency and
CC output of several steps in drug discovery and development process,
CC including target validation, identifying lead compounds, and early phase
CC clinical trials. The polynucleotides of the invention can be used to
CC treat disorders related to the CCBP2 gene by gene therapy. This
CC polynucleotide sequence represents a preferred ASO probe for detecting
CC CCBP2 gene polymorphisms relating to the invention
XX
SQ Sequence 15 BP; 0 A; 5 C; 5 G; 4 T; 0 U; 1 Other;
Query Match 7.9%; Score 11; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 4.9e+02;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1659 CCAGGCTCAGC 1671
DB 13 CCAGGSACAGC 1
RESULT 877
AAQ89557
ID AAQ89557 standard; DNA; 16 BP.
XX
XX AAQ89557;
AC
DT 11-DEC-1995 (first entry)
XX
XX Rat CYP7 gene steroid regulatory element (-1151 to -1135).
DE
XX CYP7; cholesterol 7 alpha hydroxylase; transcription factor;
KW regulatory element; ss.
KW
XX Rattus rattus.
OS

```

```

XX EP648840-A2.
XX
XX 19-APR-1995.
XX
XX 07-OCT-1994; 94BP-00115856.
XX
XX 13-OCT-1993; 93US-00135488.
XX 13-OCT-1993; 93US-00135510.
XX 13-OCT-1993; 93US-00135511.
XX 28-JAN-1994; 94US-00187453.
XX
XX (UYNE-) UNIV NORTHEASTERN OHIO.
PA
XX Chiang JYL;
XX WPI; 1995-148718/20.
XX
XX Cholesterol 7-hydroxylase (CYP7) gene regulatory elements - including
PT bile responsive elements, useful for identifying CYP7 transcription
PT factors.
XX
XX Claim 1; Page 17; 84pp; English.
XX
XX AAQ89556 and AAQ89557 are steroid regulatory elements of rat cholesterol
CC 7 alpha-hydroxylase (CYP7). CYP7 gene expression is controlled by DNA
CC regulatory elements that are located within the gene. The location of
CC these regulatory elements has been identified and they have been
CC isolated. These DNA fragments are useful in the identification of CYP7
CC transcription factors
XX
XX Sequence 16 BP; 3 A; 8 C; 0 G; 5 T; 0 U; 0 Other;
SQ
Query Match 7.9%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1740 CAACCTCCTCCC 1750
DB 1 CAACCTCCTCCC 11
RESULT 878
AAQ89026
ID AAQ89026 standard; DNA; 16 BP.
XX
XX AAQ89026;
AC
XX
XX 26-SEP-2001 (first entry)
DT
XX Human SAPI140 exon 9-intron 9 boundary genomic sequence.
DE
XX
XX Human; 140kDa Shc associated protein; SAPI40; tyrosine phosphatase Lyp1;
KW chromosome 9; haematopoietic; B-cell; T-cell; acute myeloid leukaemia;
KW AML; acute lymphoblastic leukaemia; ALL; hyperproliferation; cancer;
KW autoimmune disorder; apoptosis; allergic disorder; immunosuppression; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH exon 1. .7
FT /*tag= a
FT /partial
FT /number= 9
FT
FT intron 8. .16
FT /*tag= b
FT /partial
FT /number= 9
XX
XX WO200151509-A2.
XX
XX 19-JUL-2001.
XX

```

Mon Aug 30 09:26:45 2004

```

PF 10-JAN-2001; 2001WO-CA000023.
XX
PR 10-JAN-2000; 2000US-0175233P.
XX
XX (HOSP-) HOSPITAL FOR SICK CHILDREN.
FA
XX Roifman CM, Sharfe N;
XX
XX WPI; 2001-442133/47.
XX
XX New Shc associated protein, useful for identifying modulators for
XX treating cancer.
PT
XX
XX Example 3; Fig 4B; 106pp; English.
PS
XX
XX The present sequence represents the human SAPI140 exon 9-intron 9 boundary
XX genomic sequence. Human 140kDa Shc associated protein (SAPI140; AAU03596)
XX is a novel non-transmembrane protein which is isolated by binding to the
XX human cytoplasmic tyrosine phosphatase Lyp1. The gene encoding for SAPI140
XX maps to chromosome 9. SAPI140 is useful for identifying compounds which
XX can bind and modulate SAPI140 protein activity. Compounds which inhibit or
XX induce SAPI140 expression or activity are useful for modulating the
XX expression/activity of SAPI140 to modulate the activity of haematopoietic
XX cells, such as a B- or T-cells, preferably leukaemic cells. SAPI140 can be
XX used for the treatment of acute myeloid leukaemia (AML), acute
XX lymphoblastic leukaemia (ALL), uncontrolled T-cell diseases,
XX haematopoietic disorders (e.g. lymphomas) and hyperproliferation
XX disorders (e.g. cancer). Modulators of SAPI140 are useful in modulating
XX disorders such as neoplasia and autoimmunity, to stimulate cell death or
XX apoptosis, and to induce cell proliferation for treatment of autoimmune
XX diseases (e.g. multiple sclerosis, lupus, arthritis, diabetes) and
XX allergic disorders (e.g. asthma). Modulators of SAPI140 regulatory
XX pathways are also useful for treating a disorder which requires
XX immunosuppression such as transplantation
XX
XX Sequence 16 BP; 9 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
SQ
Query Match 7.9%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1649 AAGGCAAGCAC 1659
DB 6 AAGGCAAGCAC 16
RESULT 879
AAQ74120/C
ID AAQ74120 standard; DNA; 14 BP.
XX
XX AAQ74120;
AC
XX
XX 02-FEB-1996 (first entry)
DT
XX
XX Platelet derived growth factor (PDGF-A) antisense oligonucleotide.
DE
XX
XX Platelet derived growth factor; PDGF-A; antisense oligonucleotide;
KW breast; pancreatic; carcinoma; glioma; melanoma; rheumatoid; arthritis;
KW angiogenesis inhibitor; tumours; cancer; ss.
XX
XX Synthetic.
OS
XX WO9516032-A1.
XX
XX 15-JUN-1995.
PD
XX
XX 09-DEC-1993; 93WO-EP003461.
PF
XX
XX 09-DEC-1993; 93WO-EP003461.
PR
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
PA
XX Schlengersiepen GF, Brysch W, Schlengersiepen R, Schlengersiepen K;
PI
10-JAN-2001; 2001WO-CA000023.
XX
PR 10-JAN-2000; 2000US-0175233P.
XX
XX (HOSP-) HOSPITAL FOR SICK CHILDREN.
FA
XX Roifman CM, Sharfe N;
XX
XX WPI; 2001-442133/47.
XX
XX New Shc associated protein, useful for identifying modulators for
XX treating cancer.
PT
XX
XX Example 3; Fig 4B; 106pp; English.
PS
XX
XX The present sequence represents the human SAPI140 exon 9-intron 9 boundary
XX genomic sequence. Human 140kDa Shc associated protein (SAPI140; AAU03596)
XX is a novel non-transmembrane protein which is isolated by binding to the
XX human cytoplasmic tyrosine phosphatase Lyp1. The gene encoding for SAPI140
XX maps to chromosome 9. SAPI140 is useful for identifying compounds which
XX can bind and modulate SAPI140 protein activity. Compounds which inhibit or
XX induce SAPI140 expression or activity are useful for modulating the
XX expression/activity of SAPI140 to modulate the activity of haematopoietic
XX cells, such as a B- or T-cells, preferably leukaemic cells. SAPI140 can be
XX used for the treatment of acute myeloid leukaemia (AML), acute
XX lymphoblastic leukaemia (ALL), uncontrolled T-cell diseases,
XX haematopoietic disorders (e.g. lymphomas) and hyperproliferation
XX disorders (e.g. cancer). Modulators of SAPI140 are useful in modulating
XX disorders such as neoplasia and autoimmunity, to stimulate cell death or
XX apoptosis, and to induce cell proliferation for treatment of autoimmune
XX diseases (e.g. multiple sclerosis, lupus, arthritis, diabetes) and
XX allergic disorders (e.g. asthma). Modulators of SAPI140 regulatory
XX pathways are also useful for treating a disorder which requires
XX immunosuppression such as transplantation
XX
XX Sequence 16 BP; 9 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
SQ
Query Match 7.8%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 4.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1726 TGGAGATTGGCTCC 1739
DB 14 TGGAGATTAGACTCC 1
RESULT 880
AAT98896
ID AAT98896 standard; DNA; 14 BP.
XX
XX AAT98896;
AC
XX
XX 23-MAR-1998 (first entry)
DT
XX
XX Probe 41w18 for HIV RT gene wild type E40W41.
XX
XX Reverse transcriptase gene; HIV; RT gene; antiviral drug susceptibility;
KW virus susceptibility; antiviral drug resistant viral strain; retrovirus;
KW Hepadnaviridae; HIV RT genotyping; probe; ss.
XX
XX Synthetic.
OS
XX Human immunodeficiency virus 1.
XX
XX WO9727332-A1.
XX
XX 31-JUL-1997.
PD
XX
XX 17-JAN-1997; 97WO-EP000211.
PF
XX
XX 26-JAN-1996; 96EP-03870005.
PR
XX
XX 25-JUN-1996; 96EP-03870081.
PR
XX
XX (INNO-) INNOGENETICS NV.
PA
XX
XX Stuyver L, Louwagie J, Rossau R;
XX
XX WPI; 1997-393716/36.
XX
XX Determining susceptibility to antiviral drugs of reverse transcriptase
XX containing viruses - useful for genotyping HIV RT and detecting antiviral
XX resistant HIV.
XX
XX Claim 13; Page 36; 59pp; English.
XX
XX This sequence represents a probe for a wild type HIV reverse
XX transcriptase (RT) gene fragment. This sequence can be used in the method
XX of the invention for determining the susceptibility to antiviral drugs of
XX viruses which contain RT genes and are present in a biological sample. It
XX comprises: (1) releasing, isolating or concentrating the polynucleic
XX acids present in a sample; (2) amplifying the relevant part of the RT
XX genes present with at least one suitable primer pair; (3) hybridising the
XX polynucleic acids of step (1) or (2) with at least two RT gene probes,
XX the probes being applied to known locations on a solid support, and are
XX capable of simultaneously hybridising to their respective target regions
XX

```

CC under appropriate hybridisation and wash condition allowing the detection  
CC of homologous targets, or with the probes hybridising specifically with a  
CC sequence complementary to any of the target sequences; (4) detecting the  
CC hybrids formed in step (3); and (4) inferring the nucleotide sequence at  
CC the codons of interest (codons 38-44, 47-53, 65-72, 73-77, 148-154, 180-  
CC 187, 212-216, and 217-220), and/or the amino acids of the codons of  
CC interest and/or antiviral drug resistance spectrum, and possible the type  
CC of viral isolates involved from the differential hybridisation signals  
CC obtained in step (4). The method is specifically used to detect antiviral  
CC drug resistant strains of viruses containing RT genes, especially HIV  
CC retroviruses and Hepadnaviridae. The method can also be used for  
CC genotyping HIV RT

SQ Sequence 14 BP; 7 A; 1 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 7.8%; Score 10.8; DB 1; Length 14;  
Best Local Similarity 85.7%; Pred. No. 4.9e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1718 TACGAGATGGAGA 1731  
||| |||||  
Db 1 TACAGATGGAAA 14

RESULT 881  
AA55199  
ID AAX55199 standard; DNA; 14 BP.  
AC AAX55199;  
XX  
XX  
DT 05-JUL-1999 (first entry)  
XX  
XX  
DE Multiple antisense oligonucleotide 20.  
XX  
XX  
KW Antisense oligonucleotide; multiple target; antisense treatment;  
KW impaired respiration; inflammation; lung disease;  
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
KW acute asthma; allergy; asthma; impeded respiration;  
KW respiratory distress syndrome; pain; cystic fibrosis;  
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
KW prostate cancer; ss.

XX Synthetic.  
OS  
XX  
XX  
PN W09913886-A1.  
XX  
XX  
XX 25-MAR-1999.  
XX  
XX 17-SEP-1998; 98WO-US019419.  
XX  
XX 17-SEP-1997; 97US-0059160P.  
PR 09-JUN-1998; 98US-00093972.  
XX

PA (UVEC-) UNIV EAST CAROLINA.  
XX  
XX Nyce JW;  
PI  
XX  
XX WPI; 1999-229400/19.  
DR

XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
PT vasoconstriction.  
PT  
XX  
XX Disclosure; Page 74; 120pp; English.  
PS

XX The specification describes antisense oligonucleotides (AAX52869-X55271)  
CC directed against at least 2 mRNAs selected from target genes, coding and  
CC non-coding regions of RNAs corresponding to target genes, gene initiation  
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
CC end and the juxta-section between coding and non-coding regions and all  
CC segments of RNAs encoding proteins associated with one or more diseases,

CC conditions or mixtures. The antisense oligonucleotides may be derived  
CC from sequences AAX55272-74. These multiple target oligonucleotides  
CC (specifically AAX55180-271) can be used for the antisense treatment of  
CC diseases and conditions. Typical diseases and conditions are those  
CC associated with impaired respiration and inflammation, including lung  
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
CC acute asthma, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
CC well as all types of cancers which may metastasize or have metastasized  
CC to the lungs, including breast and prostate cancer

SQ Sequence 14 BP; 0 A; 9 C; 2 G; 3 T; 0 U; 0 Other;  
Query Match 7.8%; Score 10.8; DB 1; Length 14;  
Best Local Similarity 85.7%; Pred. No. 4.9e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1733 TGGCTCCCACTCC 1746  
||| |||||  
Db 1 TGGCTCCCCCTCC 14

RESULT 882  
AAX14792  
ID AAX14792 standard; DNA; 14 BP.  
XX  
XX AAX14792;  
AC  
XX  
XX 24-MAR-1999 (first entry)  
DT  
XX  
XX Triple helix forming nucleotides 727-740 of Hepatitis B virus.  
DE  
XX Triple-helix forming region; Triplex formation; DNA detection;  
KW identification; bacteria; oncogene; virus; ds.

XX Hepatitis B virus.  
OS  
XX US5861244-A.  
PN  
XX  
XX 19-JAN-1999.  
PD  
XX  
XX 22-DEC-1993; 93US-00173489.  
PF  
XX 29-OCT-1992; 92US-00968436.  
PR

XX (PROF-) PROFILE DIAGNOSTIC SCI INC.  
FA  
XX Hepburn AG, Wang C;  
XX  
XX WPI; 1999-130384/11.  
DR  
XX

XX Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria.

XX Disclosure; Col 19-20; 168pp; English.  
PS  
XX  
XX The present sequence represents a potential triple-helix forming region.  
CC It can be used to demonstrate the assay of the invention. The assay  
CC comprises adding a sample containing double-stranded DNA test sequences,  
CC e.g. containing the present sequence, to an aqueous medium containing at  
CC least one complex of anchor DNA, attached to a solid support, and  
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is  
CC designed to form a triple-strand structure with part of the test  
CC sequence. Triplex formation results in displacement of the reporter DNA  
CC which is detected as an indication of the presence of the DNA test  
CC sequence. The method is used to detect DNA sequences, particularly for  
CC identification of bacteria (by detecting genes for ribosomal RNA) in

CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONS from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 14 BP; 0 A; 5 C; 2 G; 3 T; 0 U; 0 Other;  
  
Query Match 7.8%; Score 10.8; DB 1; Length 14;  
Best Local Similarity 85.7%; Pred. No. 4.9e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1733 TGGCTCCCAACTCC 1746  
DB 1 TGGCTCCCAACTCC 14  
  
RESULT 884  
AAF20768  
ID AAF20768 standard; DNA; 14 BP.  
XX  
AC AAF20768;  
XX  
DT 14-MAR-2001 (first entry)  
XX  
DE Human multiple target antisense (MTA) oligonucleotide #2335.  
XX  
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2000062736-A2.  
XX  
PD 26-OCT-2000.  
XX  
PF 24-MAR-2000; 2000WO-US008020.  
XX  
PR 06-APR-1999; 99US-0127958P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
XX  
PI Nyce JW;  
XX  
PS WPI; 2000-679539/66.  
XX  
CC Low adenosine (A) content antisense oligonucleotides which do not trigger  
CC adenosine receptors during metabolism, useful e.g. for treating cancers  
CC and respiratory obstructions.  
XX  
PS Claim 14; Page 625; 1592pp; English.  
XX  
CC The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and/or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and

CC clinical samples, but also detection of oncogenes and Hepatitis B virus  
XX  
SQ Sequence 14 BP; 0 A; 7 C; 0 G; 7 T; 0 U; 0 Other;  
  
Query Match 7.8%; Score 10.8; DB 1; Length 14;  
Best Local Similarity 85.7%; Pred. No. 4.9e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1743 CTCCTCCCTATCCT 1756  
DB 1 CTCCTCCCTATCCT 14  
  
RESULT 883  
AAA34646  
ID AAA34646 standard; DNA; 14 BP.  
XX  
AC AAA34646;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2335.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiasthmatic; cytostatic; analgesic; hypotensive; cytostatic;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US017712.  
XX  
PR 03-AUG-1998; 98US-0095212P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
PS WPI; 2000-205971/18.  
XX  
CC New antisense oligonucleotides useful for treating e.g. pulmonary  
CC vasoconstriction, inflammation, allergies, asthma, hypertension, or  
CC bronchitis, emphysema, respiratory distress syndrome, ischemia or  
CC cancers.  
XX  
PS Disclosure; Page 557; 1343pp; English.  
XX  
CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiasthmatic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present



CC chemokines, endogenously produced specific and non-specific enzymes.  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides and (I) can be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention

XX SQ Sequence 14 BP; 0 A; 9 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 14;  
 Best Local Similarity 85.7%; Pred. No. 4.9e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1733 TGGCTCCCAACTCC 1746

Db 1 TGGCTCCCACTCC 14

RESULT 885

AAF21471

ID AAF21471 standard; DNA; 14 BP.

AC AAF21471;

DT 14-MAR-2001 (first entry)

XX Human multiple target antisense (MTA) oligonucleotide #3038.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antialsthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary obstruction; impeded respiration;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.

XX Homo sapiens.

OS WO200062736-A2.

PN 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

PF 06-APR-1999; 99US-0127958P.

XX (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

PI Nyce JW;

XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.

XX

PS Disclosure; Page 297; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antialsthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with the  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention

XX SQ Sequence 14 BP; 0 A; 9 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 14;

Best Local Similarity 85.7%; Pred. No. 4.9e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1733 TGGCTCCCAACTCC 1746

Db 1 TGGCTCCCACTCC 14

RESULT 886

ABZ96462

ID ABZ96462 standard; DNA; 14 BP.

AC ABZ96462;

DT 17-OCT-2003 (first entry)

XX Human nucleic acid sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antialsthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

PF 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;  
XX  
XX  
XX  
XX WPI: 2003-229219/22.  
XX  
XX Pharmaceutical composition for treating ailments associated with impaired  
XX respiration, has oligo(s) antisense to specific gene(s) or its  
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX ubiquinone.  
XX  
XX  
XX Disclosure; SEQ ID NO 12407; 872bp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
XX first active agent comprising an oligonucleotide antisense to the  
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,  
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
XX junctions of genes encoding a polypeptide associated with lung and/or  
XX nasal airway dysfunction and a second active agent comprising an  
XX antiinflammatory steroid and ubiquinone. A composition of the invention  
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
XX immunosuppressive, and cytostatic activity. The composition may have a  
XX use in antisense gene therapy. The composition is useful for treating or  
XX preventing a respiratory, lung or malignant disease or condition, also  
XX for enhancing the prophylactic or therapeutic respiratory effect of an  
XX antiinflammatory steroid in a subject, for reducing or depleting levels  
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine  
XX receptor, producing bronchodilation, increasing levels of ubiquinone or  
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,  
XX lung inflammation, lung allergies, or a respiratory disease or condition.  
XX Note: The sequence data for this patent is not represented in the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 14 BP; 0 A; 9 C; 2 G; 3 T; 0 U; 0 Other;  
SQ

Query Match 7.8%; Score 10.8; DB 1; Length 14;  
Best Local Similarity 85.7%; Pred. No. 4.9e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps

QY 1733 TGGCTCCCAATCC 1746  
Db 1 TGGCTCCGCCCTCC 14  
|||||  
|||||

RESULT 898  
AAQ22446/c  
ID AAQ22446 standard; DNA; 15 BP.  
XX  
XX AC AAQ22446;  
XX  
XX DT 05-AUG-1992 (first entry)  
XX  
XX DE Probe (6) for DNA fingerprint analysis.  
XX  
XX KW M13; consensus; hypervariable region; HVR; ss.  
XX  
XX OS Synthetic.  
XX  
XX PN US5097024-A.  
XX  
XX PD 17-MAR-1992.  
XX  
XX PF 25-SEP-1989; 89US-00411823.  
XX  
XX PR 25-SEP-1989; 89US-00411823.  
XX  
XX PA (HODE/) HODES M E.  
XX  
XX PI Hodes ME, Norris FH, Hodes MZ;  
XX  
XX PF 1992-113708/14.  
XX  
XX  
XX New DNA sequences as DNA probes - for use in paternity and maternity  
XX testing, analysis of tumour cells, animal or plant breeding, etc.  
PT

XX PS Claim 1; Page 13; 13pp; English.

XX CC The DNA probes represented in AAQ22441-76 are 15 nucleotide sequences

CC wherein 8 nucleotides of each sequence are G, 3 are T, 1 is C, 1 is A and

CC 2 are N, except that the nucleotide sequence is not the M13 consensus

CC sequence GAGGGTGGGNGTCT. The probes can detect hyper- variable regions

CC (HVRs) in genomic DNA with such precision as to enable individuals to be

CC identified or fingerprinted by reference to variations in their DNA in

CC these regions. The DNA probes can be used in paternity and maternity

CC testing, zygosity testing in twins, cell chimerism studies, e.g.

CC detection of donor versus recipient cells after bone marrow

CC transplantation, forensic medicine, family sp. verification, tests for

CC inbreeding, pedigree analysis, identification of loci or genetic

CC diseases, animal or plant breeding and pedigree analysis authentication,

CC quality control of cell lines and analysis. Preparation: The M13 sequence

CC was initially randomised manually by the method of random sampling

CC without replacement to produce random sequences. Later a computer

CC programme was written that implemented an algorithm that produced a

CC random sequence by sampling without replacement. Several of the random

CC sequences that were obtd. were synthesised, labelled and used as DNA

CC probes

XX SQ Sequence 15 BP; 2 A; 1 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 5.4e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 CTCCTCACTCTCTCC 1749

DB 15 CCCACACTCTCTCC 2

RESULT 889

AAQ45774

ID AAQ45774 standard; DNA; 15 BP.

XX AC AAQ45774;

XX DT 25-MAR-2003 (revised)

DT 08-DEC-1993 (first entry)

XX DE Human prostate transglutaminase gene PCR primer ZC4048.

XX KW Degenerate; polymerase chain reaction; enzyme; inter alia;

KW therapeutic wound repair; skin graft closure; food prepn; preparation;

KW stabilising; marker; identifying agent; agonists; antagonists;

KW cellular apoptosis; ss.

XX OS Synthetic.

XX PN WO9313207-A2.

XX PD 08-JUL-1993.

XX PF 30-DEC-1992; 92WO-US011353.

XX PR 31-DEC-1991; 91US-00816284.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Ohara PV, Grant FJ, Sheppard PO;

XX DR WPI; 1993-227323/28.

XX PT Isolated polynucleotide molecule, for stabilising good prepn. - utilised

PT for coding human prostatic or placental trans glutaminase(s) and DNA, for

PT repairing wounds, ulcerated lesions, skin grafts, and cellular markers.

XX PS Example; Page 43; 48pp; English.

XX CC The sequence is that of oligonucleotide ZC4048 which was used in a PCR to

CC confirm the presence of additional 5' sequences, as part of the

CC generation of a full-length human prostate transglutaminase cDNA clone.

CC It was designed to hybridise to the antisense lambda sequences near the

CC EcoRI site of the lambda-gt11 vector. (Updated on 25-MAR-2003 to correct

CC PN field.)

XX SQ Sequence 15 BP; 3 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 5.4e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1663 GCTCACAGCTGAA 1676

DB 1 GCGCTCAGCTGAA 14

RESULT 890

AAQ88720

ID AAQ88720 standard; DNA; 15 BP.

XX AC AAQ88720;

XX DT 27-FEB-1996 (first entry)

XX DE c-Ha-ras modified antisense oligonucleotide.

XX KW antisense; analogue; non-terminal pyrimidine; phosphorothioate; backbone;

KW treatment; HIV; human immunodeficiency virus; HSV; herpes simplex virus;

KW cancer; integrin; cell adhesion receptor; infection; diagnosis;

KW nuclease resistance; ss.

XX OS Homo sapiens.

XX PN EP653439-A2.

XX PD 17-MAY-1995.

XX PF 07-NOV-1994; 94EP-00117513.

XX PR 12-NOV-1993; 93DE-04338704.

XX PA (FARH ) HOECHST AG.

XX PI Peyman A, Uhlmann E, Mag M, Kretzschmar G, Helsing M, Winkler I;

XX DR WPI; 1995-180677/24.

XX PT New anti-sense oligo:nucleotide analogues - with modified non-terminal

PT pyrimidine nucleotide units, useful for treating viral infections,

PT cancer, etc.

XX PS Claim 1; Page 23; 36pp; German.

XX CC The antisense oligonucleotide (ON) shown is a derivative of an equivalent

CC wild type Human c-Ha-ras ON, in which at least one, esp. 2-10, non-

CC terminal pyrimidine nucleotide(s) is/are modified. The modification may

CC be: (a) replacement of a phosphodiester linkage by a phosphorothioate

CC (PS), -dithioate, -aramidate; borano-, alkyl-, aralkyl-phosphate; 2,2,2-

CC trichloro-1,1dimethyl-, alkyl- or aryl- phosphate linkage; or (3'-

CC thio)formacetal, methylhydroxylamine, oxime, methylenedimethylhdrazo,

CC dimethylene sulphone or silyl linkage; (b) replacement of a sugar

CC phosphate backbone by a morpholinonucleoside, oligomer; (c) replacement

CC of beta-D-2-deoxyribose by another sugar or carbocyclic, open-chain or

CC bicyclic sugar analogue; or (c) replacement of the natural nucleoside

CC base by an analogue, e.g. 5-hydroxymethyl-uridine. The 5' and/or 3'

CC terminus may also be modified with a lipophilic gp., eg. a farnesyl. The

CC modifications increase nuclease resistance and thus improve stability and

CC activity

XX SQ Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 5.4e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCCCTG 1681  
||||| |||||  
Db 1 CAGCTGCAACCCAG 14

RESULT 891  
AAT56203/C  
ID AAT56203 standard; RNA; 15 BP.  
XX AAT56203;  
XX  
XX  
XX 25-MAR-2003 (revised)  
XX 14-MAY-1997 (first entry)  
XX  
XX  
XX Mouse TNF-a hammerhead ribozyme target sequence (nt position 615).  
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
XX intercellular adhesion molecule; rel A; tumour necrosis factor;  
XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
XX translocation; chronic myelogenous leukaemia; CML; cancer;  
XX Philadelphia chromosome; inflammation; autoimmune disease;  
XX atherosclerosis; myocardial infarction; stroke; restenosis;  
XX transplant rejection; rheumatoid arthritis; psoriasis;  
XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
XX human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
XX ss.  
XX  
XX Mus musculus.  
XX  
XX  
XX  
XX W09523225-A2.  
XX  
XX  
XX 31-AUG-1995.  
XX  
XX  
XX 23-FEB-1995; 95WO-IB000156.  
XX  
XX 23-FEB-1994; 94US-00201109.  
XX 29-MAR-1994; 94US-00218934.  
XX 04-APR-1994; 94US-00222795.  
XX 07-APR-1994; 94US-00224483.  
XX 15-APR-1994; 94US-00227958.  
XX 15-APR-1994; 94US-00228041.  
XX 18-MAY-1994; 94US-00245736.  
XX 06-JUL-1994; 94US-00271280.  
XX 15-AUG-1994; 94US-00291932.  
XX 16-AUG-1994; 94US-00291433.  
XX 17-AUG-1994; 94US-00292620.  
XX 19-AUG-1994; 94US-00293520.  
XX 02-SEP-1994; 94US-00300000.  
XX 08-SEP-1994; 94US-00303039.  
XX 23-SEP-1994; 94US-00311486.  
XX 23-SEP-1994; 94US-00311749.  
XX 28-SEP-1994; 94US-00314397.  
XX 03-OCT-1994; 94US-00316771.  
XX 07-OCT-1994; 94US-00319492.  
XX 11-OCT-1994; 94US-00321893.  
XX 04-NOV-1994; 94US-00334847.  
XX 10-NOV-1994; 94US-00337608.  
XX 28-NOV-1994; 94US-00345516.  
XX 16-DEC-1994; 94US-00357577.  
XX 23-DEC-1994; 94US-00363233.  
XX 30-JAN-1995; 95US-00380734.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;  
XX Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;  
XX Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
XX Tracz D, Usman N, Wincott FE, Woolf T;

DR WPI; 1995-351090/45.  
XX  
XX Ribozymes having modified bases and methods for producing them - for use  
XX in inhibiting disease related genes.  
XX  
XX PS  
XX Claim 2; Page 250; 407pp; English.  
XX  
XX The present sequence represents a preferred target sequence for an  
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves TNF-alpha mRNA at  
XX the nucleotide base position indicated in the DE line. Regions of the  
XX mRNA that do not form secondary folding structures and that contain  
XX potential hammerhead and hairpin ribozyme cleavage sites were identified  
XX by computer analysis. Ribozymes directed against these mRNA sequences  
XX were designed and synthesised with modifications that improve their  
XX nuclease resistance. The ribozymes are designed to cleave the target  
XX sequences and thereby inhibit TNF-alpha expression, making them  
XX potentially useful for treating rheumatoid arthritis, septic shock and  
XX other inflammatory disorders including psoriasis, as well as for  
XX treatment of AIDS. (Updated on 25-MAR-2003 to correct PI field.)  
XX  
XX Sequence 15 BP; 2 A; 8 C; 2 G; 0 T; 3 U; 0 Other;  
SQ

Query Match 7.8%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 5.4e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1708 GGGTTAGGACTACG 1721  
||||| |||||  
Db 15 GGGTGAGGAGCAG 2

RESULT 892  
AAQ97685  
ID AAQ97685 standard; DNA; 15 BP.  
XX  
XX  
XX AAQ97685;  
XX  
XX 22-MAR-1996 (first entry)  
XX  
XX Biotinylated antisense oligonucleotide against c-Ha-ras.  
XX  
XX antisense; c-ras; antigen; monoclonal antibody; avidin; biotinylation;  
XX non-viral vector; complex; Lewis Y antigen; bladder carcinoma; ss.  
XX Synthetic.  
XX  
XX  
XX Key Location/Qualifiers  
XX modified\_base 1 /\*tag= a  
XX /mod\_base= 5'-biotin-C  
XX  
XX W09521195-A1.  
XX  
XX 10-AUG-1995.  
XX  
XX 06-FEB-1995; 95WO-US0001161.  
XX  
XX 07-FEB-1994; 94US-00192655.  
XX  
XX (RERE-) RES DEV FOUND.  
XX  
XX Rosenblum MG, Donato NJ;  
XX  
XX WPI; 1995-283733/37.  
XX  
XX A non-viral vector having a cell binding component - used to introduce  
XX genetic material into. or to deliver a cytotoxic moiety to a specific  
XX cell.  
XX  
XX Example 14; Page 18; 35pp; English.  
XX  
XX A non-viral vector comprising a cell binding component having a biotin-  
XX binding element (eg. avidin or streptavidin) conjugated to a biotinylated  
XX

CC moiety is claimed. The cell binding element is a monoclonal antibody  
 CC (Mab) or a ligand which binds a cell surface receptor or a nucleic acid,  
 CC pref. a triplex forming oligonucleotide or an antisense oligonucleotide.  
 CC A Mab (BR96) which specifically binds Lewis Y antigen on several human  
 CC carcinomas was chemically conjugated to avidin. AAO97685 is complementary  
 CC to the c-Ha-ras 5' flanking mRNA sequence and was synthesised with a  
 CC biotinylated cytosine at the 5' terminal position. The biotinylated  
 CC oligonucleotide was incubated with the BR96-Avidin and complexes of BR96-  
 CC avidin:antisense c-Ha-ras were purified. The complexes were incubated  
 CC with T24 bladder carcinoma cells which express Lewis Y antigen and also  
 CC contain the c-Ha-ras oncogene. After incubation the product of the ras  
 CC oncogene, p21, was monitored by western blotting. Cell growth was also  
 CC monitored. Neutralisation of the effects of ras oncogene by intracellular  
 CC delivery of antisense molecules through internalisation of the Lewis Y  
 CC antigen was demonstrated  
 XX  
 SQ Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 5.4e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCCCTG 1681  
 Db 1 CAGCTGCAACCCAG 14

RESULT 893  
 AAT44432  
 ID AAT44432 standard; DNA; 15 BP.  
 AC AAT44432;  
 XX  
 DT 27-JAN-1997 (first entry)  
 XX  
 DE Antisense oligonucleotide VIII against c-Ha-ras.  
 XX  
 KW 8-azapurine; modification; stronger complex; inhibition; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN EP680969-R2.  
 XX  
 PD 08-NOV-1995.  
 XX  
 PF 26-APR-1995; 95EP-00106230.  
 XX  
 PR 02-MAY-1994; 94DE-04415370.  
 XX  
 PA (FARH ) HOECHST AG.  
 XX  
 PI Seela F, Lampe S;  
 XX  
 DR WPI; 1995-375165/49.  
 XX  
 FT New oligo:nucleotide(s) contg. 8-aza:purine base - useful as therapeutic  
 PT and diagnostic agents with more stable hybridisation to target nucleic  
 PT acid.  
 XX  
 PS Disclosure; Page 37; 51pp; German.  
 XX

CC AAT44425-54 are antisense oligonucleotides which have at least one 8-  
 CC azapurine base. The presence of an 8-azapurine base results in  
 CC significantly stronger complexing when hybridising to target nucleic  
 CC acids. The present sequence is against c-Ha-ras  
 XX  
 SQ Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;  
 Query Match 7.8%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 5.4e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCCCTG 1681

Db ||||| ||||| ||||| ||||| |||||  
 1 CAGCTGCAACCCAG 14  
 RESULT 894  
 AAT44237  
 ID AAT44237 standard; DNA; 15 BP.  
 AC AAT44237;  
 XX  
 DT 22-JUL-1997 (first entry)  
 XX  
 DE c-Ha-ras antisense component of capped oligonucleotide.  
 XX  
 KW Antisense therapy; cellular ras oncogene; c-Ha-ras; guanosine;  
 KW nuclease resistance; stability; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN DE19502912-Al.  
 XX  
 PD 01-AUG-1996.  
 XX  
 PF 31-JAN-1995; 95DE-01002912.  
 XX  
 PR 31-JAN-1995; 95DE-01002912.  
 XX  
 PA (FARH ) HOECHST AG.  
 XX  
 PI Peyman A, Uhlmann E;  
 XX  
 DR WPI; 1996-355223/36.  
 XX  
 PT Oligo:nucleotide(s) with series of G residues at at least one end have  
 PT increased stability against nuclease and cell penetration, - are partic.  
 PT anti:sense sequences for treating and diagnosing cancer, viral diseases  
 PT etc.  
 XX  
 PS Claim 3; Page 13; 15pp; German.  
 XX  
 CC Ten- to 40-mer oligonucleotides which have a cap of 1-10 (esp. 4) G  
 CC residues on at least one end are provided; if caps are present at both  
 CC ends, they can be of the same or different lengths. A cap sequence  
 CC increases nuclease resistance of the oligonucleotide and also increases  
 CC cell penetration. The present sequence is that of a preferred  
 CC oligonucleotide, directed against c-Ha-ras sequences, which can be capped  
 CC for use in anticancer therapy  
 XX  
 SQ Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;  
 Query Match 7.8%; Score 10.8; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 5.4e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAACCCCTG 1681  
 Db 1 CAGCTGCAACCCAG 14

RESULT 895  
 AAX33907  
 ID AAX33907 standard; DNA; 15 BP.  
 AC AAX33907;  
 XX  
 DT 30-JUN-1999 (first entry)  
 XX  
 DE c-Ha-ras expression inhibitor.  
 XX  
 KW Gene expression inhibitor; probe; nucleic acid detection; growth factor;  
 KW viral infection; therapy; HSV-1; cancer; restenosis; integrin;  
 KW cell-cell adhesion receptor; c-Ha-ras; ss.  
 XX

OS	Synthetic.
OS	Homo sapiens.
XX	
PN	AU9648028-A.
XX	
PD	26-SEP-1996.
XX	
XX	12-MAR-1996; 96AU-00048028.
PF	
XX	13-MAR-1995; 95DE-01008923.
PR	
PR	24-NOV-1995; 95DE-01043865.
XX	
PA	(FARH ) HOECHST AG.
XX	
PI	Peyman A, Uhlmann E, Breipohl G, Wallmeier H;
XX	
DR	WPI; 1996-455932/46.
XX	
XX	New phosphono-mono-ester oligo:nucleotide analogues - inhibitors of gene
PT	expression for treating viral infections, cancer, restenosis, etc.
XX	
PS	Disclosure; Page 41; 129pp; English.
XX	
CC	This sequence represents an inhibitor of c-Ha-ras expression, and is an
CC	example of an oligonucleotide analogue of the invention. The
CC	oligonucleotide analogues of the invention are used as inhibitors of gene
CC	expression (antisense oligonucleotides, ribozymes, sense oligonucleotides
CC	and triplex-forming oligonucleotides), as probes for the detection of
CC	nucleic acids, and as auxiliaries in molecular biology. As gene
CC	expression inhibitors they may be used for treating viral infections
CC	(especially where the virus is HSV-1, HSV-2, an influenza virus, VSV,
CC	hepatitis B or papilloma virus), cancer, restenosis, medical conditions
CC	mediated by integrins or cell-cell adhesion receptors, and medical
CC	conditions induced by growth factors (especially TNF-alpha)
XX	
SQ	Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;
	Query Match 7.8%; Score 10.8; DB 1; Length 15;
	Best Local Similarity 85.7%; Pred. No. 5.4e+02;
	Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	1668 CAGCTGGAACCCCTG 1681
DB	1 CAGCTGCAACCAG 14
	RESULT 896
	AAT14843
ID	AAT14843 standard; DNA; 15 BP.
XX	
AC	AAT14843;
XX	
DT	25-MAR-2003 (revised)
DT	14-NOV-1996 (first entry)
XX	
DE	Human prostatic transglutaminase primer ZC4048.
XX	
KW	Human; prostatic; prostate; placental; transglutaminase; primer;
KW	calcium dependent crosslinking; tissue adhesive; wound repair; PCR;
KW	skin graft; food; protozoan deterioration; dried fish; meat texture;
KW	cleavable crosslink; apoptosis; degenerative nerve disease; amplify;
KW	hyperproliferation; factor XIII; blood; immunogenicity; stability;
XX	half life; ss.
XX	
OS	Synthetic.
XX	
PN	US5514579-A.
XX	
PD	07-MAY-1996.
XX	
PF	30-DEC-1992; 92US-00998973.
XX	
XX	31-DEC-1991; 91US-00816284.
XX	

XX  
FA  
XX  
PI  
XX  
DR  
XX  
PT  
XX  
PS  
XX  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
SQ

The sequences given in AAT14838-45 are primers which were used in the amplification and cloning of the full length DNA which encodes human prostatic transglutaminase. See also AAT14825. These primers are based on the unique clone PTG561/2 which was isolated using the primer sequences given in AAT14827-36. The primers are based on regions of conserved amino acid sequences identified from a multiple alignment of known transglutaminase sequences, human erythrocyte membrane protein band 4.2 and the rat dorsal protein-1. One region of homology chosen for primer design corresponds to the active site of factor XIII, and two other regions were chosen which seemed to have structural importance based on the presence of hydrophobic residues and Pro residues. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 15 BP; 3 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 7.8%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 95.7%; Pred. No. 5.4e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1663 GCTCACACTGGAA 1676  
|||||  
DB 1 GCGCTCAGCTGGAA 14

RESULT 897  
AAX66553  
ID AAX66553 standard; RNA; 15 BP.  
XX  
AC AAX66553;  
XX  
DT 20-JUL-1999 (first entry)  
XX  
DE Human CD40 hammerhead ribozyme target SEQ ID NO:3185.  
XX  
KW Arthritic condition; graft tolerance; immune response; target; cleavage;  
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase  
KW streptolysin; synovial membrane; joint; arthritis; osteoarthritis;  
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
KW diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9618736-A2.  
XX  
PD 20-JUN-1996.  
XX  
PF 22-NOV-1995; 95WO-US015516.  
XX  
PR 13-DEC-1994; 94US-00354920.  
PR 23-DEC-1994; 94US-00363253.  
PR 23-DEC-1994; 94US-00363254.  
PR 17-FEB-1995; 95US-00390850.  
PR 20-APR-1995; 95US-00426124.  
PR 02-MAY-1995; 95US-00432874.  
PR 04-MAY-1995; 95US-00434509.  
PR 07-JUL-1995; 95US-0000951P.  
PR 07-JUL-1995; 95US-0000974P.  
PR 07-AUG-1995; 95US-00512861.  
PR 05-OCT-1995; 95US-00541365.

OS	Synthetic.
OS	Homo sapiens.
PX	AU9648028-A.
PN	
PD	26-SEP-1996.
XX	
XX	12-MAR-1996; 96AU-00048028.
PF	
XX	13-MAR-1995; 95DE-01008923.
PR	
PR	24-NOV-1995; 95DE-01043865.
XX	
PA	(FARH ) HOECHST AG.
XX	
PI	Peyman A, Uhlmann E, Breipohl G, Wallmeier H;
XX	
DR	WPI; 1996-455932/46.
XX	
XX	New phosphono-mono-ester oligo:nucleotide analogues - inhibitors of gene expression for treating viral infections, cancer, restenosis, etc.
PT	
PS	Disclosure; Page 41; 129pp; English.
XX	
CC	This sequence represents an inhibitor of c-Ha-ras expression, and is an example of an oligonucleotide analogue of the invention. The
CC	oligonucleotide analogues of the invention are used as inhibitors of gene expression (antisense oligonucleotides, ribozymes, sense oligonucleotides and triplex-forming oligonucleotides), as probes for the detection of nucleic acids, and as auxiliaries in molecular biology. As gene expression inhibitors they may be used for treating viral infections (especially where the virus is HSV-1, HSV-2, an influenza virus, VSV, hepatitis B or papilloma virus), cancer, restenosis, medical conditions mediated by integrins or cell-cell adhesion receptors, and medical conditions induced by growth factors (especially TNF-alpha)
XX	
SQ	Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;
Query Match	7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity	85.7%; Pred. No. 5.4e+02;
Matches 12; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
OY	1668 CAGCTGGAACCCCTG 1681       1 CAGCTGCACCAG 14
DB	
RESULT 896	
AAT14843	
ID	AAT14843 standard; DNA; 15 BP.
XX	
AC	AAT14843;
XX	
DT	25-MAR-2003 (revised)
DT	14-NOV-1996 (first entry)
XX	
DE	Human prostatic transglutaminase primer ZC4048.
XX	
KW	Human; prostatic; prostate; placental; transglutaminase; primer;
KW	calcium dependent crosslinking; tissue adhesive; wound repair; PCR;
KW	skin graft; food; protozoan deterioration; dried fish; meat texture;
KW	cleavable crosslink; apoptosis; degenerative nerve disease; amplify;
KW	hyperproliferation; factor XIII; blood; immunogenicity; stability;
half life; ss.	
XX	
OS	Synthetic.
US514579-A.	
XX	
PD	07-MAY-1996.
XX	
PF	30-DEC-1992; 92US-00999973.
XX	
XX	31-DEC-1991; 91US-00816284.

XX	(ZYMO) ZYMOGENETICS INC.
XX	Sheppard PO, Grant FC, O'hara PJ;
XX	
XX	WPI; 1996-238771/24.
XX	
PT	DNA encoding human prostatic and placental trans:glutaminase - used e.g. as tissue adhesive, food stabiliser or to screen cpds. that modulate apoptosis.
XX	
PS	Example 1; Col 33; 19pp; English.
XX	
CC	The sequences given in AAT14838-45 are primers which were used in the amplification and cloning of the full length DNA which encodes human prostatic transglutaminase. See also AAT14825. These primers are based on the unique clone PTGS61/2 which was isolated using the primer sequences given in AAT14827-36. The primers are based on regions of conserved amino acid sequences identified from a multiple alignment of known transglutaminase sequences, human erythrocyte membrane protein band 4.2 and the rat dorsal protein-1. One region of homology chosen for primer design corresponds to the active site of factor XIII, and two other CC regions were chosen seemed to have structural importance based on the presence of hydrophobic residues and Pro residues. (Updated on 25-MAR-2003 to correct PF field.)
XX	
SQ	Sequence 15 BP; 3 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
Query Match	7.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity	95.7%; Pred. No. 5.4e+02;
Matches 12; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
OY	1663 GCTCACACTGGAA 1676       1 GCCTCATCACTGGAA 14
DB	
RESULT 897	
AAX66553	
ID	AAX66553 standard; RNA; 15 BP.
XX	
AC	AAX66553;
XX	
DT	20-JUL-1999 (first entry)
XX	
DE	Human CD40 hammerhead ribozyme target SEQ ID NO:3185.
XX	
KW	Arthritis condition; graft tolerance; immune response; target; cleavage;
KW	hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase
KW	stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
KW	rheumatoid arthritis; autoimmune disease; allergy; inflammation;
diagnosis; ss.	
XX	
OS	Homo sapiens.
WO9618736-A2.	
PN	
XX	
PD	20-JUN-1996.
XX	
PF	22-NOV-1995; 95WO-US015516.
XX	
PR	13-DEC-1994; 94US-00354920.
PR	23-DEC-1994; 94US-00363253.
PR	23-DEC-1994; 94US-00363254.
PR	17-FEB-1995; 95US-00390850.
PR	20-APR-1995; 95US-00426124.
PR	02-MAY-1995; 95US-00432874.
PR	04-MAY-1995; 95US-00434509.
PR	07-JUL-1995; 95US-0000951P.
PR	07-JUL-1995; 95US-0000974P.
PR	07-AUG-1995; 95US-00512861.
PR	05-OCT-1995; 95US-00541365.

```

PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;
XX WPI; 1996-321852/32.
XX
XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX useful for preventing or treating initial development, progression or
XX regression of vascular diseases, esp. familial hypercholesterolaemia.
XX
XX Claim 4; Page 32; 72pp; English.
XX
XX AAT49608-T49863 represent target sequences for the human cholesterol
XX ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
XX T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
XX transfer between plasma lipoproteins. The numbering of the targets refers
XX to the position of the cleavage site in full length CETP. The ribozyme
XX binds to 5 nucleotides either side of this site, provided the sequence
XX is immediately upstream. The ribozymes are able to cleave mRNA from the
XX gene encoding CETP, thereby blocking synthesis and/or expression of the
XX mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
XX can be inhibited (or eliminated) thereby preventing the reduction in size
XX density of the high density lipoproteins (HDL), prolonging HDL half life,
XX and therefore increasing HDL levels. The ribozymes can be used to treat
XX hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
XX hypobetalipoproteinaemia, dyslipidaemia,
XX angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
XX density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
XX (a decrease in LDL levels, and a corresponding increase in HDL levels).
XX The HH ribozymes can also be used diagnostically to study genetic drift
XX and mutations in diseased cells, and to detect CETP mRNA. As the HH
XX ribozymes target specific regions of the CETP gene, they have low non-
XX specific activity
XX
XX Sequence 15 BP; 1 A; 6 C; 4 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 10.8%; Score 15; DB 1; Length 15;
XX Best Local Similarity 73.3%; Pred. No. 65;
XX Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1684 GTCCTCTCCAGCGTG 1698
Db 1 GTCUCCUCCAGCGUG 15
||:|:|:|:|:|:|
|:|:|:|:|:|:|

RESULT 33
AAT49817
ID AAT49817 standard; RNA; 15 BP.
XX
XX AC AAT49817;
XX
XX DT 07-MAR-1997 (first entry)
XX
XX DE Human CETP HH ribozyme target sequence #1688.
XX
XX KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
XX neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
XX reverse cholesterol transport; high density lipoprotein; therapy; CETP;
XX familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
XX peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
XX angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
XX LDL; ss.
XX
XX OS Homo sapiens.
XX
XX XX WO9620279-A1.
XX
XX PD 04-JUL-1996.
XX
XX XX 11-DEC-1995; 95WO-US016000.
XX
XX PF 23-DEC-1994; 94US-00363240.
XX

```

```

PA (RIBO-) RIBOZYME PHARM INC.
PA (WARN ) WARNER LAMBERT CO.
XX
XX PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;
XX
XX DR WPI; 1996-321852/32.
XX
XX PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX useful for preventing or treating initial development, progression or
XX regression of vascular diseases, esp. familial hypercholesterolaemia.
XX
XX Claim 4; Page 32; 72pp; English.
XX
XX AAT49608-T49863 represent target sequences for the human cholesterol
XX ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
XX T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
XX transfer between plasma lipoproteins. The numbering of the targets refers
XX to the position of the cleavage site in full length CETP. The ribozyme
XX binds to 5 nucleotides either side of this site, provided the sequence
XX is immediately upstream. The ribozymes are able to cleave mRNA from the
XX gene encoding CETP, thereby blocking synthesis and/or expression of the
XX mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
XX can be inhibited (or eliminated) thereby preventing the reduction in size
XX density of the high density lipoproteins (HDL), prolonging HDL half life,
XX and therefore increasing HDL levels. The ribozymes can be used to treat
XX hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
XX hypobetalipoproteinaemia, dyslipidaemia,
XX angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
XX density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
XX (a decrease in LDL levels, and a corresponding increase in HDL levels).
XX The HH ribozymes can also be used diagnostically to study genetic drift
XX and mutations in diseased cells, and to detect CETP mRNA. As the HH
XX ribozymes target specific regions of the CETP gene, they have low non-
XX specific activity
XX
XX Sequence 15 BP; 1 A; 6 C; 4 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 10.8%; Score 15; DB 1; Length 15;
XX Best Local Similarity 73.3%; Pred. No. 65;
XX Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1681 GGTGTCTCTCCAGC 1695
Db 1 GGTGUCUCCUCCAGC 15
||:|:|:|:|:|:|
|:|:|:|:|:|:|

RESULT 34
AAT49833
ID AAT49833 standard; RNA; 15 BP.
XX
XX AC AAT49833;
XX
XX DT 07-MAR-1997 (first entry)
XX
XX DE Human CETP HH ribozyme target sequence #1745.
XX
XX KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
XX neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
XX reverse cholesterol transport; high density lipoprotein; therapy; CETP;
XX familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
XX peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
XX angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
XX LDL; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9620279-A1.
XX
XX XX 04-JUL-1996.
XX
XX PD 11-DEC-1995; 95WO-US016000.
XX
XX PF

```

```

XX 23-DEC-1994; 94US-00363240.
XX (RIBO-) RIBOZYME PHARM INC.
XX (WARN) WARNER LAMBERT CO.
XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;
XX WPI; 1996-321852/32.
XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX useful for preventing or treating initial development, progression or
XX regression of vascular diseases, esp. familial hypercholesterolaemia.
XX Claim 4; Page 32; 72pp; English.
XX AAT49608-T49863 represent target sequences for the human cholesterol
XX ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
XX T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
XX transfer between plasma lipoproteins. The numbering of the targets refers
XX to the position of the cleavage site in full length CETP. The ribozyme
XX binds to 5 nucleotides either side of this site, provided the sequence
XX is immediately upstream. The ribozymes are able to cleave mRNA from the
XX gene encoding CETP, thereby blocking synthesis and/or expression of the
XX mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
XX can be inhibited (or eliminated) thereby preventing the reduction in size
XX density of the high density lipoproteins (HDL), prolonging HDL half life,
XX and therefore increasing HDL levels. The ribozymes can be used to treat
XX conditions associated with abnormal levels of CETP, specifically familial
XX hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
XX hyperbetalipoproteinaemia, hypopalipoproteinaemia, dyslipidaemia,
XX vascular complications of diabetes, transplant, atherectomy and
XX angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
XX density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
XX (a decrease in LDL levels, and a corresponding increase in HDL levels).
XX The HH ribozymes can also be used diagnostically to study genetic drift
XX and mutations in diseased cells, and to detect CETP mRNA. As the HH
XX ribozymes target specific regions of the CETP gene, they have low non-
XX specific activity
XX Sequence 15 BP; 3 A; 9 C; 0 G; 0 T; 3 U; 0 Other;
SQ Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 65;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1738 CCCAACTCTCCCTA 1752
DB 1 CCCAACUCCUCCUA 15
RESULT 35
AAT49839
ID AAT49839 standard; RNA; 15 BP.
AC AAT49839;
XX 07-MAR-1997 (first entry)
XX Human CETP HH ribozyme target sequence #1754.
XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
XX neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
XX reverse cholesterol transport; high density lipoprotein; therapy; CETP;
XX familial hypercholesterolaemia; dyslipidaemia; hypopalipoproteinaemia;
XX peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
XX angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
XX LDL; ss.
XX Homo sapiens.
XX WO9602079-A1.
XX
XX 04-JUL-1996.
XX 11-DEC-1995; 95WO-US016000.
XX 23-DEC-1994; 94US-00363240.
XX (RIBO-) RIBOZYME PHARM INC.
XX (WARN) WARNER LAMBERT CO.
XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;
XX WPI; 1996-321852/32.
XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX useful for preventing or treating initial development, progression or
XX regression of vascular diseases, esp. familial hypercholesterolaemia.
XX Claim 4; Page 32; 72pp; English.
XX AAT49608-T49863 represent target sequences for the human cholesterol
XX ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
XX T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
XX transfer between plasma lipoproteins. The numbering of the targets refers
XX to the position of the cleavage site in full length CETP. The ribozyme
XX binds to 5 nucleotides either side of this site, provided the sequence
XX is immediately upstream. The ribozymes are able to cleave mRNA from the
XX gene encoding CETP, thereby blocking synthesis and/or expression of the
XX mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
XX can be inhibited (or eliminated) thereby preventing the reduction in size
XX density of the high density lipoproteins (HDL), prolonging HDL half life,
XX and therefore increasing HDL levels. The ribozymes can be used to treat
XX conditions associated with abnormal levels of CETP, specifically familial
XX hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
XX hyperbetalipoproteinaemia, hypopalipoproteinaemia, dyslipidaemia,
XX vascular complications of diabetes, transplant, atherectomy and
XX angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
XX density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
XX (a decrease in LDL levels, and a corresponding increase in HDL levels).
XX The HH ribozymes can also be used diagnostically to study genetic drift
XX and mutations in diseased cells, and to detect CETP mRNA. As the HH
XX ribozymes target specific regions of the CETP gene, they have low non-
XX specific activity
XX Sequence 15 BP; 4 A; 5 C; 2 G; 0 T; 4 U; 0 Other;
SQ Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 65;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1747 TCCCTATCTCTAAGG 1761
DB 1 UCCCUAUCUCAAAGG 15
RESULT 36
AAT49813
ID AAT49813 standard; RNA; 15 BP.
AC AAT49813;
XX 18-MAR-1997 (first entry)
XX Human CETP HH ribozyme target sequence #1666.
XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
XX neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
XX reverse cholesterol transport; high density lipoprotein; therapy; CETP;
XX familial hypercholesterolaemia; dyslipidaemia; hypopalipoproteinaemia;
XX peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
XX angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
XX LDL; ss.
XX Homo sapiens.
XX

```



```

XX PN W09620279-A1.
XX OS Homo sapiens.
XX PD 04-JUL-1996.
XX PF 11-DEC-1995; 95WO-US016000.
XX PR 23-DEC-1994; 94US-00363240.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (WARN ) WARNER LAMBERT CO.
XX PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;
XX DR WPI; 1996-321852/32.
XX PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX PT useful for preventing or treating initial development, progression or
XX PT regression of vascular diseases, esp. familial hypercholesterolaemia.
XX PS Claim 4; Page 32; 72pp; English.
XX CC AAT49608-T49863 represent target sequences for the human cholesterol
XX CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
XX CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
XX CC transfer between plasma lipoproteins. The numbering of the targets refers
XX CC to the position of the cleavage site in full length CETP. The ribozyme
XX CC binds to 5 nucleotides either side of this site, provided the sequence UH
XX CC is immediately upstream. The ribozymes are able to cleave mRNA from the
XX CC gene encoding CETP, thereby blocking synthesis and/or expression of the
XX CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
XX CC can be inhibited (or eliminated) thereby preventing the reduction in size
XX CC and therefore increasing HDL levels. The ribozymes can be used to treat
XX CC conditions associated with abnormal levels of CETP, specifically familial
XX CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
XX CC hyperbetalipoproteinemia, hypopalipoproteinemia, dyslipidaemia,
XX CC vascular complications of diabetes, transplant, atherectomy and
XX CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
XX CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
XX CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
XX CC The HH ribozymes can also be used diagnostically to study genetic drift
XX CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
XX CC ribozymes target specific regions of the CETP gene, they have low non-
XX CC specific activity
XX SQ Sequence 15 BP; 3 A; 6 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 65;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1659 CCAGGCTCACAGCTG 1673
Db 1 CCAGGCUCACAGCUG 15
|||||:|||||:|
|:|:|:|:|:|:|

RESULT 37
AAT49835
ID AAT49835 standard; RNA; 15 BP.
XX AC AAT49835;
XX DT 07-MAR-1997 (first entry)
XX DE Human CETP HH ribozyme target sequence #1748.
XX KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
XX KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
XX KW reverse cholesterol transport; high density lipoprotein; therapy; CETP;
XX KW familial hypercholesterolaemia; dyslipidaemia; hypopalipoproteinemia;
XX KW peripheral vascular disease; hyperbetalipoproteinemia; RCT; inhibitor;
XX KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;

```

```

KW LDL; ss.
XX OS Homo sapiens.
XX PN W09620279-A1.
XX PD 04-JUL-1996.
XX PF 11-DEC-1995; 95WO-US016000.
XX PR 23-DEC-1994; 94US-00363240.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (WARN ) WARNER LAMBERT CO.
XX PI Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;
XX DR WPI; 1996-321852/32.
XX PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX PT useful for preventing or treating initial development, progression or
XX PT regression of vascular diseases, esp. familial hypercholesterolaemia.
XX PS Claim 4; Page 32; 72pp; English.
XX CC AAT49608-T49863 represent target sequences for the human cholesterol
XX CC ester transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
XX CC T50137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
XX CC transfer between plasma lipoproteins. The numbering of the targets refers
XX CC to the position of the cleavage site in full length CETP. The ribozyme
XX CC binds to 5 nucleotides either side of this site, provided the sequence UH
XX CC is immediately upstream. The ribozymes are able to cleave mRNA from the
XX CC gene encoding CETP, thereby blocking synthesis and/or expression of the
XX CC mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
XX CC can be inhibited (or eliminated) thereby preventing the reduction in size
XX CC and therefore increasing HDL levels. The ribozymes can be used to treat
XX CC conditions associated with abnormal levels of CETP, specifically familial
XX CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
XX CC hyperbetalipoproteinemia, hypopalipoproteinemia, dyslipidaemia,
XX CC vascular complications of diabetes, transplant, atherectomy and
XX CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
XX CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
XX CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
XX CC The HH ribozymes can also be used diagnostically to study genetic drift
XX CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
XX CC ribozymes target specific regions of the CETP gene, they have low non-
XX CC specific activity
XX SQ Sequence 15 BP; 3 A; 8 C; 0 G; 0 T; 4 U; 0 Other;

Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 65;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1741 AACTCCTCCCTATCC 1755
Db 1 AACUCCUCCUACUCC 15
|||||:|:|:|:|:|
|:|:|:|:|:|:|

RESULT 38
ABS60987/c
ID ABS60987 standard; DNA; 20 BP.
XX AC ABS60987;
XX DT 05-NOV-2002 (first entry)
XX DE Human genotyping PCR primer #140.
XX KW Human; ss; aminopeptidase P; XNPEP2; bradykinin receptor B1; primer;
XX KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NE;
XX KW kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;

```

angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4; polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma; cardiovascular disease; angina pectoris; hypertension; heart failure; myocardial infarction; ventricular hypertrophy; vascular disease; aneurysm; embolism; thrombosis; coronary artery disease; angioedema; arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR; autoimmune disease; inflammatory arthritis; cancer; wound; genotyping; viral infection; bacterial infection; fungal infection; COPD; Chronic obstructive pulmonary disease; enterocolitis.

Homo sapiens.

WO200261131-A2.

08-AUG-2002.

03-DEC-2001; 2001WO-US047235.

04-DEC-2000; 2000US-0251015P.

23-JAN-2001; 2001US-0263678P.

02-MAR-2001; 2001US-0273037P.

(BRIM ) BRISTOL-MYERS SQUIBB CO.  
(TSUC/) TSUCHIHASHI Z.  
(HUII/) HUI L.

Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
Swanson BN, Powell JR;  
WPI; 2002-619265/66.

New isolated nucleic acid with at least one polymorphic position, useful for detecting, diagnosing and treating disorders such as angioedema, cancer, viral, bacterial or fungal infection, cardiovascular and autoimmune diseases.

Example 3; Page 911; 977pp; English.

The invention relates to an isolated nucleic acid from a human gene encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1), tachykinin receptor B1 (TACR1), Cl esterase inhibitor (CINH), kallikrein 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one polymorphic position. Also included are (1) a probe that hybridises to a nucleotide polymorphism comprising additional 5' and 3' flanking genomic sequence; (2) analysing (M1) at least one nucleic acid sample comprising the sample from one or more individuals and determining the nucleic acid sequence at one or more polymorphic positions in a gene encoding a protein selected from the group above; (3) constructing (M2) haplotypes using the genes comprising grouping at least two nucleic acids upon administration of an ACE inhibitor and/or vasopeptidase inhibitor; (4) identifying (M3) an individual at risk of developing a disorder using the polymorphic data; (5) a library of nucleic acids, each of which comprises one or more polymorphic positions within a gene encoding a human protein selected from the group above; and (6) genotyping (M4) an individual comprising obtaining a nucleic acid sample, determining the nucleotide present in at least one polymorphic position, and comparing at least one position with a known data set. The genes (M1, M2, M3 and M4) and compositions are useful for detecting, diagnosing, treating, preventing various disorders such as angioedema and diseases which involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's disease, trachomas, and cardiovascular diseases like angina pectoris, hypertension, heart failure, myocardial infarction, ventricular hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary artery disease, arteriosclerosis and/or atherosclerosis, and hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic obstructive pulmonary disease (COPD) and enterocolitis (many other diseases and disorders are listed in the specification). The polynucleotides are also useful for chromosome identification. Antibodies against the proteins may be utilised for immunophenotyping of cell lines and biological samples. The present sequence is a genotyping PCR primer

CC for the gene encoding one of the proteins listed above

XX Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

SQ Query Match 10.6%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. NO. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1669 ACCTGGACCTGGGTC 1686  
|||||||

Db 19 AGCTGGAACTTGGTTC 2

RESULT 39  
ABZ85226  
ID ABZ85226 standard; DNA; 20 BP.

XX AC ABZ85226;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Claim 15; SEQ ID NO 468; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing levels of adenosine  
CC or, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 10.6%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 1.1e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAAACCTGGT 1683

DB 2 CAAAGCTGGATCCCTGGT 19

RESULT 40

AAA11514/c

ID AAA11514 standard; DNA; 21 BP.

XX AC AAA11514;

XX AC AAA11514;

DT 30-JUN-2000 (first entry)

XX Human dysferlin PCR primer #159.

DE Human dysferlin PCR primer #159.

XX Dysferlin; anti-dystrophic; gene therapy; muscular dystrophy; human;

KW skeletal muscle cell; hereditary; Miyoshi myopathy; diagnosis;

KW limb girdle muscular dystrophy-2B; brain-specific; PCR primer; ss.

XX Homo sapiens.

OS Homo sapiens.

XX WO200011157-A1.

PN 02-MAR-2000.

PD 25-AUG-1999;

PF 25-AUG-1998;

XX (GEO) GEN HOSPITAL CORP.

PA Brown RH, Liu J, Aoki M, Ho MF, Matsuda-Asada C;

XX WPI; 2000-237646/20.

DR Novel dysferlin genes and related proteins useful for diagnosis, risk

XX identification and treatment of hereditary muscular dystrophies and other

PT dysferlin related disorders.

PS Claim 8; Page 137; 146pp; English.

XX This invention describes a novel human dysferlin nucleic acid (I) and its

XX encoding protein (II), which has anti-dystrophic activity and can be used

CC for gene therapy. Introduction of (I), a vector comprising (I) or

CC dysferlin into a cell of a mammal can be used to decrease the symptoms of

CC muscular dystrophy. The dysferlin gene is normally expressed in skeletal

CC muscle cells and is selectively mutated in several families with the

CC hereditary muscular dystrophies, e.g. Miyoshi myopathy and limb girdle

CC muscular dystrophy-2B. The primers and oligonucleotides derived from (I)

CC can be used in diagnosis of or risk identification for dysferlin-related

CC disorders in patients, fetus, or pre-embryos. Expression of brain-

CC specific dysferlin may be important as a marker for normal neural

CC development. Dysferlin DNA or subgenomic coding sequences can be used for

CC therapy of the hereditary muscular dystrophies. AAX82919-X82945 represent

CC PCR primers used in the method of the invention

XX Sequence 21 BP; 4 A; 6 C; 9 G; 2 T; 0 U; 0 Other;

QY Query Match 10.5%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 1.3e+02;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1677 CCTGTGTCTCTCCAGCGT 1697

DB 21 CCGTGGGTCCCTCCAGCAT 1

XX Query Match 10.5%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 1.3e+02;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1677 CCTGTGTCTCTCCAGCGT 1697

DB 21 CCGTGGGTCCCTCCAGCAT 1

XX Query Match 10.5%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 1.3e+02;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1677 CCTGTGTCTCTCCAGCGT 1697

DB 21 CCGTGGGTCCCTCCAGCAT 1

RESULT 41

AAA36969/c

ID AAA36969 standard; DNA; 21 BP.

XX AAA36969;

XX 03-AUG-2000 (first entry)

DT Human dysferlin exon amplification primer SEQ ID NO:231.

XX Human; dysferlin; mutant; identification; chromosome 2p12-14; detection;

XX muscular dystrophy; diagnosis; hereditary muscular dystrophy;

XX Miyoshi myopathy; limb girdle muscular dystrophy; primer; amplification;

XX screening; ss.

XX Homo sapiens.

XX WO200011016-A1.

PN 02-MAR-2000.

PD 25-AUG-1999;

XX 99WO-US019394.

XX 25-AUG-1998;

PR 98US-0097930P.

XX (GEO) GEN HOSPITAL CORP.

XX (UYPI-) UNIV PITTSBURGH.

XX Brown RH, Liu J, Hoffman E, Chou F;

XX WPI; 2000-246531/21.

XX Dysferlin polynucleotide, its mutant form useful for diagnosis and

XX treatment of hereditary muscular dystrophies e.g. Miyoshi myopathy and

XX limb girdle muscular dystrophy.

XX Disclosure; Page 34; 136pp; English.

XX The present invention describes an isolated dysferlin DNA of 20-25

XX nucleotides in length, comprising a nucleotide sequence specifically

XX selected from nucleotides 911-913, 929-948, 1019-1038, 1392-1411, 1424-

XX 1443, 1484-1503, 1499-1518, 1543-1565, 1715-1734, 1714-1759, 2241-2260,

XX 2864-2883, 2978-2997, 3057-3076, 3198-3217, 3252-3271, 4356-4375, 4665-

XX 4684, 5015-5034, 5610-5629, 5726-5735, 6035-6054, 6179-6198, 6243-6263

XX and 6529-6548 of the human dysferlin nucleotide sequence given in

XX AAA36744. Dysferlin nucleotide sequences containing specific mutations

XX can be used for diagnosing a patient, a fetus or a pre-embryo at risk of

XX developing a dysferlin associated disorder by detecting mutations in the

XX dysferlin gene in biological samples from patients. Alternatively, the

XX biological sample containing genomic DNA can be incubated with a

XX restriction enzyme, preferably BstEII, BstEII, PstI, HaeI, AclI, AclI,

XX Bsp1286, NlaIV, NlaIII, BglI, BstEII, PstI, HaeI, AclI, AclI,

XX Tsp509I, SalI, HincII, TagI, HinfI, TfiI, SfiI or PstI and the presence

XX or absence of a restriction enzyme site in the sample is detected as an

XX indication of the presence or absence of a particular mutation in the

XX sample. Dysferlin polynucleotides are useful for treating hereditary

XX muscular dystrophies such as Miyoshi myopathy (MM) and limb girdle

XX muscular dystrophy-2B (LGM2-2B). MM and LGM2-2B map to the human

XX chromosome 2p12-14 region between the genetic markers D2S292 and D2S286.

XX The present sequence represents a primer for human dysferlin

XX Sequence 21 BP; 4 A; 6 C; 9 G; 2 T; 0 U; 0 Other;

QY Query Match 10.5%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 1.3e+02;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1677 CCTGTGTCTCTCCAGCGT 1697

DB 21 CCGTGGGTCCCTCCAGCAT 1

```

XX OS Synthetic.
XX PN JP2002233380-A.
XX PD 20-AUG-2002.
XX PF 08-FEB-2001; 2001JP-00031958.
XX PR 08-FEB-2001; 2001JP-00031958.
XX PA (CHCC) CHISSO CORP.
XX DR WPI; 2002-736476/80.
XX PT A nucleic acid molecule derived from a plasmid of Streptomyces albulus.
XX PS Example 3; Page 4; 17pp; Japanese.
XX CC The invention relates to a DNA molecule which is derived from plasmid
XX CC pNO33 of Streptomyces albulus. In the scope of the invention, a microbe
XX CC host may be transformed by the vector. The vector is used for the
XX CC preparation of epsilon-polylysine. The current sequence represents an S.
XX CC albulus plasmid pNO33 related PCR primer sequence
XX SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 10.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 94.8%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1636 GGGCTTGTAGCAGAG 1651
DB 17 GGGCTTGTAGCAGATG 2
RESULT 44
ABZ31506
ID ABZ31506 standard; DNA; 20 BP.
XX AC ABZ31506;
XX DT 30-JAN-2003 (first entry)
XX DB Candida albicans GRACE strain PCR primer SEQ ID NO 5725.
XX KW Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
XX KW signal transduction; DNA replication; cell division; growth;
XX KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX OS Candida albicans.
XX PN WO200253728-A2.
XX PD 11-JUL-2002.
XX PF 26-DEC-2001; 2001WO-US049486.
XX PR 29-DEC-2000; 2000US-0259128P.
XX PR 20-FEB-2001; 2001US-00792024.
XX PR 22-AUG-2001; 2001US-0314050P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX DR WPI; 2002-566694/60.
XX PT Constructing strains for identifying gene products as effective targets
XX PT for therapeutic intervention, by inactivating in the strain one allele of
XX PT a gene and placing other allele of the gene under conditional expression.
XX PS Claim 36; SEQ ID NO 5725; 167pp + Sequence Listing; English.

```

---

```

XX OS Synthetic.
XX PN ABL58444 standard; DNA; 18 BP.
XX PD 30-JUL-2002 (first entry)
XX PF 09-MAR-2000; 2000WO-IB000246.
XX PR 09-MAR-2000; 2000WO-IB000246.
XX PA (CHIC/) CHICHEPORTICHE Y.
XX PI Chicportiche Y, Ody C;
XX DR WPI; 2002-055092/07.
XX KW Promoting (M1) the success rate of in vitro production of embryoid bodies
XX KW from mammalian embryonic stem cells useful for regenerative medicine
XX KW comprises increasing the quantity of MAMA.
XX PS Disclosure; Page 14; 32pp; English.
XX CC The invention relates to a method of promoting the success rate of in
XX CC vitro production of embryoid bodies from mammalian embryonic stem cells
XX CC by increasing the quantity of MAMA or its homologues. MAMA is useful as
XX CC an agent of differentiation in an in vitro culture medium of mammalian
XX CC embryonic stem cells. An in vitro culture medium which contain MAMA and
XX CC the methods are useful for promoting the success rate of in vitro
XX CC production of embryoid bodies from embryonic stem cells which contain
XX CC MAMA. MAMA, cultures and vectors containing MAMA and the methods may be
XX CC used for regenerative medicine. MAMA may be used as a promoter of the
XX CC implantation of eggs obtained in vitro and to promote the successful
XX CC attachment of in vitro-fertilized eggs to the uterine membrane. The
XX CC present sequence represents a primer used for generating cyp-C specific
XX CC probes by RT-PCR, for northern hybridisation analysis of MAMA, galectin-3
XX CC and cyp-C mRNAs in transfected embryonic stem cells
XX SQ Sequence 18 BP; 1 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 10.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1672 TGGAGCCCTGGTGCTCT 1687
DB 2 TGGAGCCCTGGTGCTCT 17
RESULT 43
ABV73609/C
ID ABV73609 standard; DNA; 20 BP.
XX AC ABV73609;
XX DT 10-JAN-2003 (first entry)
XX DE S. albulus plasmid pNO33 related primer #1.
XX KW Plasmid; epsilon-polylysine; pNO33; PCR; primer; ss.

```

XX The invention relates to constructing (M1) a strain of diploid fungal  
 CC cells in which both alleles of a gene are modified, comprising  
 CC one allele by insertion or replacement by a cassette having an  
 CC expressible selectable marker and modifying other allele by  
 CC recombination, of a promoter replacement fragment with a heterologous  
 CC promoter, so that expression of the second allele is regulated by the  
 CC promoter. (M1) is useful for constructing a strain of diploid fungal  
 CC cells in which both alleles of a gene are modified. The diploid fungal  
 CC cells having both alleles modified are useful for identifying a gene that  
 CC is essential to the survival or growth of a fungus, a gene that  
 CC contributes to the virulence and/or pathogenicity of a fungus, a gene that  
 CC that contributes to the resistance of a diploid fungus to an antifungal  
 CC agent, an antifungal agent that inhibits the growth of a diploid fungus  
 CC and for identifying a therapeutic agent for treatment of a diploid fungus  
 CC disease. (M1) is useful for identifying a compound which modulates the  
 CC activity of a gene product, preferably enzymatic activity, carbon  
 CC compound catabolism, biosynthetic, transporter, transcriptional,  
 CC translational, signal transduction, DNA replication and cell division  
 CC activity. The method is useful for identifying a compound having the  
 CC ability to inhibit growth or proliferation of *C. albicans* cells and for  
 CC treating infection by *C. albicans*. The present sequence is that of a PCR  
 CC primer used in the method of the invention. Note: The sequence data for  
 CC this patent is not represented in the printed specification but is based  
 CC on sequence information supplied to Derwent by the European Patent Office  
 XX  
 SQ Sequence 20 BP; 4 A; 9 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 10.4%; Score 14.4; DB 1; Length 20;  
 Best Local Similarity 93.8%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1737 TCCCAACTCTCCCTA 1752  
 Db 1 TCCCAACTCTCCCAA 16  
 |||||  
 |||||

RESULT 45  
 ABI93783/c  
 ID ABI93783 standard; DNA; 20 BP.  
 AC ABI93783;  
 DT 16-FEB-2002 (first entry)  
 DE Capture oligonucleotide Zip ID#870 oligo #9.  
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;  
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;  
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;  
 KW oncogene; tumour suppressor; human papillomavirus; forensic;  
 KW environmental monitoring; food industry; feed industry; ss.  
 XX Synthetic.  
 OS  
 XX WO200179548-A2.  
 PN  
 XX 25-OCT-2001.  
 PD  
 XX 04-APR-2001; 2001WO-US010958.  
 PF  
 XX 14-APR-2000; 2000US-0197271P.  
 PR  
 XX (CORR ) CORNELL RES FOUND INC.  
 PA  
 XX Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;  
 PI WPI; 2002-034366/04.  
 DR  
 XX Designing capture oligonucleotide probes for use on a support to which  
 PT complementary oligonucleotides hybridize with little mismatch.  
 XX Example 5; Fig 29; 300pp; English.  
 PS

XX The present invention describes a method (M1) for designing capture  
 CC oligonucleotide probes (I) for use on a support to which complementary  
 CC oligonucleotide probes (II) will hybridize with little mismatch, where  
 CC (I) have melting temperatures within a narrow range. The method is useful  
 CC for detecting infectious diseases caused by bacterial infectious agents  
 CC e.g. *Salmonella*, *Listeria* monocytogenes and *Haemophilus influenzae*, fungal  
 CC infectious agents e.g. *Cryptococcus neoformans* and *Candida albicans* and  
 CC *Aspergillus fumigatus*, viruses e.g. T-cell lymphocytotropic virus,  
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents  
 CC selected from *Onchocerca volvulus*, *Entamoeba histolytica* and *Dracunculus*  
 CC medinensis. The method is also useful for detecting genetic diseases such  
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.  
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes  
 CC involved in DNA amplification, replication, recombination or repair, the  
 CC cancer is specifically associated with a gene selected from BRCA1 gene,  
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The  
 CC method is also used for environmental monitoring, forensics and the food  
 CC and feed industry, detecting comprises scanning (using e.g. a scanning  
 CC electron microscope and infrared microscope) the support at the  
 CC particular sites and identifying if ligation of the oligonucleotide probe  
 CC sets occurred and correlating (using a computer) identified ligation to a  
 CC presence or absence of the target nucleotide sequences. ABI82074 to  
 CC ABI97546 represent oligonucleotide sequences used in the exemplification  
 CC of the present invention  
 XX

SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;  
 Query Match 10.4%; Score 14.4; DB 1; Length 20;  
 Best Local Similarity 93.8%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1728 GAGATTGGCTCCCAAC 1743  
 Db 18 GAGATTGGCTCCCAAC 3  
 |||||  
 |||||

RESULT 46  
 ABQ93591/c  
 ID ABQ93591 standard; DNA; 21 BP.  
 AC ABQ93591;  
 DT 16-OCT-2002 (first entry)  
 DE Human DISC1/DISC2 PCR primer disc09 fl.  
 KW Human; Disrupted In Schizophrenia 1; DISC1; neuroleptic; gene therapy;  
 KW neuropsychiatric disorder; schizoaffective disorder; bipolar disorder;  
 KW unipolar affective disorder; adolescent conduct disorder; schizophrenia;  
 KW PCR; primer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200258637-A2.  
 PN  
 XX 01-AUG-2002.  
 PD  
 XX 23-JAN-2002; 2002WO-US002186.  
 PF  
 XX 24-JAN-2001; 2001US-00770107.  
 PR  
 XX (MILL-) MILLENIUM PHARM INC.  
 PA  
 XX Meyer JM, Barrington-Martin R, Parker A, Barnes GT;  
 PI WPI; 2002-590791/63.  
 DR  
 XX New human disrupted-in-Schizophrenia (DISC) 1 and DISC2 genes containing  
 PT single nucleotide polymorphisms, useful for preventing or treating  
 PT neuropsychiatric disorders e.g. schizophrenia.  
 XX Claim 17; Fig 4; 169pp; English.  
 PS

esp. useful for the targeted intracellular hydrolysis of mRNA; inhibiting gene expression. They may also be used for the treatment of liver disease, as hormone regulation agents and as hydrolysis reagents for the detoxification of alkyl phosphate esters. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 20 BP; 2 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 10.2%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAGCTG 1673  
DB 19 AACACCCGGCTCACAGATG 1

RESULT 48  
AAQ80880/c  
ID AAQ80880 standard; DNA; 20 BP.

XX AAQ80880;  
XX 25-MAR-2003 (revised)  
DT 30-AUG-1995 (first entry)  
XX Europium (III) texaphyrin (EuTx) DNA conjugate 9B.  
XX Europium (III) texaphyrin (EuTx) DNA conjugate 9B; liver disease;  
KW targeted intracellular mRNA hydrolysis; gene expression inhibition;  
KW hormone regulation; hydrolysis reagents; alkyl phosphate esters;  
KW detoxification; ss.  
XX Synthetic.

Key Location/Qualifiers  
modified\_base 1 /\*tag= a  
/mod\_base= OTHER  
/note= "EuTx-NH(CH2)6-PO4-cytosine"

WO9429316-A2.  
22-DEC-1994. 94WO-US006284.  
09-JUN-1994; 94WO-US006284.  
09-JUN-1993; 93US-00075123.  
14-APR-1994; 94US-00227370.  
(TEXA) UNIV TEXAS SYSTEM.  
(PHAR-) PHARMACYCLICS INC.  
Sessler JL, Ross KL, Wright M, Hemmi GW, Dow WC, Smith DA;  
Kral VA, Iverson B, Mody T, Miller RA, Magda D;  
WPI; 1995-036382/05.  
Texaphyrin metal complex mediated ester hydrolysis - esp. useful for targeted intracellular hydrolysis of mRNA and for inhibiting gene expression.

Example 7; Fig 9; 125pp; English.  
AAQ80879-Q80892 are texaphyrin lanthanide metal DNA conjugates, which are esp. useful for the targeted intracellular hydrolysis of mRNA; inhibiting gene expression. They may also be used for the treatment of liver disease, as hormone regulation agents and as hydrolysis reagents for the detoxification of alkyl phosphate esters. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 20 BP; 2 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

The invention relates to a novel Disrupted-In-Schizophrenia (DISC) 1 allelic variant polynucleotide. The polypeptides of the invention have neuroleptic activity. The polynucleotides may have a use in gene therapy. DISC1 or DISC2 nucleic acid molecules are useful for diagnosing or treating a subject having a disease or disorder associated with specific DISC1 or DISC2 alleles and/or aberrant DISC1 expression or activity e.g. neuropsychiatric disorder such as schizoaffective, bipolar, unipolar, affective or adolescent conduct disorder or schizophrenia. Similarly, the compound that inhibits DISC1 protein activity may be used in the method for treating such neuropsychiatric disorders. The sequences shown in CC ABQ93575-ABQ93658 represent the PCR primers used in the invention to CC amplify the sequences of DISC2 and DISC2

Sequence 21 BP; 3 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 10.4%; Score 14.4; DB 1; Length 21;  
Best Local Similarity 93.8%; Pred. No. 1.4e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1640 TTGTAGCAGAGGCAA 1655  
DB 19 TTGCAGCAGAGGCAA 4

RESULT 47  
AAQ80879/c  
ID AAQ80879 standard; DNA; 20 BP.

XX AAQ80879;  
XX 25-MAR-2003 (revised)  
DT 30-AUG-1995 (first entry)  
XX Europium (III) texaphyrin (EuTx) DNA conjugate 9A.  
XX Europium (III) texaphyrin (EuTx) DNA conjugate 9A; liver disease;  
KW targeted intracellular mRNA hydrolysis; gene expression inhibition;  
KW hormone regulation; hydrolysis reagents; alkyl phosphate esters;  
KW detoxification; ss.  
XX Synthetic.

Key Location/Qualifiers  
modified\_base 7 /\*tag= a  
/mod\_base= OTHER  
/note= "EuTx-NH(CH2)6 alkylamidated thymidine"

WO9429316-A2.  
22-DEC-1994. 94WO-US006284.  
09-JUN-1994; 94WO-US006284.  
09-JUN-1993; 93US-00075123.  
14-APR-1994; 94US-00227370.  
(TEXA) UNIV TEXAS SYSTEM.  
(PHAR-) PHARMACYCLICS INC.  
Sessler JL, Ross KL, Wright M, Hemmi GW, Dow WC, Smith DA;  
Kral VA, Iverson B, Mody T, Miller RA, Magda D;  
WPI; 1995-036382/05.  
Texaphyrin metal complex mediated ester hydrolysis - esp. useful for targeted intracellular hydrolysis of mRNA and for inhibiting gene expression.

Example 7; Fig 9; 125pp; English.  
AAQ80879-Q80892 are texaphyrin lanthanide metal DNA conjugates, which are

```
Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1655 AGCACCAGGCTCACAGCTG 1673
DB      19 AACACCCGGCTCACAGATG 1

RESULT 49
AAQ91455/c
ID      AAQ91455 standard; DNA; 20 BP.
XX
AC      AAQ91455;
XX
DT      25-MAR-2003 (revised)
XX
DT      30-AUG-1995 (first entry)
XX
DE      Dysprosium (III) texaphyrin (DyTx) DNA conjugate.
XX
XX      Dysprosium (III) texaphyrin (DyTx) DNA conjugate; liver disease;
KW      targeted intracellular mRNA hydrolysis; gene expression inhibition;
KW      hormone regulation; hydrolysis reagents; alkyl phosphate esters;
KW      detoxification; ss.
XX
OS      Synthetic.
XX
FH      Key
FT      modified_base 1
FT      Location/Qualifiers
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "DyTx-NH(CH2)6-P04-cytosine"
XX
XX      WO9429316-A2.
XX
XX      22-DEC-1994.
XX
XX      09-JUN-1994; 94WO-05006284.
XX
XX      09-JUN-1993; 93US-00075123.
XX      14-APR-1994; 94US-00227370.
XX
XX      (TEXA ) UNIV TEXAS SYSTEM.
XX      (PHAR-) PHARMACYCLICS INC.
XX
XX      Sessler JL, Ross XL, Wright M, Hemmi GW, Dow WC, Smith DA;
XX      Kral VA, Iverson B, Mody T, Miller RA, Magda D;
XX      WPI; 1995-036382/05.
XX
XX      Texaphyrin metal complex mediated ester hydrolysis - esp. useful for
XX      targeted intracellular hydrolysis of mRNA and for inhibiting gene
XX      expression.
XX
XX      Disclosure; Fig 21; 125pp; English.
XX
XX      AAQ91451-Q91457 are texaphyrin lanthanide metal DNA conjugates, which are
XX      esp. useful for the targeted intracellular hydrolysis of mRNA; inhibiting
XX      gene expression. They may also be used for the treatment of liver disease,
XX      as hormone regulation agents and as hydrolysis reagents for the
XX      detoxification of alkyl phosphate esters. (Updated on 25-MAR-2003 to
XX      correct PN field.)
XX
XX      Sequence 20 BP; 2 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1655 AGCACCAGGCTCACAGCTG 1673
DB      19 AACACCCGGCTCACAGATG 1
```

```
RESULT 50
AAQ81567/c
ID      AAQ81567 standard; DNA; 20 BP.
XX
AC      AAQ81567;
XX
DT      04-SEP-1995 (first entry)
XX
DE      Hepatitis B virus polypeptide cDNA PCR primer p142.
XX
XX      Hepatitis B virus; HBV; polypeptide; diagnosis and detection;
KW      PCR primer p142; ss.
XX
OS      Synthetic.
XX
PN      JP06321991-A.
XX
PD      22-NOV-1994.
XX
XX      14-MAY-1993; 93JP-00113136.
XX      14-MAY-1993; 93JP-00113136.
XX
XX      (MITU ) MITSUBISHI KASEI CORP.
XX
XX      WPI; 1995-041293/06.
XX
XX      Polypeptide derived from type B hepatitis virus and gene to code it -
XX      used in diagnosis of type B hepatitis virus.
XX
XX      Example 2; Page 5; 13pp; Japanese.
XX
XX      AAQ81567 and AAQ81568 are a pair of primers for the PCR amplification of
XX      the cDNAs encoding the hepatitis B virus (HBV) polypeptides described in
XX      AAR68865-R68871. The polypeptides or their fragments can be used in the
XX      diagnosis and detection of HBV
XX
XX      Sequence 20 BP; 4 A; 1 C; 12 G; 3 T; 0 U; 0 Other;

Query Match      10.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1736 CTCCTCACTCTCTCCATC 1754
DB      19 CCCCCCACTCTCTCCAGTC 1

RESULT 51
AAT08224/c
ID      AAT08224 standard; DNA; 20 BP.
XX
AC      AAT08224;
XX
DT      23-MAY-1996 (first entry)
XX
XX      p142, PCR primer used for isolation of antisense HBV strain X region.
XX      Hepatitis B virus; X region; antisense; antibody; vector; diagnosis;
XX      hepatoma; hepatitis; antiviral; anticancer; transcription; ss.
XX
OS      Synthetic.
XX
XX      WO9527788-A1.
XX
XX      19-OCT-1995.
XX
XX      10-APR-1995; 95WO-JP000700.
XX
XX      11-APR-1994; 94JP-00095458.
XX
XX      (DAIN-) DAINABOT CO LTD.
PA
```

Mon Aug 30 09:26:45 2004

of oligonucleotides in cells. It comprises contacting a targeted intracellular RNA in a cell with a metallotexaphyrin-oligonucleotide conjugate. The contact is carried out under physiological conditions for a time sufficient to hydrolyse the phosphate ester bond of the targeted RNA. The metallotexaphyrin of the conjugate has catalytic activity for phosphate ester bond hydrolysis. The oligonucleotide of the conjugate may be complementary binding affinity to the targeted RNA. The conjugate may be used in antisense therapies for treating, e.g. cancer, viral infections, autoimmune diseases and restenosis. The conjugate may also be used as hydrolysis reagents for the detoxification of di- and trialkyl phosphate esters, which are used in solvents, insecticides and chemical nerve gases. The metallotexaphyrin complex enhances the therapeutic activity of the oligonucleotide, not only by facilitating cellular uptake of the oligonucleotide but also by hydrolysing target RNA within the cell, independent of RNase H. Attachment to the complex may also cause the oligonucleotide to take on some of the pharmacodynamic and biodistribution properties of the texaphyrin, such as selective localisation in tumours. The present oligonucleotide is shown in the specification

Sequence 20 BP; 2 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 10.2%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCAGCTG 1673  
DB 19 AACACCCGGCTCAGAGT 1

RESULT 53  
AAV07037/c  
ID AAV07037 standard; DNA; 20 BP.

XX AC AAV07037;  
XX 08-JUL-1998 (first entry)  
XX Texaphyrin oligonucleotide conjugate.

XX Texaphyrin oligonucleotide conjugate; dysprosium; metal complex;  
KW hydrolytic cleavage activity; ss.  
XX Synthetic.

XX Key modified\_base 1 Location/Qualifiers  
FT /tag= a  
FT /note= "A texaphyrin dysprosium metal complex, bound to  
FT cytosine via a linking phosphate group"

XX WO9807733-A1.

XX 26-FEB-1998.

XX 20-AUG-1997; 97WO-US014692.

XX 20-AUG-1996; 96US-03700277.

XX (PHAR-) PHARMACYCLICS INC.

XX Magda D, Crofts SP, Wright M;

XX WPI; 1998-179049/16.

XX New conjugates which have hydrolytic cleavage activity for RNA - comprise  
PT a texaphyrin metal complex bound to an internal linkage of an  
PT oligonucleotide.

XX Example 4; Page 51; 77pp; English.

XX This sequence is shown in the specification. The invention relates to  
XX texaphyrin oligonucleotide conjugates which have hydrolytic cleavage  
CC

XX Uchida T, Shikata T;  
XX WPI; 1995-366392/47.  
XX X region anti-sense DNA sequence of new hepatitis B strain, related  
PT peptide(s) and antibodies - useful for diagnosis and investigation of HBV  
PT infection.  
XX Example 2; Page 22; 61pp; Japanese.

XX AAR08224-53 are PCR primers used for the isolation and amplification of 2  
CC antisense DNA sequences derived from the X region of a new strain of  
CC hepatitis B. The DNA codes for a viral peptide ASXP. The ASXP peptide and  
CC antibodies recognising it are useful in the diagnosis of hepatitis caused  
CC by the virus, in the investigation of transcription activated and  
CC enhanced by the presence of the ASXP peptide, and in the development of  
CC effective antiviral and anticancer drugs for the treatment of hepatitis  
CC and hepatoma

XX Sequence 20 BP; 4 A; 1 C; 12 G; 3 T; 0 U; 0 Other;  
Query Match 10.2%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 CTCGCAACTCTCCCTATC 1754  
DB 19 CCGCCAACTCTCCCAATC 1

RESULT 52  
AAV07290/c  
ID AAV07290 standard; DNA; 20 BP.

XX AC AAV07290;  
XX 14-AUG-1998 (first entry)  
XX Oligonucleotide #4.

XX Metallotexaphyrin; dysprosium; europium; conjugate; RNase H;  
KW antisense therapy; ss.

XX Synthetic.

XX US5763172-A.

XX 09-JUN-1998.

XX 07-JUN-1995; 95US-00486962.

XX 21-JAN-1992; 92US-00822964.

XX 09-JUN-1993; 93US-00075123.

XX 14-APR-1994; 94US-00227370.

XX 09-JUN-1994; 94WO-US006284.

XX 26-MAY-1995; 95US-00452261.

XX 07-JUN-1995; 95US-00485581.

XX (PHAR-) PHARMACYCLICS INC.  
XX (TEXA ) UNIV TEXAS SYSTEM.

XX Sessler JL, Wright M, Miller RA, Dow WC, Magda D;

XX WPI; 1998-347306/30.

XX Enhancing therapeutic activity of oligo-nucleotides in cells - using  
PT conjugate comprising metallotexaphyrin, which hydrolyses phosphate ester  
PT bonds of RNA, and oligo-nucleotide, which binds to targeted RNA.  
XX Disclosure; Col 37-38; 34pp; English.

XX The invention relates to a method of enhancing the therapeutic activity  
CC



CC activity for RNA. They comprise a texaphyrin metal complex bound to an  
 CC internal linkage of an oligonucleotide or oligonucleotide analogue. The  
 CC conjugates may be used for the destruction of retroviral RNA, messenger  
 CC RNA, ribosomal RNA, RNA cofactors, transfer RNA, small nuclear RNA and  
 CC small cytoplasmic RNA. They may be used for eliminating diseased or  
 CC cancerous cells or tissues, in blood purification protocols (in vivo or  
 CC in vitro), in antiviral treatments, or as diagnostic probes (e.g. in  
 CC determination of the nucleotide sequence of RNA or to detect  
 CC polymorphisms in RNA). Administration of the conjugates is, e.g., oral,  
 CC topical or parenteral, especially topical or intravenous. The conjugates  
 CC are especially effective under conditions where the concentration of RNA  
 CC target exceeds that of available conjugate

SQ Sequence 20 BP; 2 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 10.2%; Score 14.2; DB 1; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 1.5e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAGCTG 1673  
 DB 19 AACACCCGGCTCACAGATG 1

RESULT 54

AAV99212/c  
 ID AAV99212 standard; DNA; 20 BP.

AC AAV99212;

XX

DT 09-MAR-1999 (first entry)

XX

DE Antisense primer for intron boundary mapping of DNA Metase exon 35-36.

KW DNA methyltransferase; DNA Metase; antisense oligonucleotide; human;  
 cellular growth; tumour growth inhibition; silenced gene activation;  
 beta thalassemia; sickle cell anemia; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9854313-A2.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-IB001107.

XX 30-MAY-1997; 97US-00866340.

XX 17-DEC-1997; 97US-0069865P.

XX (UYMC-) UNIV MCGILL.

XX

PI Szyf M, Bigey P, Ramchandani S;

XX WPI; 1999-059833/05.

XX

PT New DNA methyltransferase nucleotide sequences - used particularly to  
 develop antisense oligonucleotides for diagnostic and therapeutic  
 purposes, particularly for inhibiting tumour growth.

XX Example 8; Page 32; 108pp; English.

XX

CC PCR primers AAV99163-220 were used to map the intron boundaries of the  
 CC exons of DNA methyltransferase (DNA Metase) genomic sequence. Antisense  
 CC oligonucleotides which inhibit DNA Metase expression can be  
 CC derived from the genomic DNA Metase sequence. The antisense  
 CC oligonucleotides can be used in investigating the role of DNA Metase in  
 CC cellular growth. They can be administered at different points in the cell  
 CC cycle, or in conjugation with promoters or inhibitors of cell growth to  
 CC determine the role of DNA Metase in the growth of the cell type of  
 CC interest. The antisense oligonucleotides can also be used for inhibiting  
 CC tumour growth in a mammal, or to activate silenced genes to provide a  
 CC missing gene function. This ameliorates disease symptoms, e.g. in beta

CC thalassemia and sickle cell anemia. The antisense oligonucleotides can  
 CC also be used as analytical and diagnostic tools and a potentiators of  
 CC transgenic plant and animal studies

SQ Sequence 20 BP; 5 A; 9 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 10.2%; Score 14.2; DB 1; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 1.5e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1681 GGTGTCCTCTCAGCGTGG 1699  
 DB 20 GGGGTCTGCTCTCTGGTGG 2

RESULT 55

AAZ88439/c

ID AAZ88439 standard; DNA; 20 BP.

XX

AC AAZ88439;

XX

DT 08-MAY-2000 (first entry)

XX

DE Exemplary texaphyrin oligonucleotide conjugate SEQ ID NO:5.

KW Texaphyrin; metal complex; catalytic; RNA hydrolysis; virucide;  
 antibacterial; cytostatic; antiinflammatory; antitumour; antiviral; ss.

XX Synthetic.

OS

PN US6022959-A.

XX

PD 08-FEB-2000.

XX

PF 20-NOV-1997; 97US-00975522.

XX

PR 20-AUG-1996; 96US-0077185P.

XX

PR 20-AUG-1997; 97WO-US014682.

XX

PA (PHAR-) PHARMACYCLICS INC.

XX

PI Wright M, Crofts SP, Magda D;

XX

DR WPI; 2000-160391/14.

XX

PT Texaphyrin metal complex derivatized ribonucleic acids possessing  
 hydrolytic cleavage activity against RNA are useful as e.g. antiviral,  
 antibacterial, antitumor and antiinflammatory agents.

XX

PS Example 4; Col 32; 30pp; English.

XX

CC The present invention describes a conjugate with hydrolytic cleavage  
 CC activity for ribonucleic acid (RNA), which comprises a texaphyrin metal  
 CC complex bound to an internal linkage of an oligonucleotide or  
 CC oligonucleotide analogue. AAZ88435 to AAZ88440 represent exemplary  
 CC texaphyrin oligonucleotide conjugates used in the exemplification of the  
 CC present invention. The novel conjugates have virucide, antibacterial,  
 CC cytostatic and antiinflammatory properties, and are involved in RNA  
 CC hydrolysis. The conjugates are useful for inhibiting the expression of a  
 CC gene by targeted intracellular mRNA (messenger ribonucleic acid)  
 CC hydrolysis. The conjugates have applications for anti-viral and anti-  
 CC bacterial therapy as well as cancers and inflammatory responses caused by  
 CC overexpression of certain proteins

SQ Sequence 20 BP; 2 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 10.2%; Score 14.2; DB 1; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 1.5e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAGCTG 1673  
 DB 19 AACACCCGGCTCACAGATG 1

Mon Aug 30 09:26:45 2004

AAD41746 standard; DNA; 20 BP.

AAD41746;  
30-OCT-2002 (first entry)

RESULT 56  
AAD05958  
ID AAD05958 standard; DNA; 20 BP.

Human RECQL2 antisense oligonucleotide, ISIS #137526.  
Antisense; RECQL2; Bloom's disorder; prophylaxis; infection; tumour;  
inflammation; therapy; human; phosphorothioate; ss.

Human diacylglycerol kinase-zeta intron 18/exon 19 junction sequence.  
Human; catalyst; diacylglycerol; DAG; phosphatidic acid; DAG modulator;  
diacylglycerol kinase zeta; DGK; ds.

Homo sapiens.

Key Location/Qualifiers  
intron 1..10  
/\*tag= a  
/number= 18  
/partial  
exon 11..20  
/\*tag= b  
/number= 19  
/partial

US6221658-B1.

24-APR-2001.

25-AUG-1999; 99US-00382911.

22-APR-1996; 96US-0016210P.

22-APR-1997; 97US-00841483.

(UTAH ) UNIV UTAH RES FOUND.

Prescott SM, Bunting M, Tang W, Topham M;

WPI; 2001-327248/34.

New DNAs of the human diacylglycerol kinase, useful for modulating the levels of diacylglycerol kinase in cells to catalyze the conversion of diacylglycerol to phosphatidic acid, therefore increasing phosphatidic acid levels.

Disclosure; Col 17-18; 74pp; English.

The patent discloses novel human diacylglycerol kinase (DGK) isoforms namely diacylglycerol kinase epsilon, diacylglycerol kinase zeta, diacylglycerol kinase zeta-2 and their corresponding cDNAs. Human diacylglycerol kinase DNA is useful for coding human diacylglycerol kinase, which is useful for catalysing the conversion of diacylglycerol to phosphatidic acid. In particular, the human diacylglycerol kinase and its DNA are useful for decreasing intracellular levels of diacylglycerol (DAG) and for increasing intracellular levels of phosphatidic acid in cells. The present DNA sequence is the exon/intron junction sequence of human diacylglycerol kinase (DGK) zeta gene

Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 10.2%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1686 CTCCTCCAGCTGTGGAA 1704

2 CGCTCCAGTGTGATGGAA 20

RESULT 57

AAD41746/c

Location/Qualifiers

1..20  
/\*tag= a  
/mod\_base= OTHER

1..5  
/\*tag= b  
/mod\_base= OTHER

9  
/\*tag= d  
/mod\_base= m5c

16..20  
/\*tag= c  
/mod\_base= OTHER

19..20  
/\*tag= e  
/mod\_base= m5c

US6399378-B1.

04-JUN-2002.

01-MAR-2001; 2001US-00798096.

01-MAR-2001; 2001US-00798096.

(ISIS-) ISIS PHARM INC.

Ward DT, Watt AT;

WPI; 2002-535979/57.

Antisense compounds targeted to nucleic acids encoding RECQL2 associated with Bloom's disorder, for modulating RECQL2 expression and treating diseases e.g. tumors associated with expression of the RECQL2 in humans.

Example 15; Col 44; 8pp; English.

The invention relates to antisense compounds targetted to nucleic acid encoding RECQL2 (gene associated with Bloom's disorder) to inhibit the expression of RECQL2. Antisense compounds of the invention are useful for treating diseases associated with expression of RECQL2, in humans. They are useful for diagnostics, therapeutics and as research reagent, e.g. prophylactically to prevent or delay infection, inflammation or tumour formation. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human RECQL2 DNA

Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 10.2%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1662 GGCTCACAGCTGGAACCT 1680

20 GGCTCACACCTGTATCT 2

RESULT 58  
 ABT23628/c  
 ID ABT23628 standard; DNA; 20 BP.  
 XX AC ABT23628;  
 XX  
 DT 22-MAY-2003 (first entry)  
 DE  
 DE Stabilising reagent method related oligo SEQ ID No 80.  
 XX  
 XX Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage;  
 KW specific amplification; pathogenic microorganism; chimeric;  
 KW genetic engineering; clinical medicine; ss.  
 OS Unidentified.  
 XX  
 PN WO2002101042-A1.  
 XX  
 PD 19-DEC-2002.  
 XX  
 PF 12-JUN-2002; 2002WO-JP005832.  
 XX  
 PR 12-JUN-2001; 2001JP-00177737.  
 PR 20-AUG-2001; 2001JP-00249689.  
 XX  
 PA (TAKI ) TAKARA BIO INC.  
 XX  
 PI Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;  
 PI Shoki T, Asada K, Kato I;  
 XX  
 DR WPI; 2003-148805/14.  
 XX  
 XX Method for stabilizing and storing reaction reagents for specific  
 PT amplification and detection of nucleic acids particularly in e.g.  
 PT identifying pathogenic microorganisms or viruses in sample.  
 XX  
 PS Example 15; Page 137; 177pp; Japanese.  
 XX  
 CC The invention relates to a novel stabilising reaction reagent for use in  
 CC the amplification and/or detection of a target nucleic acid comprising:  
 CC preparing a reaction mixture with e.g. a nucleic acid as template, at  
 CC least 1 primer and RNaseH; and incubation of the reaction mixture for a  
 CC defined period of time to form a reaction product during the  
 CC amplification of such target nucleic acid. The method is useful for  
 CC stabilising and long-term storage of reaction reagents for highly  
 CC sensitive and specific amplification and detection of nucleic acids  
 CC particularly in identifying pathogenic microorganisms or viruses in a  
 CC sample using chimeric oligonucleotide primers, which is useful in genetic  
 CC engineering and clinical medicine. This polynucleotide sequence  
 CC represents an oligo relating to the novel stabilising reaction reagent  
 CC method of the invention  
 XX  
 SQ Sequence 20 BP; 4 A; 1 C; 12 G; 3 T; 0 U; 0 Other;  
 Query Match 10.2%; Score 14.2; DB 1; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 1.5e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1736 CTCCTCACTCTCCCTATC 1754  
 Db 19 CCCCCAACTCTCCCACTC 1  
 RESULT 59  
 ACD13735  
 ID ACD13735 standard; DNA; 20 BP.  
 XX AC ACD13735;  
 XX  
 DT 14-AUG-2003 (first entry)  
 XX  
 DE STS187T7 amplification primer F.

XX RIEG; ss; ophthalmological; neoplastic disorder; hyperplastic disorder;  
 KW abnormal cell proliferation; umbilical artery expression; PCR; primer;  
 KW Rieger's syndrome; vitelline artery expression; human; STS.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6518411-B1.  
 XX  
 PD 11-FEB-2003.  
 XX  
 PF 22-NOV-1996; 96US-00754477.  
 XX  
 PR 22-NOV-1996; 96US-00754477.  
 XX  
 PA (UNIP ) UNIV IOWA.  
 XX  
 PI Murray JC, Semina E;  
 XX  
 DR WPI; 2003-465605/44.  
 XX  
 XX New RIEG polypeptides and nucleic acids, useful in antisense therapy, in  
 PT drug screening assays, and in treating Rieger syndrome or associated  
 PT conditions related to umbilical and vitelline artery expression.  
 XX  
 PS Example 1; Col 57; 101pp; English.  
 XX  
 CC The invention relates to an isolated RIEG nucleic acid. The nucleic acids  
 CC are useful as probes to detect transcripts or genomic sequences encoding  
 CC the same or homologous proteins, in predictive and therapeutic evaluation  
 CC of allelic mutations which might be manifested in neoplastic or  
 CC hyperplastic disorders or abnormal cell proliferation, in antisense  
 CC therapy, in drug screening assays and in the treatment of Rieger's  
 CC syndrome or associated conditions related to umbilical and vitelline  
 CC artery expression. The present sequence represents a STS amplification  
 CC primer  
 XX  
 SQ Sequence 20 BP; 3 A; 9 C; 1 G; 7 T; 0 U; 0 Other;  
 Query Match 10.2%; Score 14.2; DB 1; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 1.5e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1733 TGGCTCCCACTCCCTCCCT 1751  
 Db 2 TCTCTCCCAATCTCTCACT 20  
 RESULT 60  
 ADB89990/c  
 ID ADB89990 standard; DNA; 20 BP.  
 XX AC ADB89990;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Antisense oligonucleotide targeting mouse C3 component, ISIS140078.  
 XX  
 KW Mouse; ss; antisense; complement component C3; inflammation;  
 KW septic shock; multiple organ failure; hyperacute organ failure;  
 KW autoimmune disorder; CNS inflammation; multiple sclerosis;  
 KW atherosclerosis; tumour.  
 XX  
 OS Mus musculus.  
 XX  
 PH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone and all cytosines are 5  
 FT -methyl cytosines"  
 FT modified\_base 1..5  
 FT /tag= a





PI Reubinoff BE, Pera MF, Yee PC, Trounson AO, Bongso A;  
XX WPI; 2000-376517/32.  
XX  
XX Novel undifferentiated human embryonic stem cells which are useful as a  
PT source of novel gene products.  
XX  
XX Disclosure; Page 31; 56pp; English.  
XX  
XX The present sequence is a RT-PCR primer for the human oct-4 transcript.  
CC It was used to measure oct-4 expression in differentiated and  
CC undifferentiated cells. These were all derived from human embryonic stem  
CC cells. Stem cells can be used to treat inherited diseases, to study the  
CC cellular and molecular biology of early human development, in functional  
CC genomics, to identify novel growth factors and to generate differentiated  
CC cells to use in transplantation, drug screening or drug discovery in  
CC vitro  
XX  
SQ Sequence 20 BP; 4 A; 8 C; 3 G; 5 T; 0 U; 0 Other;  
Query Match 10.1%; Score 14; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1656 GCACGAGGCTCACA 1669  
DB 7 GCACGAGGCTCACA 20  
RESULT 65  
AAV91006/c  
ID AAV91006 standard; RNA; 17 BP.  
XX AC AAV91006;  
XX  
DT 18-FEB-1999 (first entry)  
XX  
DE Human C-raf target site nucleotide position 581.  
XX  
KW Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
KW screening; identification; synthesis; deprotection; purification; cancer;  
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
KW restenosis; rheumatoid arthritis; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9850530-A2.  
XX  
PD 12-NOV-1998.  
XX  
PF 05-MAY-1998; 98WO-US009249.  
XX  
XX 09-MAY-1997; 97US-0046059P.  
PR 09-JUN-1997; 97US-0049002P.  
PR 03-JUL-1997; 97US-0051718P.  
PR 22-AUG-1997; 97US-0056808P.  
PR 02-OCT-1997; 97US-0061321P.  
PR 02-OCT-1997; 97US-0061324P.  
PR 05-NOV-1997; 97US-0064866P.  
PR 19-DEC-1997; 97US-0068212P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;  
PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
XX WPI; 1999-009494/01.  
XX  
XX Identifying new catalytic nucleic acid that modulates selected processes  
PT - especially ribozymes that cleave Raf RNA for treating cancer,  
PT restenosis, and also new ribozymes and modified nucleoside triphosphates

PT used as antiviral agents and synthons.  
XX  
PS Claim 177; Page 147; 259pp; English.  
XX  
XX A method has been developed for the identification of a nucleic acid  
CC capable of modulating a process in a biological system. The method  
CC comprises: (a) introducing into the system a random library of nucleic  
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
CC in systems where modulation has occurred and/or determining the sequence  
CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
CC endonuclease activity and catalytic activity, from the present invention,  
CC are used to modulate gene expression in plant and mammalian cells and to  
CC cleave target nucleic acid, particularly for treating systemic diseases  
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
CC ascites and infection. They may also be used to detect genetic drift and  
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs  
CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
CC generally any condition associated with the level of c-raf. Introduction  
CC of sugar/phosphate modifications increases stability against nuclease and  
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the  
CC method, specifically for modulating the expression of a Raf gene  
XX  
SQ Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;  
Query Match 9.9%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1641 TGTCACAGAGGCAAGC 1657  
DB 17 TGTCACAGAGGCAAGC 1  
RESULT 66  
AAV91005/c  
ID AAV91005 standard; RNA; 17 BP.  
XX  
XX AC AAV91005;  
XX  
DT 18-FEB-1999 (first entry)  
XX  
DE Human C-raf target site nucleotide position 576.  
XX  
KW Human; C-raf; A-raf; E-raf; hammerhead ribozyme; hairpin ribozyme;  
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
KW screening; identification; synthesis; deprotection; purification; cancer;  
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
KW restenosis; rheumatoid arthritis; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9850530-A2.  
XX  
PD 12-NOV-1998.  
XX  
PF 05-MAY-1998; 98WO-US009249.  
XX  
XX 09-MAY-1997; 97US-0046059P.  
PR 09-JUN-1997; 97US-0049002P.  
PR 03-JUL-1997; 97US-0051718P.  
PR 22-AUG-1997; 97US-0056808P.  
PR 02-OCT-1997; 97US-0061321P.  
PR 02-OCT-1997; 97US-0061324P.  
PR 05-NOV-1997; 97US-0064866P.  
PR 19-DEC-1997; 97US-0068212P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;  
PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
XX WPI; 1999-009494/01.  
XX  
XX Identifying new catalytic nucleic acid that modulates selected processes  
PT - especially ribozymes that cleave Raf RNA for treating cancer,  
PT restenosis, and also new ribozymes and modified nucleoside triphosphates

```
XX WPI; 1999-009494/01.
XX
XX Identifying new catalytic nucleic acid that modulates selected processes
XX - especially ribozymes that cleave Raf RNA for treating cancer,
XX restenosis, and also new ribozymes and modified nucleoside triphosphates
XX used as antiviral agents and synthons.
XX
XX Claim 177; Page 147; 259pp; English.
XX
XX A method has been developed for the identification of a nucleic acid
XX capable of modulating a process in a biological system. The method
XX comprises: (a) introducing into the system a random library of nucleic
XX acid catalysts (NAC) having a substrate binding domain (SBD), comprising
XX a random sequence, and a catalytic domain (CD); and (b) identifying NAC
XX in systems where modulation has occurred and/or determining the sequence
XX of at least part of the SBDs in such systems. Nucleic acid molecules with
XX endonuclease activity and catalytic activity, from the present invention,
XX are used to modulate gene expression in plant and mammalian cells and to
XX cleave target nucleic acid, particularly for treating systemic diseases
XX caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
XX ascites and infection. They may also be used to detect genetic drift and
XX mutations in diseased cells and to determine c-raf RNA. Specifically NACs
XX with RNA-cleaving activity that modulate expression of the Raf gene, are
XX used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
XX generally any condition associated with the level of c-raf. Introduction
XX of sugar/phosphate modifications increases stability against nuclease and
XX activity. AA90922 to AA93877 represent NACs that can be used in the
XX method, specifically for modulating the expression of a Raf gene
XX
XX Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 9.9%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1646 CAGAGGCGAAGCACCAG 1662
XX |||||
XX Db 17 CAGAGGCGAGCTTCAG 1
XX
XX RESULT 67
XX ACD50855
XX ID ACD50855 standard; RNA; 17 BP.
XX AC ACD50855;
XX XX
XX DT 23-SEP-2003 (first entry)
XX XX
XX DE HBV hammerhead ribozyme substrate sequence #270.
XX XX
XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
XX amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.
XX
XX OS Hepatitis B virus.
XX
XX PN WO200281494-A1.
XX XX
XX PD 17-OCT-2002.
XX
XX XX
XX PF 26-MAR-2002; 2002WO-US009187.
XX
XX PR 26-MAR-2001; 2001US-00817879.
XX
XX PR 08-JUN-2001; 2001US-00877478.
XX
XX PR 08-JUN-2001; 2001US-0296876P.
XX
XX PR 24-OCT-2001; 2001US-0335059P.
XX
XX PR 05-DEC-2001; 2001US-0337055P.
```

```
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MACE/) MACEJAK D.
XX (MCSW/) MCSWIGGEN J.
XX (MORR/) MORRISSEY D.
XX (PAVC/) PAVCO P.
XX (LEEP/) LEE P.
XX (DRAP/) DRAPER K.
XX (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
XX Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
XX hepatocellular carcinoma, or condition associated with hepatitis C virus
XX infection.
XX
XX Example 1; Page 141; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,
XX inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
XX are nucleic acid decoy molecules, and aptamers that bind to HBV reverse
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX as oligonucleotides that specifically bind the Enhancer I region of HBV
XX DNA. The nucleic acids may be used to modulate the expression of HBV
XX genes and HBV viral replication. Also disclosed is a method for screening
XX compounds and/or potential therapies directed against HBV, and compounds
XX that modulate the expression and/or replication of HCV. The compounds and
XX methods of the invention are useful for the treatment of degenerative and
XX disease states related to HBV and HCV infection, replication and gene
XX expression such as cirrhosis, liver failure, and hepatocellular
XX carcinoma. The present sequence represents a substrate for one of the HBV
XX ribozyme, inozyme, G-cleaver, zinzyme, DNzyme or amberyne sequences
XX disclosed in the present invention
XX
XX SQ Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 9.9%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 64.7%; Pred. No. 1.5e+02;
XX Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1673 GGAACCCCTGGTGCTCC 1689
XX ||||| : ||: ||
XX Db 1 GGAACCCUUGUGUCUCC 17
XX
XX RESULT 68
XX ACD55655/c
XX ID ACD55655 standard; RNA; 17 BP.
XX AC ACD55655;
XX XX
XX DT 23-SEP-2003 (first entry)
XX
XX DE HBV amberyne substrate sequence #165.
XX
XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
XX amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.
XX
XX OS Hepatitis B virus.
```

PN WO200281494-A1.  
XX 17-OCT-2002.  
XX 26-MAR-2002; 2002WO-US009187.  
XX 26-MAR-2001; 2001US-00817879.  
PR 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX WPI; 2003-229207/22.  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX Example 1; Page 206; 387pp; English.  
XX The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HBV  
CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences  
CC disclosed in the present invention  
XX Sequence 17 BP; 3 A; 0 C; 11 G; 0 T; 3 U; 0 Other;  
SQ Query Match 9.9%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1738 CCCAACTCTCCCTATC 1754  
DB 17 CCCAACTCTCCCACTC 1  
RESULT 69  
ACD50854  
ID ACD50854 standard; RNA; 17 BP.  
XX ACD50854;  
AC ACD50854;  
XX 23-SEP-2003 (first entry)  
DT HBV hammerhead ribozyme substrate sequence #269.  
XX

KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
KW amberyze; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX Hepatitis B virus.  
OS WO200281494-A1.  
XX 17-OCT-2002.  
XX 26-MAR-2002; 2002WO-US009187.  
XX 26-MAR-2001; 2001US-00817879.  
PR 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX WPI; 2003-229207/22.  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX Example 1; Page 141; 387pp; English.  
XX The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HBV  
CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences  
CC disclosed in the present invention  
XX Sequence 17 BP; 2 A; 4 C; 4 G; 0 T; 7 U; 0 Other;  
SQ Query Match 9.9%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 58.8%; Pred. No. 1.5e+02;  
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 1672 TGGAAACCTCGTGCTC 1688  
DB 1 UGGAAACCTCGTGCTC 17



SQ	Sequence	17 BP; 2 A; 5 C; 3 G; 0 T; 7 U; 0 Other;
Query Match	9.9%; Score 13.8; DB 1; Length 17;	
Best Local Similarity	58.8%; Pred. No. 1.5e+02;	
Matches	10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;	
QY	1674 GAACCTGTGTCTCTCT 1690	
DB	1 GAACCTGTGTCTCTCT 17	
RESULT 71		
AAX28045		
ID	AAX28045 standard; DNA; 18 BP.	
XX	AAX28045;	
AC	AAX28045;	
XX	10-JUN-1999 (first entry)	
DT	PCR primer for human GDNF promoter sequence.	
XX	GDNF promoter; human; glial cell line-derived neurotrophic factor;	
XX	KW neurodegenerative disease; Parkinson's disease; renal disease; therapy;	
KW	KW urogenital disease; gastrointestinal disease; physical nerve trauma;	
KW	KW PCR primer; ss.	
XX	Synthetic.	
OS	Homo sapiens.	
XX	WO9907843-A1.	
PN	18-FEB-1999.	
XX	23-JUL-1998; 98WO-EP004620.	
PF	05-AUG-1997; 97US-0054812P.	
XX	14-APR-1998; 98US-0081751P.	
PR	(HOFF ) HOFFMANN LA ROCHE & CO AG F.	
XX	Baecker PA, Johnson RM, Lee WH, Verity AN;	
PI	WPI; 1999-180491/15.	
XX	New human glial cell line-derived neurotrophic factor promoters - useful	
XX	in the treatment of neurodegenerative conditions including Parkinson's	
PT	disease.	
XX	Example 1; Page 34; 100pp; English.	
PS	This sequence is a primer for a human glial cell line-derived	
CC	neurotrophic factor (hGDNF) promoter. The promoters can be used to	
CC	identify hGDNF modulators. hGDNF modulators are used to treat a mammal	
CC	exhibiting neurodegenerative disease-like symptoms, particularly,	
CC	Parkinson's disease, as well as renal, urogenital, and gastrointestinal	
CC	diseases, and neurodegenerative sequelae of physical nerve trauma. The	
CC	hGDNF modulator has anti-neurodegenerative activity and the promoters	
CC	regulate GDNF expression. GDNF has a developmental role in survival of	
CC	mid-brain dopaminergic neurons, cerebellar Purkinje neurons, and cranial	
CC	and spinal cord motor neurons. In the peripheral nervous system, GDNF	
CC	supports the development of multiple neuronal populations, including	
CC	sympathetic, parasympathetic, sensory, and autonomic neurons. Delivery of	
CC	a small molecule GDNF expression modulator is less pulsatile and less	
CC	invasive than prior art treatment involving intraparenchymal, ICV, or	
CC	intrathecal injection of GDNF	
XX	Sequence 18 BP; 6 A; 7 C; 5 G; 0 T; 0 U; 0 Other;	
QY	9.9%; Score 13.8; DB 1; Length 18;	
Best Local Similarity	88.2%; Pred. No. 1.6e+02;	
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	

QY 1655 AGCACCAGGCTCACAGC 1671  
 Db 2 AGCACCAGGCTCACAGC 18

RESULT 72  
 ID ADEL15603/c  
 AC ADEL15603 standard; DNA; 19 BP.  
 XX ADEL15603;  
 DT 29-JAN-2004 (first entry)  
 XX Tricyclic dextrocannabinoids related primer, mouse SOCS-3 reverse.

KW non-psychoactive cannabinoid derivative; pro-inflammatory mediator;  
 KW anti-inflammatory cytokine; anti-inflammatory; analgesic; antiallergic;  
 KW vasotropic; antitubercular; tuberculostatic; antiarteriosclerotic;  
 KW antirheumatic; antiarthritic; antiasthmatic; dermatological; cytostatic;  
 KW neuroprotective; nootropic; antiparkinsonian; antibacterial;  
 KW antiparasitic; virucide; immunosuppressive; nephrotropic; antidiabetic;  
 KW hepatotropic; cardiant; anti-HIV; anticonvulsant; osteopathic;  
 KW inflammatory; immune disorder; demyelinating;  
 KW chronic degenerative disease; cardiovascular protection; primer;  
 KW tricyclic dextrocannabinoid; ss; mouse; murine.

XX Mus sp.  
 XX WO2003077832-A2.  
 XX 25-SEP-2003.  
 XX 16-MAR-2003; 2003WO-IL000223.  
 XX 18-MAR-2002; 2002IL-00148736.  
 XX (PHAR-) PHARMOS CORP.  
 XX Garzon A, Avraham A, Fink G;  
 XX WPI; 2003-779073/73.  
 XX Use of non-psychoactive cannabinoid derivative for decreasing the  
 XX transcription of at least one pro-inflammatory mediator cyclooxygenase-2  
 XX or increasing the transcription of at least one anti-inflammatory cytokine  
 XX interleukin-10.

XX Example 1; Page 29; 81pp; English.

XX The invention relates to the novel use of a composition comprising non-  
 XX psychoactive cannabinoid derivative, its salt, ester or solvate used for  
 XX decreasing the transcription of at least one pro-inflammatory mediator or  
 XX increasing the transcription of at least one anti-inflammatory cytokine.  
 XX The novel composition has the following activities: antiinflammatory,  
 XX analgesic, antiallergic, vasotropic, antitubercular, tuberculostatic,  
 XX antiarteriosclerotic, antirheumatic, antiarthritic, antiasthmatic,  
 XX dermatological, cytostatic, neuroprotective, nootropic, antiparkinsonian,  
 XX antibacterial, antiparasitic, virucide, immunosuppressive, nephrotropic,  
 XX antidiabetic, hepatotropic, cardiant, anti-HIV, anticonvulsant, and  
 XX osteopathic. The novel non-psychoactive cannabinoid derivative  
 XX composition can be used in the preparation of a medicament for  
 XX preventing, alleviating or treating a disease or disorder by regulating  
 XX pro and anti-inflammatory mediators. The diseases/disorders include:  
 XX inflammatory and immune disorders, pain, allergic inflammation, diseases  
 XX caused by monocyte infiltration (e.g. sarcoidosis, Wegener's  
 XX granulomatosis and tuberculosis), atherosclerosis, rheumatoid arthritis,  
 XX aschma, inflammatory lung disorders, inflammatory pulmonary diseases,  
 XX diseases, osseous inflammation, pancreatitis, inflammatory skin  
 XX diseases involving immune-mediated or post-traumatic inflammation,  
 XX inflammatory demyelinating neuropathies, multiple sclerosis,  
 XX neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's  
 XX disease, bacterial, parasitic or viral infections, sepsis, renal

CC disorders, diabetic nephropathy and liver disorders), postoperative  
 CC complications in cardiovascular surgery, in transplants or organs or  
 CC tissue replacements and in prosthetic implants and transplant rejection.  
 CC The diseases/disorders can also be used for treating demyelinating  
 CC disorders and chronic degenerative diseases (e.g. AIDS dementia,  
 CC Huntington's chorea, amyotrophic lateral sclerosis, Kennedy's syndrome,  
 CC motor neuron disease and prion-associated neurodegeneration) and are also  
 CC useful in cardiovascular protection and treatment of atheroma,  
 CC restenosis, angioplasty, myocardial ischaemia and myocardial infarction.  
 CC This polynucleotide sequence represents a primer used in the method to  
 CC test the impact of tricyclic dextrocannabinoids on gene expression  
 CC relating to the invention.

XX SQ Sequence 19 BP; 5 A; 3 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 9.9%; Score 13.8; DB 1; Length 19;  
 Best Local Similarity 88.2%; Pred. No. 1.7e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1683 TGTCCTCCCTCCAGCGGG 1699  
 Db 19 TCTCTCTCCCAACGGG 3

RESULT 73  
 AAV26436  
 ID AAV26436 standard; DNA; 20 BP.  
 XX AAV26436;  
 AC AAV26436;  
 DT 30-JUL-1998 (first entry)  
 XX PCR primer "A gamma-globin" gene.  
 XX Beta-globin; adeno-associated virus vector; therapeutic; liver;  
 KW hepatic disease; ss; PCR; primer; amplification.  
 XX Synthetic.  
 XX Homo sapiens.  
 XX WO9809524-A1.  
 XX 12-MAR-1998.  
 XX 02-SEP-1997; 97WO-US015453.  
 XX 06-SEP-1996; 96US-0025616P.  
 XX 11-SEP-1996; 96US-0025649P.  
 XX (CHIR) CHIRON CORP.  
 XX (INDV) UNIV INDIANA.  
 XX Srivastava A, Ponnazhagan S, Chloemer RH, Wang X, Yoder MC;  
 XX Zhou S, Escobedo J, Dwarki V;  
 XX WPI; 1998-193255/17.  
 XX Novel adeno-associated viral vectors - for liver specific delivery of  
 XX therapeutic molecule.  
 XX Example 2; Page 20; 32pp; English.

XX The human beta-globin promoter- A gamma-globin gene-specific primers  
 XX (AAV26435 and 26436) were used to amplify and detect the human A gamma-  
 XX globin gene which had been injected into C57Bl/6 mice using a recombinant  
 XX adeno-associated virus (AAV) vector. This confirmed the adeno-associated  
 XX virus vector can be used to deliver a therapeutic molecule to the liver  
 XX of a mammal. This can be used for the expression of therapeutic molecules  
 XX such as secretory proteins, antisense molecules or ribozymes, in the  
 XX liver, especially to treat hepatic diseases

XX SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

```

Query Match      9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1681 GGTTCTCTCTCCAGGT 1697
DB 2 GGTTCTCTCTCCAGCAT 18

RESULT 74
AAC65593/C
ID AAC65593 standard; DNA; 20 BP.
XX
AC AAC65593;
XX
DT 14-FEB-2001 (first entry)
XX
DE Human uteroglobin SNP PCR primer HUG38R.
XX
KW Mouse; uteroglobin; immunoglobulin A mediated disease; IGA nephropathy;
KW autoimmune disorder; pulmonary inflammation; Wegener's granulomatosis;
KW Goodpasture's disease; diabetic glomerulosclerosis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200062795-A2.
XX
PD 26-OCT-2000.
XX
PF 13-APR-2000; 2000WO-US009979.
XX
PR 21-APR-1999; 99US-0130434P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Mukherjee AB, Zheng F, Zhang Z;
XX
WPI; 2000-687100/67.
XX
DR Use of a composition comprising uteroglobin (or a fragment, derivative,
PT mimetic or variant), for inhibiting or treating an immunoglobulin-A
PT mediated autoimmune disorders, e.g. diabetic glomerulosclerosis and
PT pulmonary inflammation.
XX
PS Example 12; Page 43; 60pp; English.
XX
CC The present invention describes the use of uteroglobin in the diagnosis
CC and prevention of IGA mediated diseases, such as IGA nephropathy,
CC Wegener's granulomatosis, Goodpasture's disease and diabetic
CC glomerulosclerosis. This is possible as uteroglobin binds to fibronectin,
CC preventing the complexing of fibronectin with IGA and the deposition of
CC immune complexes in the kidney
XX
SQ Sequence 20 BP; 7 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match      9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1722 GAGATGGAGATTGGCTC 1738
DB 20 GAGATGGAGTTTCGCTC 4

RESULT 75
AAH78641
ID AAH78641 standard; DNA; 20 BP.
XX
AC AAH78641;
XX
DT 10-DEC-2001 (first entry)
XX
DE Probe for mechanically sensitive potassium channel gene fragment.

```

```

XX Human; mechanically sensitive potassium channel; riluzole; TWICK;
KW polyunsaturated fatty acid; arachidonic acid; hTRAAC; Chromosome 11q13;
KW neuronal excitation; muscle excitation; cardiac rhythm; anoxia;
KW hormone secretion; cardiac disease; vascular disease; ischemia;
KW nervous system disorder; endocrinal disease; muscle disease;
KW retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration; probe;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200168670-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-FR000758.
XX
PR 14-MAR-2000; 2000FR-00003264.
XX
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI Lazdunski M, Lesage F, Maingret F;
XX
WPI; 2001-590037/66.
XX
DR New mechanically sensitive potassium channel, useful for treating
XX cardiovascular diseases and in drug screening, is activated by
XX polyunsaturated fatty acids.
XX
PS Disclosure; Page 15; 37pp; French.
XX
CC The present probe was used to detect a gene fragment of the human
XX mechanically sensitive potassium channel gene. The channel is activated
XX by polyunsaturated fatty acids (particularly arachidonic acid (AA)) and
XX by riluzole. The polypeptide is designated human TWICK-related AA-
XX activated potassium channel (hTRAAC). The hTRAAC gene is located on
XX chromosome 11q13. hTRAAC is involved in regulation of neuronal and muscle
XX excitation, cardiac rhythm and secretion of hormones. Cells that express
XX hTRAAC, designated to screen for modulators of hTRAAC activity. Such
XX modulators are potentially useful for prevention or treatment, in humans
XX and animals, of: cardiac and/or vascular disease; nervous system
XX disorders associated with ischemia and anoxia; endocrinal diseases; and
XX associated with anomalous hormone secretion or muscle diseases; and
XX retinal diseases. Typical examples are epilepsy, cardiac arrhythmia and
XX neurodegeneration
XX
SQ Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Query Match      9.9%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1659 CCAGGCTCACAGCTGGA 1675
DB 1 CCAGGCTGCCAGCTGGA 17

RESULT 76
AAD19416/C
ID AAD19416 standard; DNA; 20 BP.
XX
AC AAD19416;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human delta-6-desaturase (h6D-1) amplifying PCR primer #1.
XX
KW Delta-6-desaturase gene; D6D; lipid metabolism disorder; atopic eczema;
KW mastalgia; rheumatoid arthritis; Sjogren's syndrome; viral infection;
KW gastrointestinal disorder; post viral fatigue; pre-menstrual syndrome;
KW endometriosis; cystic fibrosis; alcoholism; Alzheimer's syndrome;
KW cardiovascular disease; Crohn's disease; congenital liver disease;
KW schizophrenia; diabetic neuropathy; nephropathy; retinopathy; cancer;

```

KW arterial hypertension; atherosclerosis; chronic inflammatory disorder;  
 KW autoimmune disorder; hypercholesterolaemia; atopic disorder; h6dD-1;  
 KW gene therapy; human; PCR primer; ss.  
 XX Homo sapiens.  
 XX WO200170993-A2.  
 XX 27-SEP-2001.  
 XX 26-MAR-2001; 2001WO-CA000398.  
 XX 24-MAR-2000; 2000CA-02301158.  
 XX (SCOT-) SCOTIA HOLDINGS PLC.  
 XX Winther MD, Smith HL, Allen SJ, Ponton A, De Antueno RJ;  
 XX WPI; 2001-611507/70.  
 XX Nucleic acid encoding delta-6-desaturase gene useful for treating atopic  
 PT eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome, and  
 PT gastrointestinal disorders, viral infections and post viral fatigue.  
 XX Example 4; Page 69; 164pp; English.  
 XX The invention relates to polynucleotides that control delta-6 desaturase  
 CC genes (d6d) and methods useful for identifying compounds which inhibit or  
 CC promote the activity of mammalian d6d. Compounds which modulate d6d gene  
 CC segments are useful for treating lipid metabolism disorders e.g. atopic  
 CC eczema, mastalgia, rheumatoid arthritis, Sjogren's syndrome,  
 CC gastrointestinal disorders, viral infections and post viral fatigue, pre-  
 CC menstrual syndrome, endometriosis, cystic fibrosis, alcoholism, cancer,  
 CC Alzheimer's syndrome, cardiovascular disease, Crohn's disease, congenital  
 CC liver disease, schizophrenia, diabetes and diabetic  
 CC complications including diabetic neuropathy, nephropathy and retinopathy.  
 CC Compounds of the invention are also useful for inhibiting progressive and  
 CC acute disorders such as arterial hypertension, atherosclerosis, chronic  
 CC inflammatory and autoimmune disorders, hypercholesterolaemia and other  
 CC atopic disorders. d6d genes are useful in gene therapy. The present  
 CC sequence is a PCR primer used to amplify human delta-6-desaturase (h6dD-  
 CC 1) sequence  
 XX  
 SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
 Query Match 9.9%; Score 13.8; DB 1; Length 20;  
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1685 TCCTCCACGCGTGGTG 1701  
 DB 19 TCTTCTCCACGCGTAGTG 3  
 RESULT 77  
 AAD22845/c  
 ID AAD22845 standard; DNA; 20 BP.  
 XX  
 AC AAD22845;  
 XX  
 XX 26-FEB-2002 (first entry)  
 DT  
 XX CD34 cell marker DNA amplifying RT-PCR up primer.  
 DE  
 XX Cell marker; CD34; vulnary; cosmetic; uropathic; cardiant; osteopathic;  
 KW myocardial infarction; dermatological; gastroesophageal reflux; weakness;  
 KW aesthetic; muscular; medicament; heart failure; gene therapy; myofiber;  
 KW urinary incontinence; faecal incontinence; muscle tissue dysfunction;  
 KW muscle-derived progenitor cell; MDC; vesico-ureteral reflux;  
 KW RT-PCR primer; ss.  
 XX Unidentified.  
 OS  
 XX

PN WO200178754-A2.  
 XX 25-OCT-2001.  
 XX 12-APR-2001; 2001WO-US012084.  
 XX 14-APR-2000; 2000US-00349937.  
 XX (UUPI-) UNIV PITTSBURGH.  
 XX Chancellor MB, Huard J, Capelli CC, Qu Z;  
 XX WPI; 2002-025967/03.  
 XX Use of a composition comprising isolated muscle-derived progenitor cells  
 PT expressing cell markers having at least desmin, and having long-term  
 PT survivability in situ for augmenting muscle or non-muscle soft tissue.  
 XX Example 9; Page 48; 92pp; English.  
 XX The invention relates to the use of a composition comprising isolated  
 CC muscle-derived progenitor cells (MDC) expressing cell markers of desmin,  
 CC CD34, Bcl-2, Sca-1 and Flk-1, and having long-term survivability in situ.  
 CC The invention is useful for the manufacture of a medicament for  
 CC augmenting and bulking muscle or non-muscle soft tissue in a mammal,  
 CC where MDC do not express CD45 and c-kit cell markers. The invention is  
 CC also useful in the treatment of a defect or void in non-muscle soft  
 CC tissue, weakness or dysfunction in muscle tissue in a mammal, an  
 CC aesthetic defect or a cosmetic defect, restoring or improving  
 CC contractility of smooth muscle tissue and producing new myofibers such  
 CC that the cells comprising the composition migrate to the sites of the  
 CC basal lamina of myofibers and develop into satellite cells to produce new  
 CC myofibers in the mammal. The invention further provides treatments and  
 CC amelioration for dermatological conditions, gastroesophageal reflux,  
 CC vesico-ureteral reflux, urinary incontinence, faecal incontinence, heart  
 CC failure and myocardial infarction. The invention also relates to a method  
 CC for genetically modifying the cells for gene transfer therapy. The  
 CC present DNA sequence is a RT (reverse transcriptase)-PCR primer which is  
 CC used for amplifying CD34 cell marker DNA related to the invention. The  
 CC CD34 marker DNA is used for the muscle-derived progenitor cells (MDC)  
 CC treatment of bone defects  
 XX  
 SQ Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;  
 Query Match 9.9%; Score 13.8; DB 1; Length 20;  
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1640 TTGTAGCAGAGGCAAG 1656  
 DB 20 TGTAGCAGAGTCAAG 4  
 RESULT 78  
 ABX78257/c  
 ID ABX78257 standard; DNA; 20 BP.  
 XX  
 AC ABX78257;  
 XX  
 XX 17-APR-2003 (first entry)  
 DT  
 XX Human bifunctional apoptosis regulator antisense oligo ISIS NO 143788.  
 DE  
 XX Human; bifunctional apoptosis regulator; antisense; phosphorothioate;  
 KW cytosstatic; antiinflammatory; inhibitor; infection; inflammation; tumour;  
 KW ss.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER

FT /note= "phosphorothioate backbone, nucleotides 1-5 and 16  
FT -20 are 2'-methoxyethoxy (MOE) nucleotides, nucleotides 7  
FT -14 are 2'-deoxy- nucleotides, all C nucleotides are 5-  
FT methyl cytosines"  
PN US6468796-B1.  
XX  
XX 22-OCT-2002.  
XX  
XX 27-APR-2001; 2001US-00844525.  
XX  
XX 27-APR-2001; 2001US-00844525.  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Watt AT;  
XX  
XX WPI; 2003-196749/19.  
XX  
XX New antisense compounds targeted to nucleic acids encoding human  
PT bifunctional apoptosis regulator, for modulating expression of the  
PT regulator and treating diseases associated with expression of the  
PT regulator in humans.  
XX  
XX Example 15; Col 45-46; 42pp; English.  
XX  
XX This invention describes a novel compound, 17-50 nucleobases in length  
CC which specifically hybridizes with a nucleic acid encoding human  
CC bifunctional apoptosis regulator (BAR) and inhibits the expression of  
CC human BAR. The products of the invention have cytostatic and  
CC antiinflammatory activity and can be used to inhibit human BAR expression  
CC during antisense therapy, useful for inhibiting the expression of human  
CC BAR in cells or tissues and for treating diseases associated with  
CC expression of BAR in an animal, particularly a human suspected of having  
CC or being prone to a disease or condition associated with expression of  
CC human BAR. In addition the antisense oligonucleotides are useful for  
CC diagnostics, therapeutics and as research reagent, e.g. prophylactically  
CC to prevent or delay infection, inflammation or tumor formation. The  
CC oligonucleotides described in the invention have 2'-methoxyethyl (2'-MOE)  
CC wings and a deoxy gap. This sequence represents a human BAR antisense  
CC oligonucleotide described in the disclosure of the invention  
XX  
XX Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 9.9%; Score 13.8; DB 1; Length 20;  
Best Local Similarity 88.2%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1662 GGCTCAGCTGGAACC 1678  
DB 17 GGCTCAGCTGGAATCC 1  
RESULT 79  
ABZ92121  
ID ABZ92121 standard; DNA; 20 BP.  
XX  
XX ABZ92121;  
XX  
XX 17-OCT-2003 (first entry)  
XX  
XX Human oligonucleotide sequence.  
XX  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiallthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO200285308-A2.  
PN

XX 31-OCT-2002.  
XX  
XX 23-APR-2002; 2002WO-US013135.  
XX  
XX 24-APR-2001; 2001US-0286137P.  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-229219/22.  
XX  
XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
XX Disclosure; SEQ ID NO 7363; 872pp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 9.9%; Score 13.8; DB 1; Length 20;  
Best Local Similarity 88.2%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1636 GGGCTTGTAGCAGAGG 1652  
DB 4 GGGCTTGTAGCAGATGG 20  
RESULT 80  
ABX10328/C  
ID ABX10328 standard; DNA; 20 BP.  
XX  
XX ABX10328;  
XX  
XX 28-JAN-2003 (first entry)  
XX  
XX Coryneform bacterium PCR primer #30.  
XX  
XX Coryneform bacterium; signal peptide domain; food processing; medicine;  
KW cosmetic; transglutaminase; human epithelial growth factor; primer; ss;  
KW PCR.  
XX  
XX Synthetic.  
XX  
XX WO200281694-A1.  
XX  
XX 17-OCT-2002.  
XX





CC in the amplification of human T cell receptor beta chain variable region  
 CC (TCRBV) DNA  
 XX Sequence 21 BP; 2 A; 7 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 9.9%; Score 13.8; DB 1; Length 21;  
 Best Local Similarity 88.2%; Pred. No. 2e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1687 TCCTCCAGCGTGTGGGA 1703  
 Db 2 TCCTCCAGCTTGTGGA 18

RESULT 85  
 ACF36406/c  
 ID ACF36406 standard; DNA; 21 BP.

XX AC ACF36406;  
 XX 18-DEC-2003 (first entry)  
 XX TRPM-2 antisense oligonucleotide #12.

XX TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;  
 XX prostate cancer; anti-apoptotic protein; antisense; ss.

XX Synthetic.

XX Homo sapiens.

XX WO2003072591-A1.

XX 04-SEP-2003.

XX 20-FEB-2003; 2003WO-US0005305.

XX 22-FEB-2002; 2002US-00080794.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;

XX WPI; 2003-689981/65.

XX New modified antisense oligonucleotide, useful particularly for treating  
 XX prostatic cancer, inhibits the testosterone-repressed prostate message-2.

XX Example 5; Page 42; 44pp; English.

XX The invention relates to a compound consisting of an oligonucleotide with  
 XX a phosphorothioate backbone throughout, in which: (a) sugars on  
 XX nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 XX remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 XX positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 XX ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 XX prostatic cancer cells to the androgen-independent state, in vivo or in  
 XX vitro; (b) to treat prostatic cancer (after initially withdrawing  
 XX androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 XX cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 XX ovarian and some breast cancer cells) that express abnormal levels of  
 XX TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 XX increase stability in vivo and activity (both in vivo or in vitro) and  
 XX result in a synergistic increase in effect when (I) is used with  
 XX chemotherapeutic agents or other antisense oligonucleotides directed  
 XX against other antiapoptotic genes. Sequences ACF36399-406 represent  
 XX antisense oligonucleotides targeted against human anti-apoptotic protein  
 XX TRPM-2 (testosterone-repressed prostate message-2) gene

XX Sequence 21 BP; 1 A; 4 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 9.9%; Score 13.8; DB 1; Length 21;  
 Best Local Similarity 88.2%; Pred. No. 2e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1734 GGCTCCCAACTCTCTCC 1750  
 Db 20 GGCCCCCAACTCG3CCC 4

RESULT 86  
 AAQ46059  
 ID AAQ46059 standard; DNA; 20 BP.

XX AC AAQ46059;

XX 25-MAR-2003 (revised)

XX 08-FEB-1994 (first entry)

XX Sequence of PCR primer L04 for the amplification of hly virulence factor.

XX Virulence factor; Listeria detection; food poisoning; hly; PCR; primer;

XX ss.

XX Synthetic.

XX CH682156-A5.

XX 30-JUL-1993.

XX 28-JUN-1990; 90CH-00002190.

XX 28-JUN-1990; 90CH-00002190.

XX (CAND/) CANDRIAN U.

XX (FURR/) FURRER B.

XX (HOEF/) HOEFELIN C.

XX (LUET/) LUETHY J.

XX Candrian U, Furrer B, Hoefelein C, Luethy J;

XX WPI; 1993-265174/34.

XX Listeria monocytogenes detection by enzymatic nucleic acid amplification  
 XX - using oligo-nucleotide(s) derived from alpha-haemolysin and/or beta-  
 XX haemo-lysin virulence factors in polymerase chain reactions.

XX Claim 2; Page 2; 2pp; German.

XX Oligos L01, L02, L03 and L04 are used for the amplification of hly (alphy  
 XX -haemolysin) virulence factor; and oligos AD07, AD08 and AD09 are used  
 XX for the amplification of iap (beta-haemolysin) virulence factor. They are  
 XX used in a detection method for Listeria monocytogenes in food samples  
 XX which is faster and more sensitive than the classical bacteriological  
 XX methods. (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 9.8%; Score 13.6; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 2e+02;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1688 CCTCCAGCGTGTGGAGTT 1707

Db 1 CCTCCAGAGTGTGATGTT 20

RESULT 87

AA42248

ID AA42248 standard; DNA; 20 BP.

XX AC AA42248;

XX 20-FEB-1997 (first entry)

XX Primer derived from hlyA gene used in modified PCR method.

XX



KW Detection; PCR; polymerase chain reaction; hybrid; antibody;  
 XX immunochemical detection; ss.

XX Synthetic.

XX CA2139070-A.

XX 24-JUN-1996.

XX 23-DEC-1994; 94CA-02139070.

XX 23-DEC-1994; 94CA-02139070.

XX (BLAI/) BLAIS B W.

XX Blais BW;

XX WPI; 1996-413110/42.

XX Detection of nucleic acid sequences - by polymerase chain reaction  
 PT amplification, transcription using RNA polymerase and detection of  
 PT RNA:DNA hybrids using antibodies.

XX Example 1; Page 16; 31pp; English.

XX A new method for the detection of nucleic acids comprises (a) amplifying  
 CC a DNA by PCR using primers to which an appropriate RNA polymerase  
 CC promoter has been appended; (b) transcribing the amplified DNA into RNA  
 CC using an RNA polymerase; (c) forming RNA:DNA hybrids; and (d)  
 CC immunochemically detecting the RNA:DNA hybrids using antibodies directed  
 CC to RNA:DNA hybrids. Two primers (AA742247, AA742248) were selected from  
 CC the hlyA gene and spanned a 730 base pair region of the gene from  
 CC nucleotides 602-1332. For further use in the invention, the primer  
 CC described in AA742247 had an additional 26 nucleotides added to it  
 CC corresponding to T7 RNA polymerase promoter sequence. The resulting  
 CC primer is described in AA742249

XX Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 9.8%; Score 13.6; DB 1; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 2e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

Qy 1684 GTCTCCTCCAGCGTGGTGA 1703

Db 1 GTATCCTCCAGAGTCATCGA 20

RESULT 88

AA766085

ID AA766085 standard; DNA; 20 BP.

XX AA766085;

XX 25-MAR-2003 (revised)

DT 18-JUN-1997 (first entry)

XX Plasmidogen activator/urokinase gene repeat sequence primer #1.

XX Polymorphism; repeat sequence; genetic marker; primer; amplification;  
 KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;  
 KW linkage analysis; genetic disease; animal; plant; breeding; locus;  
 KW hybridisation; chromosome; ds.

XX Synthetic.

XX US5582979-A.

XX 10-DEC-1996.

XX 04-APR-1994; 94US-00222177.

XX 21-APR-1989; 89US-00341562.

PR 05-SEP-1991; 91US-00754351.

XX (MARS-) MARSHFIELD CLINIC.

XX Weber JL;

XX WPI; 1997-042299/04.

XX Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -  
 using novel nucleic acid mols. as primers.

XX Example 9; Col 59-60; 186pp; English.

XX The invention relates to the isolation of polymorphic repeat sequences  
 CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic  
 CC markers. Primers based on these sequences can be used to detect these  
 CC repeats, especially for use in e.g paternity or maternity testing, human  
 CC genetic analysis such as linkage analysis of genetic disease, commercial  
 CC animal or plant breeding or pedigree analysis. The sequences AAT66084-  
 CC 166107 represent repeat sequences of low informativeness found in  
 CC specific human genes. The primers AAT66085-6 were used to amplify a 111  
 CC bp fragment of the plasmidogen activator/urokinase gene which contains  
 CC the repeat sequence of AAT66084. (Updated on 25-MAR-2003 to correct PF  
 CC field.)

XX Sequence 20 BP; 5 A; 1 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 9.8%; Score 13.6; DB 1; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 2e+02;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1713 AGGAGTACGAGATCGAGAT 1732

Db 1 AGGAGTTAGGAGCTGGAGGT 20

RESULT 89

AAV62008

ID AAV62008 standard; DNA; 20 BP.

XX AAV62008;

XX 25-MAR-2003 (revised)

DT 11-JAN-1999 (first entry)

XX L monocytogenes hlyA gene PCR primer B.

XX Detection; pathogen; amplification; RNA enhancement product; PCR primer;  
 KW DNA/RNA hybrid; Listeria sp; Streptococcus sp; Lactobacillus sp;  
 KW Lactococcus sp; Micrococcus sp; Enterococcus sp; Staphylococcus sp;  
 KW Bacillus sp; Pseudomonas sp; Escherichia coli; Salmonella typhimurium;  
 KW Yersinia enterocolitica; ss.

XX Synthetic.

XX Listeria monocytogenes.

XX US5827661-A.

XX 27-OCT-1988.

XX 23-SEP-1996; 96US-00718596.

XX 23-DEC-1994; 94CA-02137070.

PR 30-DEC-1994; 94US-00366619.

XX (KALY-) KALYX BIOSCIENCES INC.

XX Blais BW;

XX WPI; 1998-593985/50.

XX Enhanced detection by nucleic acid amplification, especially of Listeria  
 PT - uses formation of DNA-RNA hybrids after amplification, and then

PT specific immuno-detection of these.  
 XX  
 PS Example 1; Col 12; 15pp; English.  
 XX  
 CC AAV62007-V62009 are PCR primers used in a novel method for the enhanced  
 CC detection of DNA sequences, via a nucleic acid amplification procedure,  
 CC especially for detecting pathogens. Minute samples of pathogens (c. 10  
 CC cells) cannot be detected effectively by PCR. The minute quantities of  
 CC product formed by PCR are then transcribed into RNA enhancement products,  
 CC which further amplifies the target sequences to detectable levels.  
 CC Detection then takes place with antibodies for DNA:RNA hybrids, which  
 CC enable detection if the product volume formed is still small, but is  
 CC specific enough just for this type of product. The method is especially  
 CC useful for detecting the following pathogens: *Listeria monocytogenes*, *L.*  
 CC *innocua*, *L. ivanovi*, *L. seeligeri*, *L. welshimeri*, *L. murrayi*, *L. grayi*,  
 CC *Streptococcus thermophilus*, *Lactobacillus casei*, *Lactococcus lactis*,  
 CC *Micrococcus luteus*, *Enterococcus faecalis*, *Staphylococcus epidermidis*,  
 CC *Bacillus cereus*, *Bacillus subtilis*, *Pseudomonas aeruginosa*, *Escherichia*  
 CC *coli*, *Salmonella typhimurium*, or *Yersinia enterocolitica*. (Updated on 25-  
 CC MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 9.8%; Score 13.6; DB 1; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 2e+02;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1684 GTCTCTCCAGCTGTGGA 1703  
 DB |||||  
 1 GTATCTCCAGAGTGATCGA 20  
 RESULT 90  
 AAX22801/c  
 ID AAX22801 standard; DNA; 20 BP.  
 XX  
 AC AAX22801;  
 DT 27-MAY-1999 (first entry)  
 XX  
 DE PCR primer 82689.  
 XX  
 KW Protein-enveloped polyribonucleic acid; viral RNA; bacteriophage RNA;  
 KW diagnostic; detection; assay; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN DE19737442-A1.  
 XX  
 PD 04-MAR-1999.  
 XX  
 PF 22-AUG-1997; 97DE-01037442.  
 XX  
 PR 22-AUG-1997; 97DE-01037442.  
 XX  
 PA (OLFE-) OLFERT LANDT TIB MOLBIOL SYNTHESELABOR.  
 XX  
 PI Landt O;  
 XX  
 DR WPI; 1999-168279/15.  
 XX  
 PS Genetically modified RNA viruses or bacteriophages - useful as RNA  
 PT standards, positive controls, etc.  
 XX  
 PS Example 14; Col 19; 12pp; German.  
 XX  
 CC This invention describes protein-enveloped polyribonucleic acids  
 CC containing viral RNA or bacteriophage RNA, characterised in that the  
 CC natural nucleic acid sequence is varied. Also described is a method for  
 CC producing a protein-enveloped polyribonucleic acid. Protein-enveloped  
 CC polyribonucleic acids are useful as standards for diagnostic methods in  
 CC which the presence of a specific ribonucleic acid is detected, and are  
 CC useful as standard or competitor sequences for methods in which the

CC amount of a defined ribonucleic acid is determined. They are also useful  
 CC as positive controls for the detection of viral RNA, where the protein-  
 CC enveloped polyribonucleic acid is added directly to the assay sample and  
 CC is isolated in parallel with the viral RNA. They can monitor the  
 CC efficiency of processes for purifying nucleic acids or the efficiency of  
 CC the reverse transcription of ribonucleic acids, and are useful a  
 CC comparison substances in assays in which nucleic acids are detected by  
 CC hybridisation or in assays in which nucleic acids are detected after or  
 CC during nucleic acid amplification. They are useful as carriers for RNA  
 CC sequences having a functional property, and for mixtures of RNA sequences  
 CC from which individual RNA sequences can be selected  
 XX  
 SQ Sequence 20 BP; 3 A; 8 C; 3 G; 6 T; 0 U; 0 Other;  
 Query Match 9.8%; Score 13.6; DB 1; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 2e+02;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1631 GGATGGGGCTGTAGCAGAA 1650  
 DB |||||  
 20 GGACAGGGCTTATGCGAGAA 1  
 RESULT 91  
 AAZ04070/c  
 ID AAZ04070 standard; DNA; 20 BP.  
 XX  
 AC AAZ04070;  
 DT 07-OCT-1999 (first entry)  
 XX  
 DE PCR primer used to amplify an ORF of Chlamydia trachomatis.  
 XX  
 KW Vaccine; eye disease; conventional trachoma; nongenodemic trachoma;  
 KW paratrachoma; inclusion conjunctivitis; genital disease; peritropatitis;  
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;  
 KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.  
 XX  
 OS Synthetic.  
 OS Chlamydia trachomatis.  
 XX  
 PN WO928475-A2.  
 XX  
 PD 10-JUN-1999.  
 XX  
 PF 27-NOV-1998; 98WO-IBC01939.  
 XX  
 PR 28-NOV-1997; 97FR-00015041.  
 PR 17-DEC-1997; 97FR-00016034.  
 PR 04-NOV-1998; 98US-01C7077P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Griffais R;  
 XX  
 DR WPI; 1999-371125/31.  
 XX  
 PT Genome sequence of Chlamydia trachomatis.  
 XX  
 PS Disclosure; Page 1658; 1755pp; English.  
 XX  
 CC PCR primers AAZ01426-206209 were used to amplify open reading frames  
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs  
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines  
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also  
 CC be used to control growth of the microorganism. Chlamydia trachomatis is  
 CC responsible for a large number of diseases, e.g. eye diseases such as  
 CC conventional trachoma, nongonodemic trachoma, paratrachoma, and inclusion  
 CC conjunctivitis; genital diseases such as nongonococcal urethritis,  
 CC epididymitis, cervicitis, salpingitis, peritropatitis, bartholinitis;  
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.  
 CC The polypeptides of the invention may be of use in treating these  
 CC diseases

```

XX SQ Sequence 20 BP; 6 A; 9 C; 1 G; 4 T; 0 U; 0 Other;
Query Match          9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1709 GGTAGGAGTACGGAGTGG 1728
Db 20 GGTGGGAATACGTGTGG 1

RESULT 92
AAX78426
ID AAX78426 standard; cDNA; 20 BP.
XX
AC AAX78426;
XX
DT 26-AUG-1999 (first entry)
XX
DE Rat GAPDH primer 35.
XX
KW GAPDH; glyceraldehyde-phosphate dehydrogenase; cytokine; rat; PCR;
KW primer; ds.
XX
OS Synthetic.
OS Rattus sp.
XX
PN JPI1155600-A.
XX
PD 15-JUN-1999.
XX
PF 28-NOV-1997; 97JP-00328171.
XX
PR 28-NOV-1997; 97JP-00328171.
XX
PA (SHIS ) SHISEIDO CO LTD.
XX
DR WPI; 1999-398081/34.
XX
Measuring expression of cytokine gene in sample cell - by extracting RNA
and amplifying cDNA.
XX
PS Claim 9; Page 15; 21pp; Japanese.
XX
CC This invention describes a novel method for measuring the expression of a
CC specific cytokine gene in a sample cell group. AAX78387-X78392 and
CC AAX78398-X78427 represent primers used to amplify the rat glyceraldehyde-
CC 2-phosphate dehydrogenase (GAPDH) gene which is used to illustrate the
CC method of the invention
XX
SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
Query Match          9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1721 GGAGATGGAGATTGGCTCCC 1740
Db 1 GAAGATGGTGGTGGCTTCC 20

RESULT 93
AAX25929
ID AAX25929 standard; DNA; 20 BP.
XX
AC AAX25929;
XX
DT 08-JUN-1999 (first entry)
XX
DE GAPDH reverse primer corresponds to bases 252-271.
XX
KW Evaluation; allergy; PCR; amplification; primer; probe; hybridisation;

gene expression; cytokine; immune response; GAPDH; ss;
glyceraldehyde-3-phosphate dehydrogenase.
Synthetic.
JPI0304880-A.
17-NOV-1998.
09-OCT-1997; 97JP-00277580.
07-MAR-1997; 97JP-00053528.
(SHIS ) SHISEIDO CO LTD.
WPI; 1999-232451/20.
Determination of a nucleic acid and a reagent for it - useful for
evaluating allergic properties of a chemical substance.
Claim 5; Page 3; 20pp; Japanese.
The invention relates to a test method for evaluating the allergic
properties of a chemical substance by PCR amplifying and determining the
levels of expression of cytokine genes involved with allergic immune
responses. Primers and probe AAX25928-X25930 are used to determine
glyceraldehyde-3-phosphate dehydrogenase (GAPDH) expression. This primer
is targeted to nucleotides 252-271 of the GAPDH gene
XX
SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
Query Match          9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1721 GGAGATGGAGATTGGCTCCC 1740
Db 1 GAAGATGGTGGTGGCTTCC 20

RESULT 94
AAX97388/c
ID AAX97388 standard; DNA; 20 BP.
XX
AC AAX97388;
XX
DT 13-SEP-1999 (first entry)
XX
DE Primer used to amplify Chlamydia pneumoniae polynucleotides.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
OS Synthetic.
OS Chlamydophila pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB001890.
XX
PR 21-NOV-1997; 97FR-00014673.
XX
PR 04-NOV-1998; 98US-0107078P.
XX
PA (GEST ) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae.

```

XX  
PS Page 1900; Disclosure; 1912pp; English.  
CC  
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames  
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae  
CC (see AAX91990). C. pneumoniae causes respiratory disease such as  
CC pneumonia and bronchitis and is thought to be a contributing factor in  
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema  
CC nodosum or pharyngitis. The polypeptides encoded by the open reading  
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used  
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae  
CC nucleotide sequences can also be used as immunogenic compositions,  
CC especially where the vector directs the expression of a neutralising  
CC epitope of C. pneumoniae  
XX  
SQ Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;  
  
Query Match 9.8%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1720 CGGAGATGGAGATTGGCTCC 1739  
Db ||||| ||||| ||||| |||||  
20 CGGATAGGGAGACTGGCTGC 1  
  
RESULT 95  
AAX97331/C  
ID AAX97331 standard; DNA; 20 BP.  
XX  
AC AAX97331;  
XX  
DT 13-SEP-1999 (first entry)  
DE  
DE Primer used to amplify Chlamydia pneumoniae polynucleotides.  
XX  
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;  
XX neutralising epitope; PCR primer; ss.  
XX  
OS Synthetic.  
OS Chlamydothila pneumoniae.  
XX  
PI WO9927105-A2.  
XX  
XX 03-JUN-1999.  
XX  
XX 20-NOV-1998; 98WO-IB001890.  
XX  
XX 21-NOV-1997; 97FR-00014673.  
XX  
XX 04-NOV-1998; 98US-0107078P.  
XX  
XX (GEST ) GENSET.  
XX  
XX Griffais R;  
XX  
XX WPI; 1999-357842/30.  
XX  
XX Genome sequence of Chlamydia pneumoniae.  
XX  
PS Page 1896; Disclosure; 1912pp; English.  
XX  
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames  
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae  
CC (see AAX91990). C. pneumoniae causes respiratory disease such as  
CC pneumonia and bronchitis and is thought to be a contributing factor in  
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema  
CC nodosum or pharyngitis. The polypeptides encoded by the open reading  
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used  
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae  
CC nucleotide sequences can also be used as immunogenic compositions,  
CC especially where the vector directs the expression of a neutralising  
CC epitope of C. pneumoniae  
XX

XX  
SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;  
  
Query Match 9.8%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1633 ATGGGCTTCTAGCAGAGG 1652  
Db ||||| ||||| ||||| |||||  
20 ATGGTGCTAGTATCAGCAGG 1  
  
RESULT 96  
AAZ76046/C  
ID AAZ76046 standard; DNA; 20 BP.  
XX  
AC AAZ76046;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human biallelic marker downstream amplification primer SEQ ID NO:10402.  
XX  
XX Human genome; biallelic marker; high density disequilibrium map;  
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;  
XX haplotyping; hybridisation; identification; characterisation;  
XX amplification; single nucleotide polymorphism; SNP; PCR primer;  
XX diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9954500-A2.  
XX  
XX 28-OCT-1999.  
XX  
XX 21-APR-1999; 99WO-IB000822.  
XX  
XX 21-APR-1998; 98US-0082614P.  
XX  
XX 23-NOV-1998; 98US-0109732P.  
XX  
XX (GEST ) GENSET.  
XX  
XX Cohen D, Blumenfeld M, Chumakov I;  
XX WPI; 2000-013267/01.  
XX  
XX Novel biallelic markers used to construct a high density disequilibrium  
XX map of the human genome.  
XX  
XX Claim 9; Page 2448; 2745pp; English.  
XX  
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present  
XX invention, which contain a polymorphic base at position 24 of their  
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
XX primers for the biallelic markers. The biallelic markers of the invention  
XX have a variety of uses: they can be used for high density mapping of the  
XX human genome, and in complex association studies and haplotyping studies  
XX which are useful in determining the genetic basis for disease states.  
XX Compositions and methods of the invention can also be useful for the  
XX identification of the targets for the development of pharmaceutical  
XX agents and diagnostic methods, as well as the characterisation of the  
XX differential efficacious responses to and side effects from  
XX pharmaceutical agents acting on a disease as well as other treatment.  
XX N.B. The SEQ ID Nos 2852, 2913, 2974, 3036, 3096, 3157, 3227, 3297 and  
XX 3367, are not actually given a sequence in the Sequence Listing from the  
XX present invention  
XX  
SQ Sequence 20 BP; 6 A; 0 C; 11 G; 3 T; 0 U; 0 Other;  
  
Query Match 5.8%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1746 CTCCTATCCTAAAGGCCCA 1765

Db 20 CTCCTATCCTCTACTCCCA 1

RESULT 97  
AAH38150/C  
ID AAH38150 standard; DNA; 20 BP.  
XX AC AAH38150;  
XX DT 14-AUG-2001 (first entry)  
XX DE SNP specific lower PCR primer SEQ ID 946.  
XX KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
XX KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
XX KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
XX KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
XX KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
XX KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
XX OS Homo sapiens.

XX FH modified\_base 1..20  
XX PN WO200129262-A2.  
XX PD 26-APR-2001.  
XX PF 13-OCT-2000; 2000WO-US028436.  
XX PR 15-OCT-1999; 99US-0160096P.  
XX PA (ORCH-) ORCHID BIOSCIENCES INC.  
XX PI Picoult-Newburg L, Pohl M;  
XX PT WPI; 2001-290930/30.

XX PT New genotyping oligonucleotide, useful for detecting the presence,  
XX PT absence or identity of single polynucleotide polymorphism in a nucleic  
XX PT acid sample.

XX PS Claim 1; Page 54; 83pp; English.

XX CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
XX CC primer extension (SNPE) primers, and the sequences of regions flanking  
XX CC sites of single nucleotide polymorphisms SNPs. The present invention  
XX CC includes kits for determining the presence or absence of a SNP, using the  
XX CC oligonucleotides of the invention. The PCR primers are used to amplify a  
XX CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
XX CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
XX CC performing a single-nucleotide primer extension reaction. The  
XX CC oligonucleotides are useful for determining the presence, absence or  
XX CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
XX CC assess by association analysis the genotype of an individual or group of  
XX CC individuals, having a pathological phenotypic trait suspected of being  
XX CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
XX CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
XX CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
XX CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
XX CC traits also include symptoms of or susceptibility to multifactorial  
XX CC disease of which a component is or may be genetic such as autoimmune  
XX CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
XX CC inflammation, cancer, nervous system diseases and infection by pathogenic  
XX CC microorganism. The method is also useful in forensic investigations and  
XX CC paternity analysis. The present sequence represents a PCR primer specific  
XX CC for a human SNP containing DNA sequence

XX SQ Sequence 20 BP; 7 A; 1 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 9.8%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1737 TCCCAACTCCTCCTATCCT 1756  
Db 20 TCCCAACTCCTCCTATCCT 1

RESULT 98  
AAH20719  
ID AAH20719 standard; DNA; 20 BP.  
XX AC AAH20719;  
XX DT 13-AUG-2001 (first entry)  
XX DE Human telomeric repeat binding factor 2 oligonucleotide 111447.

XX KW Antisense; phosphorothioate; human; telomeric repeat binding factor 2;  
XX KW inhibitor; premature aging; hyperproliferative disorder; cancer;  
XX KW cytostatic; ss.  
XX OS Homo sapiens.

XX FH modified\_base 1..20  
XX PN WO200143752-A1.  
XX PD 21-JUN-2001.  
XX PF 14-DEC-2000; 2000WO-US033954.  
XX PR 17-DEC-1999; 99US-00467642.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Cowsert LM;  
XX DR WPI; 2001-398071/42.

XX PT Antisense compounds targeted to nucleic acid encoding telomeric repeat  
XX PT binding factor 2 useful for treating conditions such as premature aging  
XX PT and diseases such as cancer.  
XX PS Example 15; Page 81; 108pp; English.  
XX CC This invention describes a novel antisense compound (I) 8-30 nucleobases  
XX CC in length targeted to a polynucleotide encoding human telomeric repeat  
XX CC binding factor 2 (II) which specifically hybridizes with, and inhibits  
XX CC the expression of (II). (I) is useful for treating a human having a  
XX CC disease or condition associated with (II) such as premature aging or a  
XX CC hyperproliferative disorder especially cancer, by inhibiting the  
XX CC expression of (II) in human cells or tissues. (I) is useful for  
XX CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.  
XX CC The products of the invention have cytostatic activity. This sequence  
XX CC represents an antisense oligonucleotide used to illustrate the method of  
XX CC the invention

XX SQ Sequence 20 BP; 7 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 9.8%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY      1640 TTGTAGCAGAGGCAAGCAC 1659
Db      1 TTGCATCAGAGGCCAGAAC 20

RESULT 99
AAH80623/c
ID      AAH80623 standard; cDNA; 20 BP.
XX
AC      AAH80623;
XX
DT      11-SEP-2001 (revised)
DT      19-SEP-2001 (first entry)
XX
XX      Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 587.
XX
XX      Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
XX      disease diagnosis; ss.
XX
XX      Human immunodeficiency virus 1.
OS
XX
XX      US6251588-B1.
PN
XX
XX      26-JUN-2001.
PD
XX
XX      10-FEB-1998; 98US-00021701.
PF
XX
XX      10-FEB-1998; 98US-00021701.
PR
XX
XX      (AGIL-) AGILENT TECHNOLOGIES INC.
PA
XX
XX      Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
PI
XX      WPI; 2001-424456/45.
DR
XX
XX      Predicting the potential of an oligonucleotide to hybridize to a target
PT      nucleotide sequence, useful for evaluating oligonucleotide probe
PT      sequences, by identifying a oligonucleotides based on the evaluation of
PT      parameters.
XX
XX      Example 2; Col 67; 342pp; English.
PS
XX
XX      The present invention describes a method for predicting the potential of
CC      an oligonucleotide to hybridize to a (complementary) target nucleotide
CC      sequence, involving identifying a subset of oligonucleotides within the
CC      predetermined number of unique oligonucleotides based on the evaluation
CC      of the parameter. Oligonucleotides in the subset are identified that are
CC      clustered along a region of the nucleotide sequence that is hybridisable
CC      to the target nucleotide sequences. This is useful for evaluating
CC      oligonucleotide probe sequences. The present sequence is an
CC      oligonucleotide described in the exemplification of the invention.
XX      (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ      Sequence 20 BP; 5 A; 5 C; 2 G; 8 T; 0 U; 0 Other;

Query Match          9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1701 GGAAGTTGGTTAGGAGTAC 1720
Db      20 GGAAGTTCAATTAGGAATAC 1

RESULT 100
ABN83384
ID      ABN83384 standard; DNA; 20 BP.
XX
AC      ABN83384;
XX
DT      15-AUG-2002 (first entry)
DT
XX
XX      Glyceraldehyde-3-phosphate dehydrogenase, GAPDH, PCR primer #1.
DE

GAPDH; glyceraldehyde-3-phosphate dehydrogenase; PCR; primer; ss.
Unidentified.
WO200243855-A1.
06-JUN-2002.
29-NOV-2001; 2001WO-FR003780.
29-NOV-2000; 2000PR-00015398.
(COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
Ugolin N, Marguerie De Rotrou G, Kortulewski T, Alibert O;
Le Roux D;
WPI; 2002-471810/50.
Array of biological or chemical probes, useful e.g. for diagnosis and
drug screening, fixed to a support magnetically, through a fixing vector.
Example 6; Page 29; 52pp; French.
The present invention relates to an organised array of biological or
chemical probes fixed to a support by magnetic coupling, by means of a
fixing vector. The arrays are useful for diagnosis and for high-
throughput screening of libraries of molecules or biological samples,
e.g. to identify therapeutic or diagnostic agents, also for
pharmacogenomic and toxicological analysis, and for studying the
structure and expression of genomes, or generally any molecular
interaction. The present sequence is a PCR primer for glyceraldehyde-3-
phosphate dehydrogenase (GAPDH) gene, which was used to illustrate the
invention
SQ      Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match          9.8%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1679 CTGCTGTCCTCCACGCGTG 1698
Db      1 CTGCTGTCCTCCACCAAG 20

RESULT 101
ABZ93876/c
ID      ABZ93876 standard; DNA; 20 BP.
XX
AC      ABZ93876;
XX
DT      17-OCT-2003 (first entry)
DT
XX
XX      Human oligonucleotide sequence.
DE
XX
XX      Human; antisense; lung dysfunction; nasal airway dysfunction;
KW      antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW      antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW      antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW      adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW      lung inflammation; respiratory disease; ds.
XX
XX      Homo sapiens.
OS
XX
XX      WO200285308-A2.
PN
XX
XX      31-OCT-2002.
PD
XX
XX      23-APR-2002; 2002WO-US013135.
PF
XX
XX      24-APR-2001; 2001US-0286137P.
PR

```

XX  
PA PA  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-329219/22.  
DR

Pharmaceutical composition for treating ailments associated with impaired PT respiration, has oligo(s) antisense to specific gene(s) or its PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or PT ubiguinone.

PS Disclosure; SEQ ID NO 9118; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct](http://ftp.wipo.int/pub/published/pct) sequences

SQ Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match	9.8%	Score 13.6;	DB 1;	Length 20;
Best Local Similarity	80.0%;	Pred. No. 2e+02;		
Matches 16;	Conservative	0;	Mismatches 4;	Indels 0;
				Gaps 0;

Qy 1655 AGCACCAGGCTCACAGCTGG 1674  
Db 20 AGCACCTGGCACACAGTAGG 1

RESULT 102  
ABZ99199  
ID ABZ99199 standard; DNA: 20 BP.

AC ABZ99199;

DT 17-OCT-2003 (first entry)

Human PDE4C oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

OS Homo sapiens.

PN WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

PR 24-APR-2001: 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.  
 PA NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 XX PI Miller S, Tang L, Shahabuddin S;  
 XX PI  
 XX WPI; 2003-229219/22.  
 DR

Pharmaceutical composition for treating ailments associated with impaired PT respiration, has oligo(s) antisense to specific gene(s) or its PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or PT ubiquinone.

PS Disclosure: SEO ID NO 14441; 872pp: English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end and genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct\\_sequences](http://ftp.wipo.int/pub/published/pct_sequences)

Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match	9.8%	Score 13.6;	DB 1;	Length 20;
Best Local Similarity	80.0%;	Pred. No. 2e+02;		
Matches 16;	Conservative	0;	Mismatches 4;	Indels 0;
				Gaps 0;

Qy	1679	CTGGTGTCCTCCAGCGTG	1698
Db	1	CTCGATTGTCCTCCAGCGTG	20

RESULT 103  
ABS55740  
ID ABS55740 standard; DNA: 20 BP.

AC ABS55740;

DT 17-JAN-2003 (first entry)

XX Glyceraldehyde-3-phosphate dehydrogenase reverse PCR primer.  
 XX Uncoupling protein-3; reducing drug; rat; PCR; primer; ss;  
 KW glyceraldehyde-3-phosphate dehydrogenase.

Rattus sp.

AA  
PN JP2002125680-A.

PD 08-MAY-2002.

24-OCT-2000; 2000JP-00324581.

PR 24-OCT-2000; 2000JP-00324581.

PA (SHIS ) SHISEIDO CO LTD.

WPI: 2003-002955/01.

XX Measurement of the nucleic acid of uncoupling protein-1, -2 or -3, useful  
PT for evaluating a reducing drug.  
XX  
PS Disclosure; Page 2; 21pp; Japanese.  
XX  
CC The invention describes measurement of an mRNA or a cDNA of uncoupling  
CC protein-1, -2 or -3 by carrying out a PCR by a DNA polymerase having 5'-  
CC 3' exonuclease activity by using a forward primer, a reverse primer and a  
CC probe having a reporter and a quencher and hybridising with a template  
CC nucleic acid in the region placed between the above both primers. The  
CC method is useful as a test method for evaluating a reducing drug. This  
CC sequence represents a PCR primer for amplification of the partial  
CC nucleotide sequence of cDNA encoding rat glyceraldehyde-3-phosphate  
CC dehydrogenase  
XX  
SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;  
Query Match 9.8%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;  
Matches 16; Conservative 0; Indels 4; Indels 0; Gaps 0;  
QY 1721 GGAGATGGAGATTGGCTCC 1740  
Db 1 GAAGATGGTATGGCTCC 20  
RESULT 104  
ADD81514/c  
ID ADD81514 standard; DNA; 20 BP.  
XX  
AC ADD81514;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE HIV PRT antisense derived probe #443.  
XX  
SS; oligonucleotide hybridisation potential; efficient hybridisation;  
KW large array; minimum oligonucleotide synthesis; probe.  
KW  
XX Human immunodeficiency virus.  
XX  
XX US2003054346-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 15-FEB-2001; 2001US-00784674.  
XX  
PR 10-FEB-1998; 98US-00021701.  
XX  
PA (SHAN/) SHANNON K W.  
PA (WOLB/) WOLBER P K.  
PA (DELE/) DELENSTARR G C.  
PA (WEBB/) WEBB P G.  
PA (KINC/) KINCAID R H.  
XX  
PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;  
XX  
XX WPI; 2003-743746/70.  
XX  
XX Predicting potential of oligonucleotides to hybridize to target  
XX nucleotide sequence comprises determining and evaluating for each  
PT oligonucleotide a parameter predictive of the oligonucleotides ability to  
PT hybridize with target.  
XX  
XX Example 2; SEQ ID NO 587; 423pp; English.  
XX  
XX The invention relates to a method of predicting the potential of  
XX oligonucleotides to hybridise to target nucleotide sequences. The method  
CC is useful for predicting the potential of an oligonucleotide to hybridise  
CC to a target nucleotide sequence, e.g. RNA or DNA or a sequence that  
CC contains chemically modified nucleotides. The method is also useful for  
CC predicting the potential of the oligonucleotides to hybridise to a

CC complementary target nucleotide sequence. The method is useful to predict  
CC efficient hybridisation oligonucleotides for each of multiple target  
CC sequences therefore very large arrays may be constructed and tested with  
CC minimum synthesis of oligonucleotides. The present sequence represents a  
CC HIV PRT antisense derived probe.  
XX  
SQ Sequence 20 BP; 5 A; 5 C; 2 G; 8 T; 0 U; 0 Other;  
Query Match 9.8%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 2e+02; Mismatches 0; Gaps 0;  
Matches 16; Conservative 0; Indels 4; Indels 0; Gaps 0;  
QY 1701 GGAAGTTGGTTAGGAGTAC 1720  
Db 20 GGAAGTTCAATTAGGATAC 1  
RESULT 105  
ACD53920/c  
ID ACD53920 standard; RNA; 17 BP.  
XX  
AC ACD53920;  
XX  
DT 24-SEP-2003 (first entry)  
XX  
DE HBV zynzyme substrate sequence #90.  
XX  
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; zynzyme;  
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX  
OS Hepatitis B virus.  
XX  
XX WO200281494-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 26-MAR-2002; 2002WO-US009187.  
XX  
PR 26-MAR-2001; 2001US-00817879.  
PR 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER X.  
PA (ROBE/) ROBERTS E.  
XX  
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
PI WPI; 2003-229207/22.  
XX  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
XX Example 1; Page 175; 337pp; English.  
XX  
XX The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or



CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HBV  
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences  
 CC disclosed in the present invention

XX SQ Sequence 17 BP; 3 A; 0 C; 11 G; 0 T; 3 U; 0 Other;  
 Query Match 9.6%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 1.8e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 CTCCTCACTCTCTCC 1750  
 Db 16 CCCCACTCTCTCC 2

## RESULT 106

ACC64154  
 ID ACC64154 standard; DNA; 17 BP.

XX AC ACC64154;

XX DT 01-JUL-2003 (first entry)

XX DE Murine oligonucleotide associated with tumour suppression, SEQ ID 1401.

XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;  
 XX viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 XX schizophrenia; ss.

XX OS Mus musculus.

XX PN WO2003025176-A2.

XX PD 27-MAR-2003.

XX PF 17-SEP-2002; 2002WO-IB004210.

XX PR 17-SEP-2001; 2001FR-00011979.

XX PS (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telleran A, Amson R, Tuijnder M;

XX DR WPI; 2003-333167/31.

XX PT New isolated nucleic acid, useful for treating viral diseases associated  
 XX with tumors and cell degeneration, also related polypeptides, antibodies  
 XX and transfected cells.

XX PS Disclosure; Page 194; 738pp; French.

XX CC The present invention relates to murine oligonucleotides (ACC62754-  
 ACC68906), which are associated with tumour suppression, tumour  
 CC reversion, apoptosis and virus resistance. The oligonucleotides are  
 CC useful as (1) as probes and primers for detecting, identifying,  
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of  
 CC recombinant polypeptides. The oligonucleotides are useful for preparation  
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that

CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia  
 XX SQ Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 9.6%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 1.8e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 GCTCCCACTCTCTCC 1749

Db 1 GATCCCACTCTCTCC 15

## RESULT 107

AAQ50940

ID AAQ50940 standard; DNA; 18 BP.

XX AC AAQ50940;

XX DT 25-MAR-2003 (revised)

XX DT 19-MAY-1994 (first entry)

XX DE T-cell antigen receptor J-beta2.7 probe.

XX KW RT-PCR; polymerase chain reaction; amplification; SSCP; J-domain;  
 XX single-strand conformation polymorphism; joining domain; subtype beta 2;  
 XX ss.

XX OS Synthetic.

XX PN WO9322455-A1.

XX PD 11-NOV-1993.

XX PF 30-APR-1993; 93WO-JP000577.

XX PR 30-APR-1992; 92JP-00111467.

XX PR 31-JUL-1992; 92JP-00205054.

XX PA (TAIS ) TAISHO PHARM CO LTD.

XX PA (LITL-) LIT INST CO LTD.

XX PI Yamamoto K, Mizushima Y, Nishioka K, Sakoda H, Ikeda Y;

XX DR WPI; 1993-368813/46.

XX PT Detection of expression of T-cell antigen receptor gene - in cancer,  
 XX viral or immune disease patients, by polymerase chain reaction  
 XX amplification of the gene and SSCP analysis.

XX PS Example 1; Page 24; 47pp; Japanese.

XX CC Primers corresp. to DNA coding for part of the beta-chain of the T cell  
 XX antigen receptor (pref. the Variable region primers AAQ50905- AAQ50926)  
 XX are used in PCR to amplify the T cell antigen receptor gene. The  
 XX amplified gene is detected by the single-strand conformation polymorphism  
 XX method using hybridisation probes corresp. to the beta-chain J domain  
 XX (see AAQ50928-Q50940). (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 18 BP; 3 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 9.6%; Score 13.4; DB 1; Length 18;  
 Best Local Similarity 93.3%; Pred. No. 1.9e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1656 GCACCAGGCTCAG 1670

Db 3 GCACCAGGCTCAGG 17

## RESULT 108

ABL88809

```

ID ABL88809 standard; DNA; 18 BP.
XX
AC ABL88809;
XX
DT 22-MAY-2002 (first entry)
XX
DE HIV-1 related binding molecule oligonucleotide sequence SEQ ID NO:31.
XX
KW Binding molecule; HIV-1; human immunodeficiency virus type 1;
KW reverse transcriptase; binding group; ss.
XX
OS Human immunodeficiency virus 1.
OS Synthetic.
XX
PN EP1174518-A1.
XX
XX 23-JAN-2002.
XX
PF 20-JUL-2000; 2000EP-00202611.
XX
PR 20-JUL-2000; 2000EP-00202611.
XX
PA (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX
XX Loukachov VV, Van Gemen B, Goudsmit J;
XX
XX WPI; 2002-156696/21.
XX
PT Collection of binding groups for determining or typing samples,
PT especially clinical samples, has groups capable to identify essentially
PT all members of the family of nucleic acids of relatively high
PT significance.
XX
PS Disclosure; Page 14; 166pp; English.
XX
CC The present invention describes a collection of binding groups for a
CC family of nucleic acids comprising members of relative high and relative
CC low significance, where the binding groups are selected to be capable to
CC identify, alone or in combination, essentially all members of the family
CC of nucleic acids of relatively high significance. The collection of
CC binding groups is useful for typing of nucleic acid in a clinical sample,
CC by contacting the nucleic acid with the collection and determining
CC whether one or more binding groups bound to the nucleic acid of the
CC sample. This method is useful for determining whether the sample
CC comprises at least a part of a member of relatively high significance of
CC a family of nucleic acids. The collection of binding groups is useful for
CC diagnosing the severity of a disease caused by a pathogen containing a
CC member of a family of nucleic acids. ABL88779 to ABL89321 represent
CC oligonucleotide sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 18 BP; 7 A; 1 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 9.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1717 GTACGAGATGGAGA 1731
DB 1 GTACAGAGATGGAGA 15

RESULT 109
AC83346
ID ACC83346 standard; DNA; 18 BP.
XX
XX ACC83346;
XX
XX ACC83346;
XX
DT 29-SEP-2003 (first entry)
XX
DE T7 forward PCR primer SEQ ID #8.
XX
KW G protein-coupled receptor; GPCR; receptor; GAVE10; antirheumatic;

antiarthritic; antiasthmatic; antiinflammatory; antiallergic;
rheumatoid arthritis; asthma; Crohn's disease; inflammation; allergy;
edema; gene therapy; PCR; primer; ss.
Bacteriophage t7.
WO2003029413-A2.
10-APR-2003.
30-SEP-2002; 2002WO-US031045.
01-OCT-2001; 2001US-0325591P.
(AVET ) AVENTIS PHARM INC.
Fishingdrelo H, Ardati A, Cai J;
WPI; 2003-381619/36.
New GAVE10 nucleic acid and polypeptide, useful for diagnosing, screening
and treating disorders with aberrant signaling activity of the GAVE10
polypeptide, such as rheumatoid arthritis, asthma, Crohn's disease,
allergy and edema.
Example 2; Page 82; 102pp; English.
The invention relates to an isolated nucleic acid encoding a GAVE10
polypeptide. GAVE10 is part of the family of G protein-coupled receptors.
The methods and compositions of the present invention are useful for
diagnosing, screening, preventing and treating disorders associated with
the signalling activity of the GAVE10 polypeptide. These include
rheumatoid arthritis, asthma, Crohn's disease, inflammation, allergy and
edema. They can also be used in chromosomal mapping, tissue typing,
forensic biology, prognostic assays, monitoring clinical trials,
pharmacogenomics, and also in gene therapy. The current sequence
represents a T7 forward primer used in an example from the invention in
the cloning of hGAVE10 cDNA
Sequence 18 BP; 2 A; 8 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 5.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 GGCTCCCAACTCTC 1748
DB 1 GGCTCCCAACTCTC 15

RESULT 110
ACF05396
ID ACF05396 standard; DNA; 18 BP.
XX
XX ACF05396;
XX
XX ACF05396;
XX
DT 06-NOV-2003 (first entry)
XX
DE Bacteriophage T7 forward primer.
XX
KW Human; GAVE7; G-protein coupled receptor; receptor; signal transduction;
KW antiinflammatory; gene therapy; PCR; primer; ss.
XX
OS Bacteriophage t7.
XX
PN WO2003054156-A2.
XX
XX 03-JUL-2003.
XX
XX 18-DEC-2002; 2002WO-US040354.
XX
XX 20-DEC-2001; 2001US-0341271P.
XX
```

PA (AVET ) AVENTIS PHARM INC.  
PA (CALJ) CAI J.  
XX Eishingdrello H, Ardatti A;  
XX WPI; 2003-559136/52.  
XX Nucleic acid molecule encoding a GAVE7 polypeptide, useful for  
PT diagnosing, preventing or treating disorders characterized by  
PT insufficient or excessive production of GAVE7 protein, e.g. inflammation  
PT associated with asthma.  
XX Example 1; Page 82; 52pp; English.  
XX  
XX The present sequence is that of a bacteriophage T7 forward primer, which  
CC was used to sequence PCR products comprising cDNA (see ACC84400) encoding  
CC GAVE7 (see ABR62587), a novel human G-protein coupled receptor, was  
CC isolated. The invention provides GAVE7 nucleic acids, expression vectors,  
CC host cells, polypeptides and methods for their production, and antibodies  
CC that bind specifically to GAVE7. Also claimed are methods for identifying  
CC an agonist, inverse agonist or antagonist of GAVE7, and a therapeutic  
CC method for modulating GAVE7 signalling activity or signal transduction  
CC using an agonist, antagonist or an inverse agonist of GAVE7  
XX  
XX Sequence 18 BP; 2 A; 8 C; 2 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 9.6%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. NO. 1.9e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1734 GGCTCCCAACTCTCC 1748  
DB 1 GGCTCCCAACTCTC 15  
RESULT 111  
AAAB2923/C  
ID AAAB2923 standard; DNA; 19 BP.  
XX AAAB2923;  
XX 04-DEC-2000 (first entry)  
DT  
DE cdk4 ribozyme binding site #104.  
XX  
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.  
XX Mammalia.  
XX W0200032765-A2.  
XX  
XX 08-JUN-2000.  
XX  
XX 06-DEC-1999; 99WO-US028772.  
XX  
XX 04-DEC-1998; 98US-0110954P.  
XX (IMMU-) IMMUSOL INC.  
XX  
XX Tritz R, Welch PJ, Barber JR, Robbins JM;  
XX WPI; 2000-412314/35.  
XX  
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
PT PCNA and Cyclin B1.  
XX  
XX Disclosure; Page 53; 109pp; English.  
XX  
XX The present invention relates to a hairpin or hammerhead ribozyme,  
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
CC Representative examples of ribozyme recognition sites are given in

CC AAAB2415 to AAA86787. The ribozyme of the invention is useful for  
CC inhibiting restenosis by introduction of the ribozyme into cells. The  
CC ribozyme is resistant to endonuclease activity and hence is efficient in  
CC restenosis treatment  
XX  
XX Sequence 19 BP; 5 A; 3 C; 9 G; 2 T; 0 U; 0 Other;  
SQ  
Query Match 9.6%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 93.3%; Pred. NO. 2.1e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1735 GCTCCCAACTCTCC 1749  
DB 16 GCTCCCAACTCTCC 2  
RESULT 112  
AAA51763  
ID AAA51763 standard; DNA; 19 BP.  
XX  
XX AAA51763;  
AC  
XX 31-OCT-2000 (first entry)  
DT  
DE Primer to amplify CYP3A5 gene in real time PCR.  
XX  
XX CYP3A5; Cytochrome P450; transcription regulatory region; polymorphism;  
KW Activator protein-3 motif; AP-3; basic transcription element;  
KW drug metabolism; phenotype; primer; ss.  
XX  
XX Homo sapiens.  
XX W0200039332-A1.  
XX  
XX 06-JUL-2000.  
XX  
XX 22-DEC-1999; 99WO-GB004380.  
XX  
XX 23-DEC-1998; 98GB-00028619.  
XX (JANC ) JANSSEN PHARM NV.  
XX Paulussen ADC, Armstrong M;  
XX WPI; 2000-452418/39.  
XX  
XX Identifying subjects with a high drug metabolizing phenotype associated  
PT with cytochrome CYP3A5 expression for establishing whether a drug will be  
PT metabolized by the subject.  
XX  
XX Disclosure; Page 21; 69pp; English.  
XX  
XX Primers AAA51762-63 were used to amplify cytochrome P450 CYP3A5 gene in a  
CC real time PCR assay to ensure specificity. Cytochrome P450 subfamily  
CC CYP3A5 transcription regulatory regions can be screened for the  
CC presence/absence of a polymorphic variant, preferably at positions -475  
CC or -147 of the DNA of the 5' flanking region adjacent to the CYP3A5  
CC coding sequence. The variants are present in an activator protein-3 (AP-  
CC 3) motif and/or a basic transcription element (BTE). The polymorphisms  
CC cause increased CYP3A5 gene expression and this has been linked to drug  
CC metabolic activity. Screening for the presence of variants can be used to  
CC identify subjects with a high or low drug metabolizing phenotype  
CC associated with cytochrome CYP3A5 expression. Primers are used which in  
CC addition to hybridizing to the site of interest, are capable of  
CC introducing a restriction site which is absent in either the wild type  
CC sequence or polymorphic variants. Restriction enzyme cleavage analysis  
CC can then be used to indicate the presence or absence of the variant. The  
CC methods are used to establish, before treatment with a drug, whether the  
CC drug will be effectively metabolized by the patient, to identify  
CC compounds and transcription factors that can bind to a DNA sequence  
CC encoding CYP3A5, diagnosing susceptibility to a disease which is caused  
CC by toxins or procarcinogens metabolized by CYP3A5 and for identifying  
CC mutagenic effects of a compound

```
XX Sequence 19 BP; 6 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
SQ Query Match 9.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1655 AGCACGAGCTCACA 1659
Db ||||| ||||| |||
5 AGCACGAGCTGACA 19

RESULT 113
AAH58085/c
ID AAH58085 standard; DNA; 19 BP.
XX AC AAH58085;
XX DT 10-SEP-2001 (first entry)
XX DE Cell-cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:509.
XX KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulneryary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisklicking; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX OS Homo sapiens.
XX SY Synthetic.
XX PN WO200130362-A2.
XX PD 03-MAY-2001.
XX PF 26-OCT-2000; 2000WO-US029500.
XX PR 26-OCT-1999; 99US-0161532P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Robbins JM, Tritz R;
XX WPI; 2001-300427/31.
XX PT Treating proliferative skin or eye diseases and scarring, using ribozymes
XX that cleave RNA encoding cytokines involved in inflammation, matrix
XX metalloproteinases, growth factors and cell-cycle dependent kinases.
XX Example 1; Page 109; 408pp; English.
XX The present invention describes a method for treating a proliferative
XX skin or eye disease and scarring. The method involves administering a
XX ribozyme (I) which cleaves RNA encoding a cytokine involved in
XX inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
XX dependent kinase, growth factor or a reductase, or administering a
XX nucleic acid molecule (II) comprising a promoter operably linked to a
XX nucleic acid segment encoding (I). (I) can have antipsoriatic,
XX dermatological, cytostatic, antiseborrheic, antidiabetic, antisklicking,
XX ophthalmological, vulneryary, keratolytic and virucide activities, and
XX cleaves RNA encoding cytokine involved in inflammation. (I) can be used
XX in gene therapy. (I) and (II) are useful for treating proliferative skin
XX diseases such as psoriasis, atopic dermatitis, actinic keratosis,
XX squamous or basal cell carcinoma and viral or seborrheic wart. They can
XX also be used for treating proliferative eye diseases such as diabetic
XX retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
XX prematurity and retinal detachment, and for treating and preventing
XX scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
```

```
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 5 A; 3 C; 9 G; 2 T; 0 U; 0 Other;
Query Match 9.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 GTCCTCAACTCTCTCC 1749
Db ||||| ||||| |||
16 GTCCTCGACTCTCTCC 2

RESULT 114
ABL43426/c
ID ABL43426 standard; DNA; 19 BP.
XX AC ABL43426;
XX DT 11-APR-2002 (first entry)
XX DE Human chromosome lp36-35 PCR primer SEQ ID NO:470.
XX KW Human; chromosome lp36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX OS Homo sapiens.
XX PN JF2001321190-A.
XX PD 20-NOV-2001.
XX PF 12-MAR-2001; 2001JP-00069285.
XX PR 10-MAR-2000; 2000JP-00066716.
XX PA (RIKA ) RIKAGAKU KENKYUSHO.
XX PA (GENO-) GENOTEX YG.
XX WPI; 2002-144136/19.
XX DR Arraying genome clones.
XX PT Claim 4; Page 14; 528pp; Japanese.
XX PS
XX CC The present invention describes a method of arraying genome clones. The
XX method comprises: (a) clones of the genomic libraries contained in
XX multiwell plates numbered for discrimination are mixed in each of the
XX multiwell plates; (b) a primer designed based on the chromosome marker
XX sequence is added to the mixture to carry out an amplification reaction;
XX (c) a signal corresponding to the marker is detected from the resultant
XX amplified product to specify the discrimination Nos. of the multiwell
XX plates containing the clones having said marker sequence; (d) the order
XX of the markers is changed so that the same discrimination Nos. succeed to
XX the maximum in the specified discrimination Nos. to array the multiwell
XX plates; (e) the clones in the multiwell plates of the specified
XX discrimination Nos. are mixed respectively in each wells of longitudinal
XX and lateral directions; (f) the mixed clones are cultured and the
XX resultant cultures are amplified by using the above primer; (g) signals
XX are detected from the amplified products; (h) the clones in the multiwell
XX plates are specified from the detected result; and (i) the clones are
XX reconstituted as the positions on the chromosome and arrayed. The
XX microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX PCR primers for human chromosome lp36-35 DNA, and ABL45323 to ABL45634
XX represent PCR primers for human chromosome 21q22.1, which are
XX specifically claimed for use in the present invention
XX
SQ Sequence 19 BP; 1 A; 6 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 5.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1644 AGCAGAGGCGAAGCA 1658  
 Db 18 AGCAGAGGCGATGCA 4

RESULT 115  
 ABL43434/c  
 ID ABL43434 standard; DNA; 19 BP.  
 XX AC ABL43434;  
 XX AC ABL43434;  
 XX AC ABL43434;  
 DT 11-APR-2002 (first entry)  
 XX Human chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;  
 DE Human chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;  
 XX PCR primer; ss.  
 KW Homo sapiens.  
 XX JP2001321190-A.  
 XX 20-NOV-2001.  
 XX 12-MAR-2001; 2001JP-00068285.  
 XX 10-MAR-2000; 2000JP-00066716.  
 XX (RIKA) RIKAGAKU KENKYUSHO.  
 XX (GENO-) GENOTEX YG.  
 XX WPI; 2002-144136/19.  
 XX Arraying genome clones.  
 PT Claim 4; Page 14; 528pp; Japanese.  
 PS The present invention describes a method of arraying genome clones. The  
 XX method comprises: (a) clones of the genomic libraries contained in  
 CC multiwell plates numbered for discrimination are mixed in each of the  
 CC multiwell plates; (b) a primer designed based on the chromosome marker  
 CC sequence is added to the mixture to carry out an amplification reaction;  
 CC (c) a signal corresponding to the marker is detected from the resultant  
 CC amplified product to specify the discrimination Nos. of the multiwell  
 CC plates containing the clones having said marker sequence; (d) the order  
 CC of the markers is changed so that the same discrimination Nos. succeed to  
 CC the maximum in the specified discrimination Nos. to array the multiwell  
 CC plates; (e) the clones in the multiwell plates of the specified  
 CC discrimination Nos. are mixed respectively in each wells of longitudinal  
 CC and lateral directions; (f) the mixed clones are cultured and the  
 CC resultant cultures are amplified by using the above primer; (g) signals  
 CC plates are detected from the amplified products; (h) the clones in the multiwell  
 CC plates are specified from the detected result; and (i) the clones are  
 CC reconstituted as the positions on the chromosome and arrayed. The  
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent  
 CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634  
 CC represent PCR primers for human chromosome 21q22.1, which are  
 CC specifically claimed for use in the present invention  
 XX Sequence 19 BP; 1 A; 6 C; 3 G; 9 T; 0 U; 0 Other;  
 SQ Query Match 9.6%; Score 13.4; DB 1; Length 19;  
 Best Local Similarity 93.3%; Pred. No. 2.1e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1644 AGCAGAGGCGAAGCA 1658  
 Db 18 AGCAGAGGCGATGCA 4

RESULT 116  
 AAF60107/c

ID AAF60107 standard; DNA; 20 BP.  
 XX AAF60107;  
 XX 27-APR-2001 (first entry)  
 DT Human ATM gene exon 1a reverse primer.  
 DE Human; ATM; ataxia telangiectasia; mutation detection;  
 XX single-stranded conformation polymorphism; SSCP; electrophoresis;  
 KW PCR primer; ss.  
 XX Homo sapiens.  
 OS WO200107660-A1.  
 XX 01-FEB-2001.  
 XX 21-JUL-2000; 2000WO-US020011.  
 XX 23-JUL-1999; 99US-00360416.  
 XX (REGC) UNIV CALIFORNIA.  
 XX Gatti RA;  
 XX WPI; 2001-168574/17.  
 DR Detecting a mutation or polymorphism in human ataxia telangiectasia gene  
 PT or polyexonic eukaryotic gene, involves using mega-single stranded  
 PT conformation polymorphism analysis.  
 XX Claim 7; Page 51; 118pp; English.  
 PS The present sequence is one of a number of primers used in a method for  
 XX detecting a mutation or a polymorphism in the human ATM gene, which is  
 CC associated with the disease ataxia telangiectasia, or a polyexonic  
 CC eukaryotic gene of at least 4 kb. The method uses an improved version of  
 CC single-stranded conformation polymorphism (SSCP) electrophoresis that  
 CC allows electrophoresis of two or three amplified segments in a single  
 CC lane. The method is useful for screening large, complex polyexonic  
 CC eukaryotic genes such as the ATM gene for mutations and polymorphisms.  
 CC The new mutations and polymorphisms in the ATM gene are useful for  
 CC performing more accurate screening of human DNA samples for mutations,  
 CC for distinguishing mutations from polymorphisms, and for improving the  
 CC efficiency of automated screening methods. The mega-SSCP method provides  
 CC a screening method of genes for multiple polymorphisms and mutations at  
 CC once. The method is particularly suitable for large, polyexonic,  
 CC eukaryotic genes, having mutations and polymorphisms at many points and  
 CC not merely at one or a few hot spots. Note: the SEQ ID assigned to this  
 CC sequence in the disclosure and claims of the the specification is one  
 CC number lower than the number given in the sequence listing  
 XX Sequence 20 BP; 7 A; 1 C; 11 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 9.6%; Score 13.4; DB 1; Length 20;  
 Best Local Similarity 93.3%; Pred. No. 2.2e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1742 ACTCTCCCTATCCT 1756  
 Db 15 ACTCTCCCTCTCCT 1

RESULT 117  
 AAF86771  
 ID AAF86771 standard; DNA; 20 BP.  
 XX AAF86771;  
 XX 25-JUL-2001 (first entry)  
 DT Human cytohesin-2 antisense oligonucleotide, SEQ ID NO:84.  
 XX

XX Human cytohesin-2; PSCD2; ARNO for ARF nucleotide binding site opener;  
 KW mSec7; ARF exchange factor; cytosolic adapter protein;  
 KW guanine nucleotide exchange factor; ADP ribosylation factor; ARF1; ARF3;  
 KW ARF6; actin cytoskeleton regulation; expression inhibition;  
 KW atherosclerosis; allograft rejection; hyperproliferative disorder;  
 KW cancer; tumour; phosphorothioate; antisense oligonucleotide; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate linkages"  
 FT modified\_base 1..5  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE  
 FT cytosines are 5-methylcytosine"  
 FT modified\_base 16..20  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE  
 FT cytosines are 5-methylcytosine"  
 XX  
 XX WO200130361-A1.  
 XX  
 XX 03-MAY-2001.  
 XX  
 XX 20-OCT-2000; 2000WO-US029088.  
 XX  
 XX 27-OCT-1999; 99US-00428583.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 XX Bennett CF, Cowsert LM;  
 XX WPI; 2001-335680/35.  
 XX  
 XX New antisense compounds modulating expression of human cytohesin-2 useful  
 PT for diagnosis, prophylaxis and treatment of diseases associated with  
 PT expression of cytohesin-2, e.g. cancer, atherosclerosis, allograft  
 PT rejection.  
 XX  
 XX Claim 3; Page 80; 104pp; English.  
 XX  
 CC The invention relates to antisense oligonucleotides targetted to the  
 CC human cytohesin-2 gene, which inhibit its expression. A series of  
 CC oligonucleotides (AAR66697-AAR66776) were designed to target different  
 CC regions of the human cytohesin-2 RNA, and were analysed for their effect  
 CC on cytohesin-2 mRNA levels by quantitative real-time PCR. Cytohesin-2 is  
 CC a member of a small family of cytosolic adapter proteins which function  
 CC as guanine nucleotide exchange factors for ADP ribosylation factors  
 CC (ARFs), small monomeric G-proteins which regulate critical vesicular  
 CC traffic pathways. Cytohesin-2 (also known as PSCD2, ARNO for ARF  
 CC nucleotide binding site opener, mSec7, and ARF exchange factor) is  
 CC localised to the plasma membrane and promotes guanine nucleotide exchange  
 CC on ARF1, ARF3 and ARF6, the latter of which regulates the assembly of the  
 CC actin cytoskeleton. Through its interaction with ARF6, and in conjunction  
 CC with protein kinase C, cytohesin-2 functions as a critical link between  
 CC cell surface receptors and the actin cytoskeleton. The oligonucleotides  
 CC of the invention are useful for diagnosis, prevention and treatment of  
 CC conditions associated with cytohesin-2 expression, such as  
 CC atherosclerosis, allograft rejection and hyperproliferative disorders,  
 CC especially cancer  
 XX  
 XX Sequence 20 BP; 0 A; 8 C; 5 G; 7 T; 0 U; 0 Other;  
 Query Match 9.6%; Score 13.4; DB 1; Length 20;  
 Best Local Similarity 93.3%; Pred. No. 2.2e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1685 TCTCTCCAGCGTGG 1699  
 |||||  
 Db 5 TCTCTCTCGGTGG 19  
 |||||  
 RESULT 118  
 AAD52270  
 ID AAD52270 standard, DNA; 20 BP.  
 XX  
 XX AAD52270;  
 AC  
 XX 02-MAY-2003 (first entry)  
 DT  
 XX Human IFNGR2 antisense oligonucleotide, ISIS #142748.  
 DE  
 XX Antisense; interferon gamma receptor 2; autoimmune disorder; cancer;  
 KW autoimmune thyroiditis; autoimmune insulinitis; multiple sclerosis;  
 KW diabetes; autoimmune arthritis; Crohn's disease; apoptosis; IFNGR2;  
 KW gene therapy; prophylaxis; human; phosphorothioate; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone; All cytidine residues  
 FT are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethyl nucleotides"  
 FT modified\_base 16..20  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethyl nucleotides"  
 XX  
 XX WO200288163-A1.  
 XX  
 XX 07-NOV-2002.  
 XX  
 XX 16-APR-2002; 2002WO-US012007.  
 XX  
 XX 26-APR-2001; 2001US-00843377.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 XX Bennett CF, Watt AT;  
 XX WPI; 2003-156688/15.  
 XX  
 XX New antisense oligonucleotides for modulating Interferon gamma receptor  
 PT 2, particularly useful for treating autoimmune disorders (e.g. multiple  
 PT sclerosis or Crohn's disease), cancers or diseases caused by aberrant  
 PT apoptosis.  
 XX  
 XX Claim 3; Page 85; 127pp; English.  
 XX  
 CC The invention relates to antisense compounds, composition and methods for  
 CC modulating the expression of human interferon gamma receptor 2 (IFNGR2).  
 CC The compositions comprise antisense compounds targetted to nucleic acids  
 CC encoding IFNGR2. Antisense compounds of the invention are useful for  
 CC treating diseases or conditions associated with IFNGR2, e.g. autoimmune  
 CC disorder (e.g. autoimmune thyroiditis, diabetes, multiple sclerosis,  
 CC autoimmune arthritis, autoimmune insulinitis or Crohn's disease), cancer,  
 CC or a disease/disorder caused by aberrant apoptosis. They are also useful  
 CC for diagnostics, therapeutics, prophylaxis or as research reagents or  
 CC kits. The invention is useful in gene therapy. The present sequence is an  
 CC antisense oligonucleotide targetted to human IFNGR2 DNA  
 XX  
 XX Sequence 20 BP; 4 A; 9 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 9.6%; Score 13.4; DB 1; Length 20;  
 Best Local Similarity 93.3%; Pred. No. 2.2e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 ATTGGCTCCCACTC 1745  
 DB 3 ACTGGCTCCCACTC 17

RESULT 119  
 AAT60161/c  
 ID AAT60161 standard; DNA; 18 BP.  
 AC AAT60161;  
 XX  
 XX 01-DEC-1997 (first entry)  
 DT  
 DE Collagen gene promoter region binding oligomer Oligo 158 APS.  
 DE  
 KW Triplex; inhibition; collagen gene; promoter; pathological fibrosis;  
 KW myocardial fibrosis; hypertensive heart disease; atherosclerosis;  
 KW restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;  
 KW hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT misc\_feature 1..18  
 FT /\*tag= a  
 FT /note= "Phosphorothioate linkages"  
 FT  
 PN W09710254-A1.  
 XX  
 XX 20-MAR-1997.  
 PD  
 XX 12-SEP-1996; 96WO-US014640.  
 XX  
 XX 15-SEP-1995; 95US-00528836.  
 PR 11-SEP-1996; 96US-00712357.  
 XX  
 XX (GUNT/) GUNTAKA R V.  
 PA  
 XX Guntaka RV, Weber KT, Kovacs A, Kandala J;  
 PI WPI; 1997-202172/18.  
 XX  
 XX Triplex forming oligomer binds to collagen gene promoter region - used to  
 PT impede pathological fibrosis etc.  
 XX  
 XX Claim 18; Page 36; 52pp; English.  
 PS  
 XX An oligomer has been produced which is capable of inhibiting expression  
 CC of a collagen gene. The present sequence represents a specifically  
 CC claimed oligomer Oligo 158 APS, which binds to the polypurine-  
 CC polypyrimidine region of the rat alpha1(I) collagen gene promoter region.  
 CC The oligomer may be used to impede pathological fibrosis which is  
 CC associated with myocardial fibrosis in hypertensive heart diseases,  
 CC atherosclerosis, restenosis, liver cirrhosis, lung fibrosis, and skin  
 CC fibrosis found in scleroderma, in hypertrophic scars and in skin  
 CC following burn injury. The oligomer inhibits expression of a collagen  
 CC gene after insertion into a cell by causing an intracellular reaction  
 CC which inhibits gene expression. The oligomer is preferably a triplex  
 CC forming oligomer (TFO) which is targeted to a 30-mer polypurine  
 CC oligonucleotide corresponding to the noncoding strand of the promoter  
 CC between -170 and -140. This section was chosen due to its binding  
 CC stability at physiological pH  
 XX  
 XX Sequence 18 BP; 6 A; 0 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 9.5%; Score 13.2; DB 1; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 CTCCCAACCTCTCCCTAT 1753  
 DB 18 CTCGCCCTCTCTCCCTTT 1

RESULT 120  
 AAT94803/c  
 ID AAT94803 standard; DNA; 18 BP.  
 XX  
 AC AAT94803;  
 XX  
 XX 19-FEB-1998 (first entry)  
 DT  
 DE Human leukocyte antigen class I gene URSTO probe 531-548.  
 XX  
 KW Human leukocyte antigen; HLA; probe; tissue transplantation; MHC gene;  
 KW major histocompatibility complex; paternity test; forensic medicine;  
 KW haematological malignancy; inherited disorder; adoptive immunotherapy;  
 KW identification; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX W09720197-A2.  
 PN  
 XX 05-JUN-1997.  
 PD  
 XX 29-NOV-1996; 96WO-GB002959.  
 PF  
 XX 29-NOV-1995; 95GB-00024381.  
 PR  
 XX (NOLA-) NOLAN BONE MARROW TRUST ANTHONY.  
 PA  
 XX Arguello R, Avakian H, Madrigal A;  
 PI WPI; 1997-310717/28.  
 XX  
 XX Identifying unknown allele(s) of a polyallelic gene using panel of  
 PT probes each recognising a sequence motif present in some allele(s) -  
 PT useful for donor matching in tissue transplantation.  
 XX  
 XX Claim 5; Page 19; 64pp; English.  
 PS  
 XX A novel method has been developed for identifying an unknown allele of a  
 CC polyallelic gene. The method involves: (a) contacting the unknown allele  
 CC with a panel of probes, each of which recognises a sequence motif that is  
 CC present in some alleles of the polyallelic gene but not in others; (b)  
 CC observing which probes recognise the unknown allele so as to obtain a  
 CC fingerprint of the unknown allele; and (c) comparing the fingerprint with  
 CC fingerprints of known alleles. The present sequence represents a  
 CC specifically claimed probe for use in the method where the polyallelic  
 CC gene is a human leukocyte antigen class I gene. The method can be used  
 CC for genes such as mammalian MHC genes, specifically the HLA class I and  
 CC II genes, the T cell receptor genes in mammals, TAP, LMP, ras,  
 CC nonclassical HLA class I genes, human complement factor genes C4 and C2,  
 CC Bf in the HLA complex, and genes located in mitochondrial DNA, bacterial  
 CC chromosomes and viral DNA. The method is particularly useful for matching  
 CC the alleles of the HLA genes in a prospective donor and a prospective  
 CC recipient in tissue or organ transplantations. The method can also be  
 CC used in paternity testing, in forensic medicine, as a follow up technique  
 CC in treatment of haematological malignancies or inherited disorders, in  
 CC adoptive immunotherapy, and in identification of bacteria and viruses.  
 CC The method can provide for the identification of alleles of the  
 CC polyallelic genes using a limited number of selected recurring motif  
 CC probes  
 XX  
 XX Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 9.5%; Score 13.2; DB 1; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1732 TTGGCTCCCACTCTCTCC 1749





```
PR 29-MAR-1999; 99US-00280409.
XX
XX (ISIS-) ISIS PHARM INC.
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Cowsett LM, Bennett CF, O'malley BW;
XX WPI; 2000-586211/55.
XX
XX Antisense compounds targeted to steroid receptor RNA activator useful for
PT diagnosis, prophylaxis and treatment of diseases associated with the
PT steroid activator, such as infection, inflammation or tumor formation.
XX
XX Claim 3; Col 41; 47pp; English.
XX
XX The present sequence is one of a large number of antisense
CC oligonucleotides which is directed against one of four human steroid
CC receptor RNA activator (SRA) nucleic acid sequences. Two series of
CC antisense oligonucleotides were synthesised. The first series comprised 8
CC -30 oligodeoxynucleotides with a phosphorothioate backbone. The second
CC series comprised chimeric oligonucleotides composed of a central gap
CC region, consisting of ten 2'-deoxynucleotides, which was flanked on both
CC sides by four-nucleotide wings. The wings were composed of 2'-
CC methoxyethyl (2'-MOE) nucleotides. Both series contained the same
CC nucleotide sequences. The antisense compounds are useful for research,
CC diagnosis, treatment and prophylaxis to prevent or delay infection,
CC inflammation or tumour formation. Therapeutically the oligonucleotides
CC are highly safe and are effectively administered to humans
XX
XX Sequence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 9.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1668 CAGCTGGAACCCCTGGTGT 1685
Db 1 CTGCTGGAAGCCTGGTAT 18
RESULT 124
AAD20365/c
ID AAD20365 standard; DNA; 18 BP.
AC AAD20365;
DT
DT 03-JAN-2002 (first entry)
DE
DE Antisense oligo, ISIS# 29889, targeted to human SRC-1 DNA.
XX
XX Human; antisense; steroid receptor coactivator-1; SRC-1; F-SRC-1; NcoA-1;
KW diagnostic; therapeutic; prophylaxis; infection; inflammation;
KW cytostatic; tumour formation; antiinflammatory; antibacterial;
KW phosphorothioate; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..4
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 1
FT /*tag= c
FT /mod_base= m5c
FT modified_base 7
FT /*tag= d
FT /mod_base= m5c
```

```
FT modified_base 8
FT /*tag= e
FT /mod_base= m5c
FT modified_base 10
FT /*tag= f
FT /mod_base= m5c
FT modified_base 11
FT /*tag= g
FT /mod_base= m5c
FT modified_base 13
FT /*tag= h
FT /mod_base= m5c
FT modified_base 15..18
FT /*tag= j
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 15
FT /*tag= i
FT /mod_base= m5c
XX US6294382-B1.
XX 25-SEP-2001.
XX 27-NOV-2000; 2000US-00723534.
XX 27-NOV-2000; 2000US-00723534.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Cowsett LM;
XX WPI; 2001-638016/73.
XX
XX New antisense oligonucleotides for inhibiting the expression of human
PT steroid receptor coactivator-1, particularly useful for preventing,
PT delaying or treating infection, inflammation or tumor formation.
XX
XX Claim 3; Col 42; 36pp; English.
XX
XX The present invention relates to an antisense compound of up to 30
CC nucleobases in length, which specifically hybridises with and inhibits
CC the expression of human steroid receptor coactivator-1 (SRC-1) (also
CC known as F-SRC-1 and NcoA-1) gene. The antisense compounds are useful for
CC diagnostics, therapeutics, prophylaxis, or as research reagents or kits.
CC The antisense oligonucleotides are useful for treating an animal,
CC particularly a human, suspected of having or being prone to a disease or
CC condition associated with the expression of SRC-1. In particular, the
CC antisense oligonucleotides are useful for preventing, delaying or
CC treating infection, inflammation or tumour formation. The present
CC sequence is an antisense oligonucleotide, ISIS# 29889, targeted to human
CC SRC-1 DNA
XX
XX Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 9.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1691 CCAGCGTGGTGAAGTTG 1708
Db 18 CCAGTGTGGTGAATTTCG 1
RESULT 125
ABA83557/c
ID ABA83557 standard; DNA; 18 BP.
XX
XX ABA83557;
AC
XX
XX 08-FEB-2002 (first entry)
XX
XX Mouse MP-1 antisense oligonucleotide SEQ ID NO 96.
DE
```

```
XX Human; mouse; rat; antisense gene therapy; MP-1; MAP kinase Partner 1;
KW antinflammatory; cyostatic; antimicrobial; infection; tumour;
KW phosphorothioate; ss.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..18
FT /tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone linkage, all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..4
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-MOE wings"
FT modified_base 15..18
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-MOE wings"
XX
XX US6306606-B1.
XX
XX 23-OCT-2001.
XX
XX 22-NOV-2000; 2000US-00721822.
XX
XX 22-NOV-2000; 2000US-00721822.
XX
XX (ISIS-) ISIS PHARM INC.
XX (UYVI-) UNIV VIRGINIA.
XX
XX Weber MJ, Wyatt J, Cowsest LM;
XX
XX WPI; 2002-040199/05.
XX
XX New antisense oligonucleotides for modulating the expression of MP-1 (MAP
XX kinase partner 1), for preventing, delaying or treating infection,
XX inflammation or tumor formation, especially in humans.
XX
XX Example 17; Col 43-44; 47pp; English.
XX
XX The invention relates to an antisense compound (ABA83459-ABA83576) which
XX is up to 30 nucleobases in length and that inhibits the expression of MP-
XX 1 (MAP kinase Partner 1) in cells or tissues comprising contacting the
XX cells or tissues in vitro with the antisense compound so that expression
XX of MP-1 is inhibited. The antisense compounds have potential
XX antinflammatory, cyostatic and antimicrobial activity. The antisense
XX compounds are useful for diagnostics, therapeutics, prophylaxis or as
XX research reagents or kits. The antisense oligonucleotides are useful in
XX gene therapy for treating an animal, particularly a human, suspected of
XX having or being prone to a disease or condition associated with the
XX expression of MP-1. In particular, the antisense oligonucleotides are
XX useful for preventing, delaying or treating infection, inflammation or
XX tumour formation. The present sequence is that of a mouse MP-1 antisense
XX oligonucleotide, comprising a chimeric oligonucleotide gapmer 18
XX nucleotides in length, composed of a central gap region of ten 2'-
XX deoxynucleotides flanked by four nucleotide 2'-MOE wings
XX
XX Sequence 18 BP; 3 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 9.5%; Score 13.2; DB 1; Length 18;
XX Best Local Similarity 83.3%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1664 CTCACAGCTGGACCCCTG 1681
XX
XX 18 CTCACCTGCAGCACCCCTG 1
XX
XX RESULT 126
XX
XX Query Match 9.5%; Score 13.2; DB 1; Length 18;
XX Best Local Similarity 83.3%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1664 CTCACAGCTGGACCCCTG 1681
XX
XX 18 CTCACCTGCAGCACCCCTG 1
XX
XX RESULT 126
XX
XX Human SRC-1 antisense oligonucleotide, ISIS 29849.
XX
```

```
ABL45037/c
ID ABL45037 standard; DNA; 18 BP.
XX
AC ABL45037;
XX
XX 11-APR-2002 (first entry)
XX
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:2081.
XX
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
XX PCR primer; ss.
XX
XX Homo sapiens.
XX
XX JP2001321190-A.
XX
XX 20-NOV-2001.
XX
XX 12-MAR-2001; 2001JP-00068285.
XX
XX 10-MAR-2000; 2000JP-00066716.
XX
XX (RIKA ) RIKAGAKU KENKYUSHO.
XX (GENO-) GENOTEX YG.
XX
XX WPI; 2002-144136/19.
XX
XX Arraying genome clones.
XX
XX Claim 4; Page 45; 528pp; Japanese.
XX
XX The present invention describes a method of arraying genome clones. The
XX method comprises: (a) clones of the genomic libraries contained in
XX multiwell plates numbered for discrimination are mixed in each of the
XX multiwell plates; (b) a primer designed based on the chromosome marker
XX sequence is added to the mixture to carry out an amplification reaction;
XX (c) a signal corresponding to the marker is detected from the resultant
XX amplified product to specify the discrimination Nos. of the multiwell
XX plates containing the clones having said marker sequence; (d) the order
XX of the markers is changed so that the same discrimination Nos. succeed to
XX the maximum in the specified discrimination Nos. to array the multiwell
XX plates; (e) the clones in the multiwell plates of the specified
XX discrimination Nos. are mixed respectively in each wells of longitudinal
XX and lateral directions; (f) the mixed clones are cultured and the
XX resultant cultures are amplified by using the above primer; (g) signals
XX are detected from the amplified products; (h) the clones in the multiwell
XX plates are specified from the detected result; and (i) the clones are
XX reconstituted as the positions on the chromosome and arrayed. The
XX microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
XX represent PCR primers for human chromosome 21q22.1, which are
XX specifically claimed for use in the present invention
XX
XX Sequence 18 BP; 6 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 9.5%; Score 13.2; DB 1; Length 18;
XX Best Local Similarity 83.3%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1720 CGGAGATGGAGATTGGCT 1737
XX
XX 18 CTGAGATGGAGTTTGGCT 1
XX
XX RESULT 127
XX AAD41916/c
XX ID AAD41916 standard; DNA; 18 BP.
XX
XX AAD41916;
XX
XX 30-OCT-2002 (first entry)
XX
XX Human SRC-1 antisense oligonucleotide, ISIS 29849.
XX
```

```
XX Human; steroid receptor coactivator-1; SRC-1; antisense compound;
KW diagnostic; therapeutic; prophylaxis; antisense therapy; antisense;
KW phosphorothioate backbone; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..4
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 1
FT /*tag= d
FT /mod_base= m5c
FT modified_base 7
FT /*tag= e
FT /mod_base= m5c
FT modified_base 8
FT /*tag= f
FT /mod_base= m5c
FT modified_base 10
FT /*tag= g
FT /mod_base= m5c
FT modified_base 11
FT /*tag= h
FT /mod_base= m5c
FT modified_base 13
FT /*tag= i
FT /mod_base= m5c
FT modified_base 15..18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 15
FT /*tag= j
FT /mod_base= m5c
XX
XX WO200244325-A2.
XX
XX 06-JUN-2002.
XX
XX 26-NOV-2001; 2001WO-US044179.
XX
XX 27-NOV-2000; 2000US-00723379.
XX
XX (ISIS-) ISIS PHARM INC.
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX O'malley BW, Bennett CF, Cowsert LM;
XX
XX WPI; 2002-537447/57.
XX
XX Novel antisense compound targeted to nucleic acid molecules encoding
XX human steroid receptor coactivator-1 (SRC-1), useful for inhibiting
XX expression of SRC-1 in human cells or tissues.
XX
XX Example 15; Page 79; 103pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
XX for modulating the expression of human steroid receptor coactivator-1
XX (SRC-1). The compositions comprise antisense oligonucleotides targeted
XX to nucleic acids encoding SRC-1. The antisense compound is useful for
XX inhibiting the expression of SRC-1 in human cells or tissues. It is also
XX useful for treating a human having a disease or condition associated with
XX SRC-1, by inhibiting expression of SRC-1. It is also useful for
XX diagnostics, therapeutics, prophylaxis and as research reagents and kits.
XX It is also used in antisense therapy. The present sequence is an
CC antisense oligonucleotide targeted to human SRC-1 DNA. This sequence is
CC used in the exemplification of the invention
XX
XX Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 9.5%; Score 13.2; DB 1; Length 18;
XX Best Local Similarity 83.3%; Pred. No. 2.1e+02;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1691 CCAGCGTGTGGAGTTG 1708
Db 18 CCAGTGTGTGGAAATTCG 1
XX
RESULT 128
AAQ91454/c
ID AAQ91454 standard; DNA; 19 BP.
XX
XX AAQ91454;
AC
XX
XX 25-MAR-2003 (revised)
DT 30-AUG-1995 (first entry)
XX
XX Dysprosium (III) texaphyrin (DyTx) DNA conjugate.
XX
XX Dysprosium (III) texaphyrin (DyTx) DNA conjugate; liver disease;
XX targeted intracellular mRNA hydrolysis; gene expression inhibition;
XX hormone regulation; hydrolysis reagents; alkyl phosphate esters;
XX detoxification; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1
XX /*tag= a
XX /mod_base= OTHER
XX /note= "DyTx-NH(CH2)6-PO4-adenine"
XX
XX WO9429316-A2.
XX
XX 22-DEC-1994.
XX
XX 09-JUN-1994; 94WO-US006284.
XX
XX 09-JUN-1993; 93US-00075123.
XX 14-APR-1994; 94US-00227370.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX (PHAR-) PHARMACYCLICS INC.
XX
XX Sessler JL, Ross KL, Wright M, Hemmi GW, Dow WC, Smith DA;
XX Kral VA, Iverson B, Mody T, Miller RA, Magda D;
XX
XX WPI; 1995-036382/05.
XX
XX Texaphyrin metal complex mediated ester hydrolysis - esp. useful for
XX targeted intracellular hydrolysis of mRNA and for inhibiting gene
XX expression.
XX
XX Disclosure; Fig 21; 125pp; English.
XX
XX AAQ91451-Q91457 are texaphyrin lanthanide metal DNA conjugates, which are
XX esp. useful for the targeted intracellular hydrolysis of mRNA; inhibiting
XX gene expression. They may also be used for the treatment of liver disease,
XX as hormone regulation agents and as hydrolysis reagents for the
XX detoxification of alkyl phosphate esters. (Updated on 25-MAR-2003 to
XX correct FN field.)
XX
XX Sequence 19 BP; 2 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 9.5%; Score 13.2; DB 1; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 2.3e+02;
XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

OY 1655 AGCACCAGGCTCACAGCT 1672  
 DB 18 AACACCCGGCTCACAGAT 1

RESULT 129  
 AAV07302/c

ID AAV07302 standard; DNA; 19 BP.  
 AC AAV07302;  
 DT 14-AUG-1998 (first entry)  
 DE Metallotexaphyrin-oligonucleotide conjugate #16.  
 KW Metallotexaphyrin; dysprosium; europium; conjugate; RNase H;  
 KW antisense therapy; ss.  
 OS Synthetic.

Key Location/Qualifiers  
 modified\_base 1 /\*tag= a  
 /mod base  
 /note= "DyTxNH-(CH2)6-PO4-adenine, where DyTx is  
 dysprosium (III) texaphyrin"

US5763172-A.  
 XX 09-JUN-1998.  
 XX 07-JUN-1995; 95US-00486962.  
 PR 21-JAN-1992; 92US-00822964.  
 PR 09-JUN-1993; 93US-00075123.  
 PR 14-APR-1994; 94US-00227370.  
 PR 09-JUN-1994; 94WO-US006284.  
 PR 26-MAY-1995; 95US-00452261.  
 PR 07-JUN-1995; 95US-00485581.  
 XX (PHAR-) PHARMACYCLICS INC.  
 XX (TEXA ) UNIV TEXAS SYSTEM.

Sessler JL, Wright M, Miller RA, Dow WC, Magda D;  
 WPI; 1998-347306/30.

Enhancing therapeutic activity of oligo-nucleotides in cells - using  
 conjugate comprising metallotexaphyrin, which hydrolyses phosphate ester  
 bonds of RNA, and oligo-nucleotide, which binds to targetted RNA.

Example 6; Fig 5; 34pp; English.

The invention relates to a method of enhancing the therapeutic activity  
 of oligonucleotides in cells. It comprises contacting a targeted  
 intracellular RNA in a cell with a metallotexaphyrin-oligonucleotide  
 conjugate. The contact is carried out under physiological conditions for  
 a time sufficient to hydrolyse the phosphate ester bond of the targeted  
 RNA. The metallotexaphyrin of the conjugate has catalytic activity for  
 phosphate ester bond hydrolysis. The oligonucleotide of the conjugate has  
 complementary binding affinity to the targeted RNA. The conjugate may be  
 used in antisense therapies for treating, e.g. cancer, viral infections,  
 autoimmune diseases and restenosis. The conjugate may also be used as  
 hydrolysis reagents for the detoxification of di- and trialkyl phosphate  
 esters, which are used in solvents, insecticides and chemical nerve  
 gases. The metallotexaphyrin complex enhances the therapeutic activity of  
 the oligonucleotide, not only by facilitating cellular uptake of the  
 oligonucleotide but also by hydrolysing target RNA within the cell,  
 independent of RNase H. Attachment to the complex may also cause the  
 oligonucleotide to take on some of the pharmacodynamic and biodistribution  
 properties of the texaphyrin, such as selective localisation in tumours.  
 The present sequence represents a metallo- texaphyrin-oligonucleotide

CC conjugate  
 XX  
 SQ Sequence 19 BP; 2 A; 3 C; 8 G; 6 T; 0 U; 0 Other;  
 Query Match 9.5%; Score 13.2; DB 1; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1655 AGCACCAGGCTCACAGCT 1672  
 DB 18 AACACCCGGCTCACAGAT 1

RESULT 130  
 AAC66840  
 ID AAC66840 standard; DNA; 19 BP.  
 XX  
 AC AAC66840;  
 XX 27-FEB-2001 (first entry)  
 DE Human tankyrase II coding sequence PCR primer UTANKII-4A.  
 KW Human; tankyrase II; telomere length; signal transduction; PCR primer;  
 KW ss.  
 OS Homo sapiens.  
 XX WO2000061813-A1.  
 XX 19-OCT-2000.  
 XX 10-APR-2000; 2000WO-US009558.  
 XX 09-APR-1999; 99US-0128577P.  
 XX 13-APR-1999; 99US-0129123P.  
 XX (GERO-) GERON CORP.  
 XX Morin GB, Funk WD, Piatyszek MA;  
 XX WPI; 2000-679503/66.  
 XX Novel mammalian Tankyrase II polypeptide and the polynucleotide encoding  
 the polypeptide useful for modulating or maintaining telomere length,  
 replicative capacity, apoptosis, chromosome packing or gene expression.

Example 4; Page 19; 52pp; English.

The present invention relates to the isolation of the protein and coding  
 sequences of human tankyrase II. This protein is thought to be involved  
 in signal transduction in the cell, and to have binding activity for  
 other telomere-associated proteins. It is possible that it plays a role  
 in the regulation of telomere length, thus affecting the replicative  
 ability of the cell. The protein is useful for ribosylating target  
 proteins, for determining tankyrase II binding activity in a sample, and  
 for modulating telomere length in a cell. The present sequence is a PCR  
 primer used to amplify the tankyrase II coding sequence

XX  
 SQ Sequence 19 BP; 6 A; 3 C; 8 G; 2 T; 0 U; 0 Other;  
 Query Match 9.5%; Score 13.2; DB 1; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1715 GAGTACGAGATGGAGAT 1732  
 DB 1 GAGCAGAGATGGAGAT 18

RESULT 131  
 ABX95438/c  
 ID ABX95438 standard; DNA; 19 BP.

XX AC ABX95438;  
 XX DT 23-JUN-2003 (first entry)  
 XX DE Human connexin 45 (Cx45) 3' RT-PCR primer #2.  
 XX KW Human pancreatic ductal cell line; human papilloma virus; HPV; E6; E7;  
 XX KW gap junctional intracellular communication competent; connexin43;  
 XX KW type-I diabetes; insulin-dependent diabetes;  
 XX KW immortalised human pancreatic ductal epithelial cell line; connexin 45;  
 XX KW Cx45; human pancreatic ductal epithelial clone 7; HPOB6c7; cell therapy;  
 XX KW human; reverse transcriptase PCR; RT-PCR; primer; ss.  
 XX OS Homo sapiens.  
 XX PN US2003003088-A1.  
 XX PD 02-JAN-2003.  
 XX PF 30-APR-2002; 2002US-00135801.  
 XX PR 03-MAY-2001; 2001US-0288473P.  
 XX PA (UNMS ) UNIV MICHIGAN STATE.  
 XX PI Tsao MS, Trosko JE, Madhukar BV, Olson LK, Vancamp L;  
 XX WP1; 2003-370821/35.  
 XX PT New human pancreatic ductal cell line immortalized with human papilloma  
 XX PT virus (HPV) genes E6 and E7, useful for expressing insulin in a mammal to  
 XX PT treat type-I diabetes or insulin-dependent diabetes.  
 XX PS Example 5; Page 11; 42pp; English.  
 XX CC The invention describes a human pancreatic ductal cell line, which is  
 XX CC immortalised with human papilloma virus (HPV) genes E6 and E7, and  
 XX CC capable of expressing insulin. The cells are a gap junctional  
 XX CC intracellular communication competent, and are capable of expressing  
 XX CC connexin43 gap junction protein upon induction by agents stimulating the  
 XX CC production of cyclic AMP. The human pancreatic ductal cell line is useful  
 XX CC for treating type-I diabetes or insulin-dependent diabetes in a mammal.  
 XX CC The cell line is particularly useful for producing or expressing insulin  
 XX CC in mammals. The human pancreatic ductal cell line is also useful in  
 XX CC assays for screening chemical agents that affect cells or production of  
 XX CC insulin, or for making an immortalised human pancreatic ductal epithelial  
 XX CC cell line for use in therapy. This sequence represents a reverse  
 XX CC transcriptase PCR primer used to isolate DNA encoding the human gap  
 XX CC junction gene connexin 45 (Cx45) from the human pancreatic ductal  
 XX CC epithelial clone 7 (HPOB6c7) cell line. Note: This sequence differs from  
 XX CC the sequence given as SEQ ID NO 2 in the sequence listing  
 XX SQ Sequence 19 BP; 4 A; 4 C; 8 G; 3 T; 0 U; 0 Other;  
 Query Match 9.5%; Score 13.2; DB 1; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1733 TGGCTCCCAACTCCTCCC 1750  
 Db 19 TGGCTTCCAAGTCCACCC 2  
 RESULT 132  
 ADE29769/c  
 ID ADE29769 standard; RNA; 19 BP.  
 XX AC ADE29769;  
 XX DT 23-JAN-2004 (first entry)  
 XX DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:391.

XX short interfering nucleic acid; siNA; downregulation; inhibition;  
 KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;  
 KW cytosolic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;  
 KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;  
 KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;  
 KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;  
 KW psoriasis; inflammatory bowel disease; drug screening;  
 KW genetic engineering; pharmacogenomic; gene mapping; ss.  
 XX OS Synthetic.  
 XX PN WO2003072590-A1.  
 XX PD 04-SEP-2003.  
 XX PF 28-JAN-2003; 2003WO-US002510.  
 XX PR 20-FEB-2002; 2002US-0358580P.  
 XX PR 11-MAR-2002; 2002US-0363124P.  
 XX PR 06-JUN-2002; 2002US-0386782P.  
 XX PR 29-AUG-2002; 2002US-0406784P.  
 XX PR 05-SEP-2002; 2002US-0408378P.  
 XX PR 09-SEP-2002; 2002US-0409293P.  
 XX PR 15-JAN-2003; 2003US-0440129P.  
 XX PA (SIRN-) SIRNA THERAPEUTICS INC.  
 XX PI Meswigen J, Beigelman L, Usman N, Haerberli P, Chowrira B;  
 XX WP1; 2003-689980/65.  
 XX PT New short interfering nucleic acid, useful e.g. for treatment and  
 XX PT diagnosis of cancer, downregulates expression of mitogen-activated  
 XX PT protein kinase genes.  
 XX PS Example 3; SEQ ID NO 391; 164pp; English.  
 XX CC The present invention describes a short interfering nucleic acid (siNA)  
 XX CC that downregulates expression of a mitogen-activated protein kinase  
 XX CC (MAPK) genes by RNA interference. Also described: (1) a method for  
 XX CC modulating expression of MAPK genes in cells, tissue explants or  
 XX CC organisms by introduction of siNA; (2) kits for in vitro or in vivo  
 XX CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)  
 XX CC vectors that express siNA and cells containing these vectors. MAPK siNAs  
 XX CC have cytostatic, anorectic, antidiabetic, antinflammatory,  
 XX CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,  
 XX CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK  
 XX CC siNAs can be used to modulate the expression of MAPK genes, in cells,  
 XX CC and in a wide range of tumours, e.g. for treating obesity; diabetes types I  
 XX CC and II; a wide range of tumours, and inflammatory diseases (asthma,  
 XX CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel  
 XX CC disease). They can also be used for drug screening; diagnosis; target  
 XX CC identification and validation; genetic engineering; pharmacogenomics;  
 XX CC studying gene function and gene mapping (e.g. of single-nucleotide  
 XX CC polymorphisms). The present sequence represents a MAPK siNA which is used  
 XX CC in the exemplification of the present invention.  
 XX SQ Sequence 19 BP; 5 A; 7 C; 5 G; 0 T; 2 U; 0 Other;  
 Query Match 9.5%; Score 13.2; DB 1; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1673 GGAACCTCGTGTCTCCT 1690  
 Db 19 GGAAGCGTCTGTCTCCT 2  
 RESULT 133  
 ADE29874  
 ID ADE29874 standard; RNA; 19 BP.  
 XX

AC ADE29874;  
 XX 29-JAN-2004 (first entry)  
 XX Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:496.  
 XX short interfering nucleic acid; siNA; downregulation; inhibition;  
 KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;  
 KW cytosolic; anorectic; antidiabetic; antiinflammatory; antisthmatic;  
 KW immunosuppressive; antibacterial; antiarthritis; antitumor;  
 KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;  
 KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;  
 KW psoriasis; inflammatory bowel disease; drug screening;  
 KW genetic engineering; pharmacogenomic; gene mapping; ss.  
 XX Synthetic.  
 XX WO2003072590-A1.  
 XX 04-SEP-2003.  
 XX 28-JAN-2003; 2003WO-US002510.  
 XX 20-FEB-2002; 2002US-0358580P.  
 XX 11-MAR-2002; 2002US-0363124P.  
 XX 06-JUN-2002; 2002US-0386782P.  
 XX 29-AUG-2002; 2002US-0406784P.  
 XX 05-SEP-2002; 2002US-0408378P.  
 XX 09-SEP-2002; 2002US-0409293P.  
 XX 15-JAN-2003; 2003US-0440129P.  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 XX Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;  
 XX WPI; 2003-689980/55.  
 XX New short interfering nucleic acid, useful e.g. for treatment and  
 PT diagnosis of cancer, downregulates expression of mitogen-activated  
 PT protein kinase genes.  
 XX Example 3; SEQ ID NO 496; 164pp; English.  
 XX The present invention describes a short interfering nucleic acid (siNA)  
 CC that downregulates expression of a mitogen-activated protein kinase  
 CC (MAPK) genes by RNA interference. Also described: (1) a method for  
 CC modulating expression of MAPK genes in cells, tissue explants or  
 CC organisms by introduction of siNA; (2) kits for in vitro or in vivo  
 CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)  
 CC vectors that express siNA and cells containing these vectors. MAPK siNAs  
 CC have cytostatic, anorectic, antidiabetic, antiinflammatory,  
 CC antisthmatic, immunosuppressive, antibacterial, antirheumatic,  
 CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK  
 CC siNAs can be used to modulate the expression of MAPK genes, in cells,  
 CC tissue explants or organisms, e.g. for treating obesity; diabetes types I  
 CC and II; a wide range of tumours, and inflammatory diseases (asthma,  
 CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel  
 CC disease). They can also be used for drug screening; diagnosis; target  
 CC identification and validation; genetic engineering; pharmacogenomics;  
 CC studying gene function and gene mapping (e.g. of single-nucleotide  
 CC polymorphisms). The present sequence represents a MAPK siNA which is used  
 CC in the exemplification of the present invention.  
 XX Sequence 19 BP; 2 A; 5 C; 7 G; 0 T; 5 U; 0 Other;  
 SQ Query Match 9.5%; Score 13.2; DB 1; Length 19;  
 Best Local Similarity 55.6%; Pred. No. 2.3e+02;  
 Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 1673 GGAAACCTGTGTCTCT 1690  
 Db 1 GGAAGCGTGTGTGTCTCT 18

RESULT 134  
 AAQ29803/c  
 ID AAQ29803 standard; DNA; 20 BP.  
 XX AC  
 XX AAQ29803;  
 XX 25-MAR-2003 (revised)  
 DT 19-MAR-1993 (first entry)  
 XX A allele probe VP68.  
 DE G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;  
 KW paternity; forensic; ss.  
 XX Synthetic.  
 XX BP512342-A2.  
 XX 11-NOV-1992.  
 PD 25-APR-1992; 92EP-00107084.  
 XX 07-MAY-1991; 91US-00696793.  
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 PA Saiki RK, Nasarabadi SL;  
 PI WPI; 1992-374679/46.  
 XX Determn. of an individuals genotype at the gamma-globin locus - using  
 PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.  
 XX Disclosure; Page 17; 29pp; English.  
 XX The sequences given in AAQ2987-816 are probes which were used within the  
 CC method of the invention for detecting the presence of a variant sequence  
 CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be  
 CC distinguished from one another by the polymorphic sequence corresponding  
 CC to the HindIII site of the A allele. The sequences of the three alleles  
 CC are given in AAQ29842-44. The methods for determining an individuals  
 CC genotype at the GGG locus with respect to a set of alleles improves the  
 CC discriminatory power of GGG typing methodology compared to previous  
 CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 20 BP; 5 A; 10 C; 2 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 9.5%; Score 13.2; DB 1; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1670 GCTGGAACCTGTGTCT 1687  
 Db 19 GGTGGAACCTGTGTGT 2  
 RESULT 135  
 AAQ80655  
 ID AAQ80655 standard; DNA; 20 BP.  
 XX AC  
 XX AAQ80655;  
 XX 22-AUG-1995 (first entry)  
 DT Primer amplifies part of 5' UTR and VP4/VP2 of enterovirus.  
 DE primer; amplification; PCR; polymerase chain reaction; enterovirus; VP4;  
 KW VP2; 5' UTR; untranslated region; detection; identification; ss.  
 XX Synthetic.  
 XX JF06311900-A.

XX 08-NOV-1994.  
 XX PD  
 XX CC  
 XX PF 28-APR-1993; 93JP-00102254.  
 XX PR 28-APR-1993; 93JP-00102254.  
 XX XX (M1TP ) MITSUBISHI YUKA BCL XK.  
 XX PA (INCU//) INOUE S.  
 XX DR WPI; 1995-027267/04.  
 XX PT Detection and identification of enterovirus - by amplification of part  
 XX PT of 5' -UTR and VP4 and VP2 protein sequences.  
 XX PS Claim 3; Page 2; 10pp; Japanese.  
 XX XX AAQ0654-55 are used to amplify a part of the 5' UTR (untranslated  
 CC region) and DNA encoding VP4 and VP2 proteins of an enterovirus. The  
 CC method can detect enterovirus and identify the serum type simply and  
 CC precisely  
 XX CC  
 XX SQ Sequence 20 BP; 3 A; 2 C; 9 G; 6 T; 0 U; 0 Other;  
 Query Match 9.5%; Score 13.2; DB 1; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1696 GTGGTGAAGTTGGTTA 1713  
 Db 3 GTGGTGAAGTTGCCTGA 20  
 RESULT 136  
 AAT39874/C  
 ID AAT39874 standard; DNA; 20 BP.  
 AC AAT39874;  
 XX 05-DEC-1996 (first entry)  
 XX DE Primer #4 for enterovirus Vp4 coding sequence.  
 XX KW Probe: enterovirus type 71; EV71; Vp4; coxsackie group A virus type 16;  
 XX KW CA16; Vp2; 5' untranslated region; polymerase chain reaction; primer;  
 XX KW amplify; PCR; ss.  
 XX OS Synthetic.  
 XX PN JP08173195-A.  
 XX PD 09-JUL-1996.  
 XX PF 17-OCT-1995; 95JP-00268660.  
 XX PR 28-OCT-1994; 94JP-00265124.  
 XX XX (M1TP ) MITSUBISHI YUKA BCL XK.  
 XX DR WPI; 1996-365607/37.  
 XX XX Differentiation between enterovirus type 71 and coxsackie gp. A virus  
 PT type 16 - by amplifying and probing the 5' non-translated region of Vp4  
 PT and Vp2 proteins.  
 XX PS Example 1; Page 22; 28pp; Japanese.  
 XX CC AAT39871-T39874 represent amplification primers for Vp4 coding sequences,  
 CC used within the scope of the invention. The invention is a method for  
 CC differentiating between enterovirus type 71 (EV71) coxsackie group A  
 CC virus type 16 (CA16) using Vp4 protein coding sequences. In this method,  
 CC part of the 5' untranslated region of the Vp4 and Vp2 proteins from these  
 CC viruses are amplified, and the Vp4 fragment is sequenced. Probes specific

CC for each serum type of EV71 and CA16 (see AAT39837-T39841 for EV71  
 CC probes, and AAT39842-T39847 for CA16 probes) are then designed, and the  
 CC binding ability of the probes with the amplified DNA is analysed. As the  
 CC 5' UTR is a sequence specific to each serum type of enterovirus, this  
 CC method can differentiate EV71 from CA16 with high precision  
 XX XX  
 XX SQ Sequence 20 BP; 6 A; 9 C; 2 G; 3 T; 0 U; 0 Other;  
 Query Match 9.5%; Score 13.2; DB 1; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1696 GTGGTGAAGTTGGTTA 1713  
 Db 18 GTGGTGAAGTTGCCTGA 1

RESULT 137  
 AAV29418/C  
 ID AAV29418 standard; DNA; 20 BP.  
 XX AC AAV29418;  
 XX DT 31-JUL-1998 (first entry)  
 XX DE Calcium ion channel alpha subunit exon 21 specific reverse primer.  
 XX KW Calcium ion channel alpha subunit; human; episodic ataxia type 2;  
 XX KW familial hemiplegic migraine; FHM; EA-2; treatment; diagnosis;  
 XX KW PCR primer; ss.  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 XX PN EP834561-A1.  
 XX PD 08-APR-1998.  
 XX PF 27-SEP-1996; 96EP-00202707.  
 XX PR 27-SEP-1996; 96EP-00202707.  
 XX XX (UYLE-) RIJKSUNIV LEIDEN.  
 XX DR WPI; 1998-195461/18.  
 XX PT New human nucleic acid associated with migraine and episodic ataxia type  
 XX PT 2 - useful for diagnosis and development of, e.g. familial hemiplegic  
 XX PT migraine and episodic ataxia type 2.  
 XX PS Disclosure; Page 9; 157pp; English.

XX This primer is used for the PCR amplification of an exon of the human  
 CC calcium ion channel alpha 1 subunit. The channel is related to familial  
 CC hemiplegic migraine (FHM) and/or episodic ataxia type 2 (EA-2) and is  
 CC derived from, related to or associated with a gene present in humans on  
 CC chromosome 19p13.1-13.2. The encoding nucleic acid can be used to  
 CC localise or identify genes related to episodic neurological disorders,  
 CC specifically migraine, FHM or EA-2, but also epilepsy. It can also be  
 CC used to distinguish between alleles of the corresponding gene. Cells and  
 CC animals containing recombinant expression vectors comprising the nucleic  
 CC acid can be useful in study, development and treatment of migraine, FHM,  
 CC EA-2 and epilepsy. Proteins or peptides encoded by the nucleic acid and  
 CC natural or synthetic antibodies against the proteins can be used to  
 CC diagnose FHM, EA-2, migraine and other neurological conditions associated  
 CC with cation channel dysfunction  
 XX XX

XX SQ Sequence 20 BP; 2 A; 8 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 9.5%; Score 13.2; DB 1; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1689 CTCACGGCTGGTGAAGT 1706  
 Db 20 CACCAGGCTGGCGGAAGT 3

RESULT 138  
 AAX96823  
 ID AAX96823 standard; DNA; 20 BP.  
 AC AAX96823;  
 DT 13-SEP-1999 (first entry)  
 DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.  
 KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;  
 KW neutralising epitope; PCR primer; ss.  
 XX Synthetic.  
 OS Chlamydia pneumoniae.  
 XX WO9927105-A2.  
 PN 03-JUN-1999.  
 PD 20-NOV-1998; 98WO-IB001890.  
 PF 21-NOV-1997; 97PR-00014673.  
 PR 04-NOV-1998; 98US-0107078P.  
 XX (GEST ) GENSET.  
 PA Griffais R;  
 XX WPI; 1999-357842/30.  
 DR Genome sequence of Chlamydia pneumoniae.  
 FT Page 1856; Disclosure; 1912pp; English.  
 PS AAX91991-X97517 represent PCR primers used to amplify open reading frames  
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae  
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as  
 CC pneumonia and bronchitis and is thought to be a contributing factor in  
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema  
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading  
 CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used  
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae  
 CC nucleotides sequences can also be used as immunogenic compositions,  
 CC especially where the vector directs the expression of a neutralising  
 CC epitope of C. pneumoniae  
 XX Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;  
 SQ

Query Match 9.5%; Score 13.2; DB 1; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1744 TCCTCCCTATCCTAAAGG 1761  
 Db 3 TGTCTCTACCTAAAGG 20

RESULT 139  
 AAA13141/C  
 ID AAA13141 standard; DNA; 20 BP.  
 XX AAA13141;  
 AC AAA13141;  
 DT 17-JUL-2000 (first entry)  
 XX PI3K antisense inhibitor oligonucleotide ISIS# 32155.  
 DE

XX Phosphatidyl inositol 3 kinase; PI3K; antisense oligonucleotide; p110;  
 KW catalytic subunit; treatment; rheumatoid arthritis; asthma; research;  
 KW diagnostic; infection; inflammation; tumour formation; inhibitor; ss.  
 XX Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1..20  
 FT /tag= a  
 FT /note= "Phosphorothioate internucleoside linkage"  
 FT modified\_base 1..5  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "Optionally 2'-methoxyethyl (2'-MOE) nucleotides"  
 FT modified\_base 16..20  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "Optionally 2'-methoxyethyl (2'-MOE) nucleotides"  
 XX  
 PN US6046049-A.  
 XX  
 XX 04-APR-2000.  
 XX 19-JUL-1999; 99US-00357070.  
 XX 19-JUL-1999; 99US-00357070.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Monia BP, Cowsert LM;  
 XX WPI; 2000-282691/24.  
 DR  
 XX New antisense compounds targeting nucleic acids encoding human PI3 kinase  
 PT p110 delta useful for treating a disease or condition associated with PI3  
 PT kinase p110 delta expression, e.g. rheumatoid arthritis, asthma.  
 XX  
 PS Claim 3; Col 41; 35pp; English.  
 XX  
 CC This sequence represents a phosphatidyl inositol 3 kinase (PI3K)  
 CC targeting antisense oligonucleotide. Phosphatidyl inositol 3 kinases act  
 CC as downstream effectors of hormone and growth factor receptors, and have  
 CC been implicated in growth factor mediated cell transformation, and  
 CC mitogenesis, protein trafficking, cell survival and proliferation, and  
 CC many other cellular activities. PI3K is a heterodimer, consisting of a  
 CC 110KD catalytic subunit (p110), and an 85KD regulatory subunit (p85). The  
 CC invention relates to antisense oligonucleotides which target the p110  
 CC delta mRNA of PI3K. The antisense oligonucleotides specifically hybridise  
 CC with various regions of the PI3K mRNA sequence, and inhibit the  
 CC expression of PI3K. The antisense oligonucleotides may be used to treat  
 CC an animal, particularly human, suspected of having or being prone to a  
 CC disease or condition associated with the expression of PI3K, e.g.  
 CC rheumatoid arthritis or asthma. The treatment works through the  
 CC modulation (preferably inhibition) of the expression of PI3K. The  
 CC antisense oligonucleotides may also be used for research and diagnostics,  
 CC in pharmaceutical compositions and formulations, in the preparation of  
 CC kits for detecting the level of PI3K in a sample, and as prophylaxis,  
 CC e.g. to prevent or delay infection, inflammation or tumour formation.  
 CC Antisense oligonucleotides, which are able to inhibit gene expression  
 CC specifically, are used to elucidate the function of particular genes, and  
 CC to distinguish between functions of various members of a biological  
 CC pathway  
 XX  
 SQ Sequence 20 BP; 5 A; 6 C; 8 G; 1 T; 0 U; 0 Other;  
 Query Match 9.5%; Score 13.2; DB 1; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1656 GCACCAAGGCTCACAGCTG 1673  
 Db 18 GCACCTGGCTCTCGGCTG 1



RESULT 140  
AAS15246/c  
ID AAS15246 standard; DNA; 20 BP.  
XX  
AC AAS15246;  
XX  
DT 16-JAN-2002 (first entry)  
XX  
DE Mouse GAPDH PCR primer, MoGAPDH251F.  
XX  
XX Mouse; GAPDH; glyceraldehyde phosphate dehydrogenase; MoGAPDH251F; ss;  
KW PCR primer; neurotropic; neuroprotective; antiinflammatory;  
KW interleukin-beta; IL-1b; tumour necrosis factoralpha; TNFalpha;  
KW macrophage inflammatory protein-1alpha; MIP-1alpha; fractalkane;  
KW glial fibrillar associated protein; GFAP; MHC; CX3CR1; CD86;  
KW major histocompatibility complex; Alzheimer's disease; cerebral ischaemia;  
KW neurodegenerative disease.  
XX  
OS Mus sp.  
XX  
PN WO200175165-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US010247.  
XX  
PR 30-MAR-2000; 2000US-0193847P.  
XX  
PA (ELAN-) ELAN PHARM INC.  
XX  
PI Mcconlogue LC, Games KD, Yednock TA, Hua T, Messersmith E;  
PI Bard F;  
XX  
XX WPI; 2001-639367/73.  
XX  
PT Selecting compounds useful for treating or preventing Alzheimer's  
PT disease, from their ability to reduce levels of specific disease markers  
PT in animal models.  
XX  
PS Example 1; Page 17; 36pp; English.  
XX  
XX The invention relates selecting compounds that reduce symptoms of  
CC Alzheimer's disease using a non-human mammal that has been subjected to  
CC cerebral ischaemia or lesion of a nerve so as to produce, in the affected  
CC region, increased levels of specific markers of Alzheimer's disease-  
CC associated inflammation. Test compounds are selected if they reduce  
CC levels of these markers significantly, in the affected region, relative  
CC to controls. The markers are interleukin-beta (IL-1b), tumour necrosis  
CC factoralpha (TNFalpha), macrophage inflammatory protein-1alpha (MIP-  
CC alpha), glial fibrillar associated protein (GFAP), MHC (major  
CC histocompatibility complex) Italpha or IL 1, CD86, fractalkane or CX3CR1  
CC (a receptor for fractalkane). The method is used to identify compounds  
CC useful in treatment or prevention of Alzheimer's disease or other  
CC neurodegenerative diseases that have an inflammatory component. The  
CC method provides fast, accurate and quantitative drug screens. The present  
CC sequence is a PCR primer used in a quantitative PCR experiment to  
CC determine the level of a transcript for GAPDH as a control for the  
CC determining the levels of the markers of the invention  
XX  
SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 9.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1723 AGATGGAGATTGGCTCC 1740  
Db 19 AGATGGTGTGGCTCC 2  
||||| ||| ||| |||  
1662 GGCTCAGCTGGACCC 1679  
||||| ||| ||| ||| |||

RESULT 141

AAC86126  
ID AAC86126 standard; cDNA; 20 BP.  
XX  
AC AAC86126;  
XX  
DT 29-AUG-2001 (first entry)  
XX  
DE Primer UNF14 to isolate APEX cDNA.  
XX  
XX Antigen presenting cell expression protein; APEX-1; APEX-2; APEX-3;  
KW extracellular domain; immunoglobulin-like domain; Ig-like structure;  
KW N-glycosylation site; transmembrane domain; cytoplasmic domain; PCR;  
KW SH2-binding motif; asthma; arteriosclerosis; AIDS; cirrhosis; primer;  
KW Crohn's disease; atopic dermatitis; autoimmune anaemia; bursitis;  
KW cholecystitis; diabetes mellitus; emphysema; atrophic gastritis;  
KW inflammatory bowel disease; multiple sclerosis; myasthenia gravis;  
KW myocardial inflammation; pericardial inflammation; osteoarthritis;  
KW osteoporosis; psoriasis; Reiter's syndrome; rheumatoid arthritis;  
KW inflammation; cancer; autoimmune disease; graft rejection; amplify;  
KW graft versus host disease; systemic lupus erythematosus;  
KW polymerase chain reaction; ss.  
XX  
OS Synthetic.

WO200146260-A2.  
XX  
PD 28-JUN-2001.  
XX  
PF 22-DEC-2000; 2000WO-US034963.  
XX  
PR 23-DEC-1999; 99US-0172025P.  
XX  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
PI Starling GC, Finger J;  
XX  
XX WPI; 2001-418044/44.  
XX  
PT Novel Antigen presenting cell expression protein useful for treating  
PT asthma, arteriosclerosis, autoimmune diseases, AIDS, cirrhosis, Crohn's  
PT disease and atopic dermatitis.  
XX  
PS Claim 50; Page 83; 112pp; English.

XX The sequences given in AAC86117-42 are primers which were used to isolate  
CC the cDNA sequences which encode antigen presenting cell expression (APEX)  
CC -1, APEX-2 and APEX-3 proteins. APEX-1 and APEX-2 comprise an  
CC extracellular domain having one immunoglobulin (Ig)-like structure and N-  
CC glycosylation site, a transmembrane domain, and a cytoplasmic domain  
CC having at least one SH2-binding motif. APEX proteins and antibodies are  
CC useful in the study, diagnosis, prevention and treatment of disease  
CC associated with the presence of an APEX protein e.g., asthma,  
CC arteriosclerosis, AIDS, cirrhosis, Crohn's disease, atopic dermatitis,  
CC autoimmune anaemia, bursitis, cholecystitis, diabetes mellitus,  
CC emphysema, atrophic gastritis, inflammatory bowel disease, multiple  
CC sclerosis, myasthenia gravis, myocardial or pericardial inflammation,  
CC osteoarthritis, osteoporosis, psoriasis, Reiter's syndrome, rheumatoid  
CC arthritis, inflammation, cancer, immune disorders, autoimmune diseases,  
CC graft rejections, graft versus host reaction and systemic lupus  
CC erythematosus. APEX proteins are useful as diagnostic and/or prognostic  
CC markers on APCs or APEX expressing cells, the ability to elicit the  
CC generation of antibodies and as targets for various therapeutic  
CC modalities. APEX proteins are also useful for identifying and isolating  
CC ligand that bind APEX

SQ Sequence 20 BP; 4 A; 8 C; 3 G; 5 T; 0 U; 0 Other;  
Query Match 9.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Db      2 GGCTCACACCTGTATATCC 19
RESULT 142
AAI69777
ID      AAI69777 standard; DNA; 20 BP.
XX
AC      AAI69777;
XX
DT      13-DEC-2001 (first entry)
XX
DE      16S/23S rRNA spacer region PCR primer #3.
XX
KW      Bacterium detection; 16S/23S rRNA spacer region; PCR primer; ss.
XX
OS      Pseudomonas putida.
XX
PN      JP2001190279-A.
XX
PD      17-JUL-2001.
XX
PF      13-JAN-2000; 2000JP-00004160.
XX
PR      13-JAN-2000; 2000JP-00004160.
XX
PA      (MITO ) MITSUBISHI JUKOGYO KK.
XX
DR      WPI; 2001-605311/69.
XX
FT      Detection method of Pseudomonas bacteria.
XX
PS      Claim 9; Page 8; 11pp; Japanese.
XX
CC      The present invention relates to a method for the detection of the
CC      16S/23S rRNA spacer region of Pseudomonas putida (see AAI69774). The
CC      method can be used to detect Pseudomonas bacteria. The present sequence
CC      is a PCR primer which was used in an example from the present invention
XX
SQ      Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
Query Match          9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1657 CACCAGGCTCACAGCTGG 1674
Db      2 CACCAGTTTCACTGCTGG 19
RESULT 143
AAD40844/c
ID      AAD40844 standard; DNA; 20 BP.
XX
AC      AAD40844;
XX
DT      30-OCT-2002 (first entry)
XX
DE      Human hepsin antisenase oligonucleotide, ISIS 107118.
XX
KW      Human; hepsin; antisenase compound; antisenase therapy; antisenase;
KW      phosphorothioate backbone; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
FH      Key Location/Qualifiers
FT      modified_base 1..20
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone"
FT      modified_base 1..5
FT      /tag= b
FT      /mod_base= OTHER
XZ
Db      1664 CTCACAGCTGGAACCTG 1681
Db      19 CTCACTGCGGGGACCTG 2
RESULT 144
AAD40662/c
ID      AAD40662 standard; DNA; 20 BP.
XX
AC      AAD40662;
XX
```

```
FT      modified_base 2
FT      /tag= d
FT      /mod_base= m5c
FT      modified_base 8
FT      /tag= e
FT      /mod_base= m5c
FT      modified_base 9
FT      /tag= f
FT      /mod_base= m5c
FT      modified_base 10
FT      /tag= g
FT      /mod_base= m5c
FT      modified_base 11
FT      /tag= h
FT      /mod_base= m5c
FT      modified_base 13
FT      /tag= i
FT      /mod_base= m5c
FT      modified_base 16..20
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "2'methoxyethyl nucleotides"
XX
WO200250247-A2.
XX
PN      27-JUN-2002.
XX
PD      14-DEC-2001; 2001WO-US048341.
XX
PR      20-DEC-2000; 2000US-00742482.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Cowsert LM;
XX
DR      WPI; 2002-519882/55.
XX
PT      Novel antisenase compound targeted to nucleic acids encoding human hepsin,
PT      useful for inhibiting the expression of hepsin in human cells or tissues,
PT      and for treating humans having a disease associated with human hepsin.
XX
PS      Claim 3; Page 95; 100pp; English.
XX
CC      The invention relates to antisenase compounds, compositions and methods
CC      for modulating the expression of hepsin. The compositions comprise
CC      antisenase compounds, particularly antisenase oligonucleotides, targeted
CC      to nucleic acids encoding hepsin. The antisenase compound is useful for
CC      inhibiting the expression of hepsin in human cells or tissues. It is also
CC      useful for treating an animal having a disease or condition associated
CC      with hepsin, by inhibiting expression of hepsin. It is useful for
CC      diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC      It is also used in antisenase therapy. The present sequence is an
CC      antisenase oligonucleotide targeted to human hepsin DNA. This sequence is
CC      used in the exemplification of the invention
XX
SQ      Sequence 20 BP; 4 A; 6 C; 8 G; 2 T; 0 U; 0 Other;
Query Match          9.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1664 CTCACAGCTGGAACCTG 1681
Db      19 CTCACTGCGGGGACCTG 2
RESULT 144
AAD40662/c
ID      AAD40662 standard; DNA; 20 BP.
XX
AC      AAD40662;
XX
```

DT 30-OCT-2002 (first entry)  
XX Human hepsin antisense oligonucleotide, ISIS 107118.  
XX Human; antisense; hepsin; inflammation; tumour; gene therapy; cytostatic;  
KW phosphorothioate backbone; ss.  
OS Homo sapiens.  
XX Synthetic.  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
FT modified\_base 1..5  
FT /tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl nucleotides"  
FT modified\_base 2  
FT /tag= d  
FT /mod\_base= m5c  
FT modified\_base 8  
FT /tag= e  
FT /mod\_base= m5c  
FT modified\_base 9  
FT /tag= f  
FT /mod\_base= m5c  
FT modified\_base 10  
FT /tag= g  
FT /mod\_base= m5c  
FT modified\_base 11  
FT /tag= h  
FT /mod\_base= m5c  
FT modified\_base 13  
FT /tag= i  
FT /mod\_base= m5c  
FT modified\_base 16..20  
FT /tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl nucleotides"  
XX WO200250248-A2.  
XX 27-JUN-2002.  
XX 14-DEC-2001; 2001WO-US048431.  
XX 20-DEC-2000; 2000US-00742703.  
XX (ISIS-) ISIS PHARM INC.  
XX (ABBO ) ABBOTT LAB.  
XX Marcotte PA, Cowsett LM;  
XX WPI; 2002-519883/55.  
XX New antisense oligonucleotides that modulate (particularly inhibit) human  
PT hepsin, useful for treating a disease or condition associated with the  
FT expression of hepsin, e.g. inflammation or tumor growth.  
XX Example 15; Page 82; 101pp; English.  
XX The invention relates to an antisense compound 8-30 nucleobases in length  
CC targeted to a nucleic acid molecule encoding human hepsin. The antisense  
CC compound specifically hybridises with and inhibits the expression of  
CC human hepsin. The antisense compound or the pharmaceutical composition is  
CC useful for treating animals and humans having a disease or condition  
CC associated with the expression of hepsin, e.g. inflammation or tumour  
CC growth. The antisense compounds are useful also for diagnostics,  
CC prophylaxis (e.g. to prevent or delay infection, inflammation or tumour  
CC formation) or as research reagents and kits. The method is useful for  
CC modulating, specifically inhibiting the expression of hepsin which may be

CC used in research, e.g to distinguish between functions of various members  
CC of a biological pathway. The invention is used in gene therapy. The  
CC present sequence is human hepsin antisense oligonucleotide  
XX Sequence 20 BP; 4 A; 6 C; 8 G; 2 T; 0 U; 0 Other;  
SQ Query Match 9.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1664 CTCACAGCTGGAGCCCTG 1681  
Db ||||| ||||| ||||| |||||  
19 CTCACCTGCGGGACCCCTG 2  
RESULT 145  
ABL94348  
ID ABL94348 standard; DNA; 20 BP.  
XX AC ABL94348;  
XX 29-JUL-2002 (first entry)  
XX Mouse C/EBP beta phosphorothioate antisense oligonucleotide, SEQ ID:114.  
KW Mouse; murine; C/EBP beta; CCAAT/enhancer-binding protein beta; C/EPB2;  
LAP; TCF5; CRP2; NFIL6; IL6DBP; NF-M; AGP/EBP; Apc/EBP;  
KW transcription factor; tissue development; cellular function;  
KW proliferation; differentiation; hormone responsiveness;  
KW oxidative stress response; IL-6 signalling mediator; interleukin-6;  
KW carbohydrate metabolism; immunity; Th1 response; female fertility;  
KW gluconeogenesis; ovarian; cancer; tumour formation; type II; diabetes;  
KW infection; inflammation; expression inhibition; phosphorothioate;  
antisense oligonucleotide; ss.  
XX Mus musculus.  
OS  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate linkages"  
FT modified\_base 1..5  
FT /tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE  
FT cytosines are 5-methylcytosine"  
FT modified\_base 16..20  
FT /tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE  
FT cytosines are 5-methylcytosine"  
XX US6271030-B1.  
XX 07-AUG-2001.  
XX 14-JUN-2000; 2000US-00593711.  
XX 14-JUN-2000; 2000US-00593711.  
XX (ISIS-) ISIS PHARM INC.  
XX Monia BP, Butler MM, Wyatt J;  
XX WPI; 2002-214451/27.  
XX Novel antisense compound targeted to nucleic acids encoding human or  
FT mouse CCAAT/enhancer binding protein (C/EBP) beta, useful in vitro for  
FT inhibiting expression of human or mouse C/EBP beta in cells/tissues.  
XX Claim 1; Col 47-48; 69pp; English.  
XX

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 4636; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiasthmatic, antiallergic, antihypertensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 3 A; 12 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 9.5%; Score 13.2; DB 1; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1699 GTGGAAGTTGGGTAGGA 1716  
 Db 20 GGGGAGTTGGGTACGA 3  
 RESULT 148  
 ABZ37372  
 ID ABZ37372 standard; DNA; 20 BP.  
 XX  
 AC ABZ37372;  
 XX  
 DT 18-FEB-2003 (first entry)  
 XX  
 DE Kappa light chain capture oligonucleotide Readapter SEQ ID NO:468.  
 XX  
 KW Library; cleavage; display; diverse family; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN WO200283872-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 17-APR-2002; 2002WO-US012405.  
 XX  
 PR 17-APR-2001; 2001US-00837306.  
 PR 24-OCT-2001; 2001US-00000516.  
 PR 25-OCT-2001; 2001US-00045674.  
 XX  
 PA (LADN/) LADNER R C.  
 PA (COHE/) COHEN E H.  
 PA (NAST/) NASTRI H G.  
 PA (ROOK/) ROOKEY K L.  
 PA (HOET/) HOET R.  
 PA (HOOG/) HOOGENDOORN H R J M.  
 XX  
 XX Ladner RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;  
 PI Hoogenboom HRJM;  
 PI WPI; 2003-093015/08.  
 DR  
 XX  
 FT Cleaving single-stranded nucleic acid sequences at a desired location by

PT contacting the nucleic acid with an single strand oligonucleotide  
 PT complementary to a nucleic acid region where cleavage is desired.  
 XX  
 PS Example 2; Page 406; 485pp; English.  
 XX  
 CC The present invention describes a method for cleaving single-stranded  
 CC nucleic acid sequences at a desired location. Also described: (1) methods  
 CC for displaying or expressing a member of a diverse family of peptides,  
 CC polypeptides or proteins on the surface of a genetic package and  
 CC collectively displaying at least a part of the diversity of the family,  
 CC where the displayed or expressed peptide, polypeptide or protein is  
 CC encoded at least in part by a nucleic acid that has been cleaved at a  
 CC desired location; (2) a method for preparing single-stranded nucleic  
 CC acids; (3) a method for preparing a library comprising a collection of  
 CC genetic packages that display a member of a diverse family of peptides,  
 CC polypeptides or proteins and that collectively display at least a portion  
 CC of the family; (4) a vector comprising a DNA sequence encoding an  
 CC antibody variable region linked to a version of PIII anchor which does  
 CC not mediate infection of phage particles, and wild-type gene III; (5) a  
 CC method for producing a population or a library of immunoglobulin genes;  
 CC and (6) a library of immunoglobulins that comprise members having at  
 CC least one variable domain in which at least one of CDR1 and CDR2 contain  
 CC synthetic diversity and CDR3 diversity is captured from B cells. The  
 CC method is useful for cleaving single-stranded nucleic acid sequences at a  
 CC desired location, which can be subsequently used to produce libraries of  
 CC genetic packages that display and/or express a diverse family of  
 CC peptides, polypeptides or proteins. ABZ36912 to ABZ37510 and ABP55464 to  
 CC ABP55499 represent sequences used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 U; 0 Other;  
 Query Match 9.5%; Score 13.2; DB 1; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1721 GGAGATGGAGATTGGCTC 1738  
 Db 3 GAAGATGGAGACTGGGTC 20  
 RESULT 149  
 ABZ25675  
 ID ABZ25675 standard; DNA; 20 BP.  
 XX  
 AC ABZ25675;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human connective tissue growth factor antisense oligo DNA (SeqID 68).  
 XX  
 KW antisense; human; ss; connective tissue growth factor; CTGF;  
 KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;  
 KW fisp-12; NOV2;  
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
 KW scleroderma; atherosclerosis; cytostatic; dermatological;  
 KW antiarteriosclerotic.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
 FT 5-methylcytidines"  
 XX  
 PN WO2003053340-A2.  
 XX  
 XX 03-JUL-2003.

XX PF 09-DEC-2002; 2002WO-US038618.  
XX PR 10-DEC-2001; 2001US-00006191.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Gaarde WA, Watt AT;  
XX DR WPI; 2003-559091/52.  
XX PT New antisense oligonucleotides for modulating connective tissue growth  
PT factor expression, particularly useful for treating cancers (e.g. breast  
PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or  
PT atherosclerosis.  
XX PS Claim 3; Page 86; 139pp; English.  
XX CC This invention relates to novel methods for modulating the expression of  
CC connective tissue growth factor (CTGF) by antisense oligonucleotides.  
CC CTGF has been mapped to human chromosome region 6q23.1, and is also known  
CC as ctgfact, fibroblast inducible secreted protein, flisp-12, NOV2,  
CC insulin-like growth factor binding protein-related protein 2, IGFBP-rP2,  
CC IGFBP-8, Hsc24 and ecogenin. It is known to stimulate DNA synthesis and  
CC promote chemotaxis of fibroblasts, however, it is also upregulated in  
CC acute lymphoblastic leukaemia and in tumour or endothelial cells  
CC associated with the vasculature. Accordingly, antisense oligonucleotides  
CC that inhibit the expression of CTGF in cells or tissues can be used in  
CC gene therapy to treat various conditions including hyperproliferative  
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),  
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As  
CC such, the present invention describes these antisense oligos as having  
CC cytotatic, dermatological and antiarteriosclerotic activities. This  
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo  
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of  
CC human CTGF of the invention.  
XX SQ Sequence 20 BP; 4 A; 9 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 9.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1651 GGCAAGCACCGGCTCAC 1668  
Db 3 GTCAGCAGCAGGCTCAC 20  
  
RESULT 150  
ABC47950  
ID ABC47950 standard; DNA; 13 BP.  
XX AC ABC47950;  
XX DT 21-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 47967 for detecting SNP TSC0013727.  
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 47968; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB102073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;  
  
Query Match 5.4%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1707 TGGGTTAGGAGTA 1719  
Db 1 TGGGTTAGGAGTA 13  
  
RESULT 151  
ABC47951/c  
ID ABC47951 standard; DNA; 13 BP.  
XX AC ABC47951;  
XX DT 21-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 47968 for detecting SNP TSC0013727.  
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX PS Claim 1; SEQ ID NO 47968; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 9.4%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1707 TGGGTTAGGAGTA 1719  
 Db 13 TGGGTTAGGAGTA 1

## RESULT 152

ABF16655  
 ID ABF16655 standard; DNA; 13 BP.

AC ABF16655;

DT 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 116652 for detecting SNP TSC0029189.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 116652; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 2 A; 8 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 9.4%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1739 CCAACTCCTCCCT 1751  
 Db 1 CCAACTCCTCCCT 13

## RESULT 153

ABF16654/C  
 ID ABF16654 standard; DNA; 13 BP.

XX AC ABF16654;

XX DT 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 116651 for detecting SNP TSC0029189.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 116651; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 3 A; 0 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 9.4%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1739 CCAACTCCTCCCT 1751  
 Db 13 CCAACTCCTCCCT 1

## RESULT 154

AAT50323

ID AAT50323 standard; RNA; 15 BP.

XX





```

Query Match          9.4%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1738 CCCAACTCTCTCC 1750
Db 16 CCCAACTCTCTCC 4

RESULT 156
ADD19353/c
ID ADD19353 standard; DNA; 17 BP.
XX AC
XX ADD19353;
XX
DT 15-JAN-2004 (first entry)
XX
DE Leptin gene-specific PCR primer #14.
XX feline; cat; leptin; leptin inhibitor; obesity; PCR; ss; primer.
XX OS Unidentified.
XX FN JP2003038187-A.
XX PD 12-FEB-2003.
XX PF 31-JUL-2001; 2001JP-00230711.
XX PR 31-JUL-2001; 2001JP-00230711.
XX PA (MOMI ) MORINAGA & CO LTD.
XX WPI; 2003-527653/50.
XX
PT Novel feline leptin polypeptide encoded by a feline ob gene which is
PT related to obesity in cats, useful for diagnosing and treating obesity.
PT Example; SEQ ID NO 20; 18pp; Japanese.
XX
CC The invention comprises the amino acid and coding sequences of feline
CC leptin proteins. The DNA and protein sequences of the invention are
CC useful for screening for a compound which inhibits the activity of
CC leptin. The DNA and protein sequences of the are also useful for
CC diagnosing and treating obesity. The present DNA sequence represents a
CC PCR primer that was used in an example of the invention.
XX
SQ Sequence 17 BP; 6 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

Query Match          9.4%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1676 ACCCTGGTGTCTC 1688
Db 13 ACCCTGGTGTCTC 1

RESULT 157
AAL60321
ID AAL60321 standard; DNA; 19 BP.
XX AC
XX AAL60321;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human Oct-4 specific reverse RT-PCR primer #2.
XX KW Human embryonic stem cells; HES; human; reverse transcription PCR; Oct-4;
XX RT-PCR; primer; ss.
XX OS Homo sapiens.

Query Match          9.4%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1676 ACCCTGGTGTCTC 1688
Db 13 ACCCTGGTGTCTC 1

RESULT 157
AAL60321
ID AAL60321 standard; DNA; 19 BP.
XX AC
XX AAL60321;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human Oct-4 specific reverse RT-PCR primer #2.
XX KW Human embryonic stem cells; HES; human; reverse transcription PCR; Oct-4;
XX RT-PCR; primer; ss.
XX OS Homo sapiens.

Query Match          9.4%; Score 13; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1656 GCACGAGGCTCAC 1668
Db 7 GCACGAGGCTCAC 19

RESULT 158
ACC40945/c
ID ACC40945 standard; DNA; 20 BP.
XX AC
XX ACC40945;
XX
DT 23-MAY-2003 (first entry)
XX
DE Human superoxide dismutase 1 antisense inhibitor # ISIS 150499.
XX
KW Human; superoxide dismutase 1; antisense; neuroprotective; cytostatic;
KW antiinflammatory; amyotrophic lateral sclerosis; apoptosis;
KW hyperproliferative disorder; therapy; infection; inflammation; tumour;
KW ss.
XX OS Homo sapiens.
XX OS Synthetic.

Key Location/Qualifiers
modified_base 1..20
/*tag= a
/mod_base= OTHER
/note= "Phosphorothioate linkages. All cytosines are 5-
methylycytosine"
modified_base 1..5
/*tag= b
/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
modified_base 16..20
/*tag= c
/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"

```

/note= 'DyTx-NH(CH2)6-PO4-cytosine'

FN WO2003000707-A2.  
 XX 03-JAN-2003.  
 PD 19-JUN-2002; 2002WO-US019664.  
 PF 21-JUN-2001; 2001US-00888360.  
 PR (ISIS-) ISIS PHARM INC.  
 XX Bennett FC, Dobie K;  
 XX WPI; 2003-184032/18.  
 XX Novel antisense compounds targeted to nucleic acids encoding human  
 PT superoxide dismutase 1, for modulating expression of the dismutase and  
 PT treating diseases or conditions, e.g. amyotrophic lateral sclerosis.  
 XX Claim 3; Page 77; 107pp; English.  
 XX The invention relates to a compound of 8-50 nucleobases in length,  
 XX targeted to a nucleic acid molecule encoding human superoxide dismutase  
 CC 1. The compound specifically hybridises with and inhibits the expression  
 CC of human superoxide dismutase 1 by hybridising with at least an 8-  
 CC nucleobase portion of the nucleic acid molecule encoding the active site  
 CC of the enzyme. The activity of compounds of the invention may be  
 CC described as neuroprotective, cytostatic and antiinflammatory. The  
 CC mechanism of action of compounds of the invention is antisense inhibition  
 CC of human superoxide dismutase 1 expression by chimeric phosphorothioate  
 CC oligonucleotides having 2'-methoxyethyl (2'-MOE) wings and a deoxy gap.  
 CC Compounds of the invention are useful for inhibiting the expression of  
 CC human superoxide dismutase 1 in human cells or tissues, and for treating  
 CC a disease or condition associated with this enzyme (antisense therapy),  
 CC especially amyotrophic lateral sclerosis, a disease or condition arising  
 CC from aberrant apoptosis and a hyperproliferative disorder. It may also be  
 CC used in diagnostics, therapeutics and as a research reagent, e.g.  
 CC prophylactically to prevent or delay infection, inflammation or tumour  
 CC formation. Sequences given in records ACC40880-ACC40957 represent human  
 CC superoxide dismutase 1 antisense inhibitor oligonucleotides  
 XX Sequence 20 BP; 1 A; 9 C; 4 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 9.4%; Score 13; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AGCAGAGGCAAG 1656  
 DB 18 AGCAGAGGCAAG 6  
 RESULT 159  
 AAQ91452/C  
 ID AAQ91452 standard; DNA; 17 BP.  
 XX AAQ91452;  
 XX 25-MAR-2003 (revised)  
 DT 30-AUG-1995 (first entry)  
 XX Dysprosium (III) texaphyrin (DyTx) DNA conjugate.  
 XX Dysprosium (III) texaphyrin (DyTx) DNA conjugate; liver disease;  
 XX targeted intracellular mRNA hydrolysis; gene expression inhibition;  
 XX hormone regulation; hydrolysis reagents; alkyl phosphate esters;  
 XX detoxification; ss.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 XX modified\_base 1  
 XX /\*tag= a  
 XX /\*mod\_base= OTHER  
 FT

FN WO9429316-A2.  
 XX 22-DEC-1994.  
 PD 09-JUN-1994; 94WO-US036284.  
 PF 09-JUN-1993; 93US-00075123.  
 PR 14-APR-1994; 94US-00227370.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX (PHAR-) PHARMACYCLICS INC.  
 PA Sessler JL, Ross KL, Wright M, Hemmi GW, Dow WC, Smith DA;  
 XX Kral VA, Iverson B, Mody T, Miller RA, Magda D;  
 XX WPI; 1995-036382/05.  
 XX Texaphyrin metal complex mediated ester hydrolysis - esp. useful for  
 PT targeted intracellular hydrolysis of mRNA and for inhibiting gene  
 PT expression.  
 XX Disclosure; Fig 21; 125pp; English.  
 XX AAQ91451-Q91457 are texaphyrin lanthanide metal DNA conjugates, which are  
 CC esp. useful for the targeted intracellular hydrolysis of mRNA; inhibiting  
 CC gene expression. They may also be used for the treatment of liver disease,  
 CC as hormone regulation agents and as hydrolysis reagents for the  
 CC detoxification of alkyl phosphate esters. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX Sequence 17 BP; 1 A; 3 C; 8 G; 5 T; 0 U; 0 Other;  
 SQ  
 Query Match 5.2%; Score 12.8; DB 1; Length 17;  
 Best Local Similarity 87.5%; Pred. No. 2.4e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1655 AGCACCAGGCTCACAG 1670  
 DB 16 AACACCCGGCTCACAG 1  
 RESULT 160  
 AAAX75159/C  
 ID AAAX75159 standard; RNA; 17 BP.  
 XX AAAX75159;  
 XX 28-JUL-1999 (first entry)  
 XX Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #687.  
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 XX foetal liver kinase 1; ss.  
 XX Mus sp.  
 XX WO9715662-A2.  
 XX 01-MAY-1997.  
 XX 25-OCT-1996; 96WO-US017480.  
 XX 26-OCT-1995; 95US-0005974P.  
 XX 11-JAN-1996; 96US-00584040.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX (CHIR ) CHIRON CORP.  
 XX

```

PI Pavco P, Meswigen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 175; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
XX treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 0 A; 4 C; 7 G; 0 T; 6 U; 0 Other;

Query Match          9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAGGCGCAAGCACCA 1661
DB ||||| ||||| |||
17 CAGAGCGCCAGCGCCA 2

RESULT 161
AAV07298/c
ID AAV07298 standard; DNA; 17 BP.
XX
XX AAV07298;
XX
XX 14-AUG-1998 (first entry)
XX
XX Metallotexaphyrin-oligonucleotide conjugate #12.
XX
XX Metallotexaphyrin; dysprosium; europium; conjugate; RNase H;
XX antisense therapy; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX /mod_base
XX /note= "DyTxNH-(CH2)6-P04-Cytosine, where DyTx is
XX dysprosium (III) texaphyrin"
XX
XX US5763172-A.
XX
XX 09-JUN-1998.
XX
XX 07-JUN-1995; 95US-00486962.
XX
XX 21-JAN-1992; 92US-00822964.
XX
XX 09-JUN-1993; 93US-00075123.
XX
XX 14-APR-1994; 94US-00227370.
XX
XX 09-JUN-1994; 94WO-US006284.
XX
XX 26-MAY-1995; 95US-00452261.
XX
XX 07-JUN-1995; 95US-00485581.
XX
XX (PHAR-) PHARMACYCLICS INC.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Sessler JL, Wright M, Miller RA, Dow WC, Magda D;
XX WPI; 1998-347306/30.
XX

```

---

```

XX Enhancing therapeutic activity of oligo-nucleotides in cells - using
XX conjugate comprising metallotexaphyrin, which hydrolyses phosphate ester
XX bonds of RNA, and oligo-nucleotide, which binds to targetted RNA.
XX
XX Example 6; Fig 5; 34pp; English.
XX
XX The invention relates to a method of enhancing the therapeutic activity
XX of oligonucleotides in cells. It comprises contacting a targeted
XX intracellular RNA in a cell with a metallotexaphyrin-oligonucleotide
XX conjugate. The contact is carried out under physiological conditions for
XX a time sufficient to hydrolyse the phosphate ester bond of the targeted
XX RNA. The metallotexaphyrin of the conjugate has catalytic activity for
XX phosphate ester bond hydrolysis. The oligonucleotide of the conjugate has
XX complementary binding affinity to the targeted RNA. The conjugate may be
XX used in antisense therapies for treating, e.g. cancer, viral infections,
XX autoimmune diseases and restenosis. The conjugate may also be used as
XX hydrolysis reagents for the detoxification of di- and trialkyl phosphate
XX esters, which are used in solvents, insecticides and chemical nerve
XX gases. The metallotexaphyrin complex enhances the therapeutic activity of
XX the oligonucleotide, not only by facilitating cellular uptake of the
XX oligonucleotide but also by hydrolysing target RNA within the cell,
XX independent of RNase H. Attachment to the complex may also cause the
XX oligonucleotide to take on some of the pharmacodynamic an biodistribution
XX Properties of the texaphyrin, such as selective localisation in tumours.
XX The present sequence represents a metallo- texaphyrin-oligonucleotide
XX conjugate
XX
SQ Sequence 17 BP; 1 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match          9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAG 1670
DB ||||| ||||| |||||
16 AACACCGCGCTCACAG 1

RESULT 162
AAV91007/c
ID AAV91007 standard; RNA; 17 BP.
XX
XX AAV91007;
XX
XX 18-FEB-1999 (first entry)
XX
XX Human C-raf target site nucleotide position 582.
XX
XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX target; substrate; catalyst; modulation; expression; Raf gene; delivery;
XX screening; identification; synthesis; deprotection; purification; cancer;
XX inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
XX restenosis; rheumatoid arthritis; ss.
XX
XX Homo sapiens.
XX
XX WO9850530-A2.
XX
XX 12-NOV-1998.
XX
XX 05-MAY-1998; 98WO-US009249.
XX
XX 09-MAY-1997; 97US-0046059P.
XX
XX 09-JUN-1997; 97US-0049002P.
XX
XX 03-JUL-1997; 97US-0051718P.
XX
XX 22-AUG-1997; 97US-0056808P.
XX
XX 02-OCT-1997; 97US-0061321P.
XX
XX 02-OCT-1997; 97US-0061321P.
XX
XX 05-NOV-1997; 97US-0064866P.
XX
XX 19-DEC-1997; 97US-0068212P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX

```

XX	Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;	02-OCT-1997; 97US-0061321P.
XX	Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;	02-OCT-1997; 97US-0061324P.
XX	Thompson J, Workman CT, Beaudry A, Sweedler D;	05-NOV-1997; 97US-0064866P.
XX	WPI; 1999-009494/01.	19-DEC-1997; 97US-0068212P.
XX	Identifying new catalytic nucleic acid that modulates selected processes	(RIBO-) RIBOZYME PHARM INC.
XX	- especially ribozymes that cleave Raf RNA for treating cancer,	
XX	restenosis, and also new ribozymes and modified nucleoside triphosphates	
XX	used as antiviral agents and synthons.	
XX	Claim 177; Page 147; 259pp; English.	
XX	A method has been developed for the identification of a nucleic acid	
XX	capable of modulating a process in a biological system. The method	
XX	comprises: (a) introducing into the system a random library of nucleic	
XX	acid catalysts (NAC) having a substrate binding domain (SBD), comprising	
XX	a random sequence, and a catalytic domain (CD); and (b) identifying NAC	
XX	in systems where modulation has occurred and/or determining the sequence	
XX	of at least part of the SBDs in such systems. Nucleic acid molecules with	
XX	endonuclease activity and catalytic activity, from the present invention,	
XX	are used to modulate gene expression in plant and mammalian cells and to	
XX	cleave target nucleic acid, particularly for treating systemic diseases	
XX	caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic	
XX	mutations in diseased cells and to determine c-raf RNA. Specifically NACs	
XX	used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or	
XX	generally any condition associated with the level of c-raf. Introduction	
XX	of sugar/phosphate modifications increases stability against nuclease and	
XX	activity. AAV90922 to AAV93877 represent NACs that can be used in the	
XX	method, specifically for modulating the expression of a Raf gene	
XX	Sequence 17 BP; 2 A; 5 C; 3 G; 0 T; 7 U; 0 Other;	
XX	Query Match 9.2%; Score 12.8; DB 1; Length 17;	
XX	Best Local Similarity 87.5%; Pred. No. 2.4e+02;	
XX	Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
XX	1641 TGTAGCAGAGGCAAG 1656	
XX	16 TGTACAGAGGCAAG 1	
XX	AAV93413 standard; RNA; 17 BP.	
XX	AAV93413;	
XX	18-FEB-1999 (first entry)	
XX	Human B-raf substrate nucleotide position 833.	
XX	Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;	
XX	target; substrate; catalyst; modulation; expression; Raf gene; delivery;	
XX	screening; identification; synthesis; deprotection; purification; cancer;	
XX	inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;	
XX	restenosis; rheumatoid arthritis; ss.	
XX	Homo sapiens.	
XX	WO9805030-A2.	
XX	12-NOV-1998.	
XX	05-MAY-1998; 98WO-US009249.	
XX	09-MAY-1997; 97US-0046059P.	
XX	09-JUN-1997; 97US-0049002P.	
XX	03-JUL-1997; 97US-0051718P.	
XX	22-AUG-1997; 97US-0056808P.	

```

PF 05-MAY-1998; 98WO-US009249.
XX
PR 09-MAY-1997; 97US-0046059P.
PR 09-JUN-1997; 97US-0049002P.
PR 03-JUL-1997; 97US-0051718P.
PR 22-AUG-1997; 97US-0056808P.
PR 02-OCT-1997; 97US-0061321P.
PR 02-OCT-1997; 97US-0061324P.
PR 05-NOV-1997; 97US-0064866P.
PR 19-DEC-1997; 97US-0068212P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
XX WPI; 1999-009494/01.
XX
XX Identifying new catalytic nucleic acid that modulates selected processes
PT - especially ribozymes that cleave Raf RNA for treating cancer,
PT restenosis, and also new ribozymes and modified nucleoside triphosphates
PT used as antiviral agents and synthons.
XX
PS Claim 177; Page 167; 259pp; English.
XX
CC A method has been developed for the identification of a nucleic acid
CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC ascites and infection. They may also be used to detect genetic drift and
CC mutations in diseased cells and to determine c-rat RNA. Specifically NACs
CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-rat. Introduction
CC of sugarphosphate modifications increases stability against nuclease and
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene
XX
SQ Sequence 17 BP; 1 A; 6 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1667 ACAGCTGGAACCCCTGG 1682
Db 16 ACAGCGGAACCCCTGG 1

RESULT 165
AAA79844
ID AAA79844 standard; DNA; 17 BP.
XX
XX AAA79844;
AC
XX
XX 20-NOV-2000 (first entry)
DT
XX
DE Hepatitis B virus related oligonucleotide probe #107.
XX
XX Hepatitis B virus; HBV; Hepatitis A virus; HAV; probe; detection;
KW mutation; high-density gene chip; ss.
XX
XX Hepatitis B virus.
OS
XX
XX CN1252452-A.
PN

```

```

XX 10-MAY-2000.
PD
XX
XX 24-SEP-1999; 99CN-00114460.
PF
XX
XX 24-SEP-1999; 99CN-00114460.
PR
XX
XX (UYDO-) UNIV DONGNAN.
PA
XX
XX Sun X, Lu Z, Wang Y;
PI
XX
XX WPI; 2000-443233/39.
DR
XX
XX High-density gene chip making process.
PT
XX
XX Example 1; Fig 15; 19pp; Chinese.
PS
XX
XX The present invention describes a method which comprises making a high-
CC density gene chip, specifically for making high-density micro-array of
CC oligonucleotide probes. An oligonucleotide probe selecting process to
CC seek preferentially length variable and coverage variable probes is
CC provided to ensure identical cross melting temperature of probes to the
CC maximum limit, and this can make the cross control of gene chip
CC relatively simple and raise the reliability of the gene chip detecting
CC results. The process proposes a specific probe selection method for
CC detecting target sequence directly, detecting mutation in both specific
CC and non-specific sites and a probe overall arrangement scheme. AAA79738
CC to AAA80201 represent oligonucleotide probe sequences which are used in
CC examples from the present invention
XX
SQ Sequence 17 BP; 4 A; 1 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1713 AGGAGTACGGAGATGG 1728
Db 1 AGGAGTACGGAGATGG 16

RESULT 166
ABS97987/C
ID ABS97987 standard; DNA; 17 BP.
XX
XX ABS97987;
AC
XX
XX 23-DEC-2002 (first entry)
DT
XX
DE Human urokinase gene (uPA) PCR primer #2.
XX
XX Human; ss; primer; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1; PCR;
KW cytochrome P450 A2; CYP450A2; cytochrome P450 2E; CYP4502E1; LTF;
KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thiolabile; STM;
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW multidrug resistance associated protein 3; cancer; prostate;
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR5;
KW altered drug metabolism; cardiovascular function; colorectal tumour;
KW central nervous system; pulmonary; immunological.
XX
XX Homo sapiens.
OS
XX
XX WO200257410-A2.
PN
XX
XX 25-JUL-2002.
PD

```

09-APR-2002	(first entry)	Human ERG G-cleaver ribozyme target sequence Seq ID No 1307.
Human,	hammerhead ribozyme; cytostatic; antitumour; antidiabetic;	
Ophthalmological;	antiarthritic; antipsoriatic; virucide; osteopathic;	
vulvar;	cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;	
tumour angiogenesis;	diabetic retinopathy; macular degeneration;	
neovascular glaucoma;	myopic degeneration; arthritis; verruca vulgaris;	
angiofibroma of tuberous sclerosis;	port-wine stain; wound healing;	
Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;		
Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;		
ambryme.		
Homo sapiens.		
WO200188124-A2.		
22-NOV-2001.		
16-MAY-2001;	2001WO-US015866.	
16-MAY-2000;	2000US-00572021.	
(RIBO-) RIBOZYME PHARM INC.		
(GLAX) GLAXO GROUP LTD.		
Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;		
WPI; 2002-082995/11.		
Novel polynucleotide which down regulates expression of Ets-related gene,		
useful for treating cancer, diabetic retinopathy, macular degeneration,		
arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.		
Claim 4; Page 84; 149pp; English.		
The invention relates to a nucleic acid molecule (I) which down regulates		
expression of an Ets-related gene (ERG). (I) is useful for treating		
conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,		
tumour angiogenesis, diabetic retinopathy, macular degeneration,		
neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca		
vulgaris, angiobroma of tuberous sclerosis, port-wine stains, Sturge		
Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu		
syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for		
treating a patient having a condition associated with the level of ERG,		
by contacting cells of the patient with (I) under conditions suitable for		
the treatment. The method comprises the use of one or more therapies		
under conditions suitable for the treatment. Leukaemia or tumour		
angiogenesis is treated by administering (I) to the patient in		
conjunction with one or more of other therapies such as radiation or		
chemotherapy treatment. (I) is useful for reducing ERG activity in a		
cell, by contacting the cell with (I). (I) is useful for cleaving RNA of		
ERG gene, by contacting (I) with RNA, in the presence of a divalent		
cation such as Mg2+. (I) is useful for diagnosis of conditions and		
diseases related to the expression of ERG, and as diagnostic tool to		
examine genetic drift and mutations within diseased cells or to detect		
the presence of ERG RNA in a cell. (I) is useful for specifically		
targeting genes that share homology with ERG gene or ERG fusion genes.		
ABK17354-ABK22719 represent nucleic acids, including antisense and		
enzymatic nucleic acid molecules which regulate expression of ERG, and		
related PCR primers of the invention		
Sequence 17 BP; 4 A; 3 C; 7 G; 0 T; 3 U; 0 Other;		
Query Match	9.2%;	Score 12.8; DB 1; Length 17;
Best Local Similarity	£7.58;	Pred. No. 2.4e+02;
Indels	0;	Gaps 0;

XX	28-NOV-2001; 2001WO-US044839.
XX	PF PF
XX	PR PR
XX	28-NOV-2000; 2000US-00724389.
XX	(DNAS-) DNA SCI LAB INC.
FA	
PI	Guida M, Hall J;
PI	WPI; 2002-698522/75.
XX	
DR	
XX	This invention relates to the sequence of an isolated nucleic acid
CC	molecule comprising at least one base variation from that of a known
CC	human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
CC	cytochrome P450 O2B1 (CYP450O2E1), adrenergic receptor beta1 (ADRB1),
CC	aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC	(ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
CC	inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
CC	protein (FLAP), glutathione-S-transferase 12 (GSTL2), histamine-N-methyl
CC	transferase (HNMT), kallikrein 2 KLK2, nicotinamide N-methyl
CC	transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC	sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC	(UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC	transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC	(MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC	(MRP3), orphan nuclear receptor (NRII2), or acetylcholine muscarinic
CC	receptor 1, 2, 3, 4, or 5 (CHRM1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC	The polymorphisms in the human genes cited in the invention are useful as
CC	genetic linkage markers for locating and characterizing the genes that
CC	are responsible for specific traits within the genome and eventually
CC	identifying the genes responsible for a variety of disorder-related
CC	traits as a result of their e.g., overexpression, constitutive
CC	expression, mutation or underexpression, which may be used in diagnosing
CC	and/or treating the disorders. The nucleic acid molecules comprising the
CC	polymorphic sequences contained in CYP450A1, CYP450A2, CYP450ZEL1,
CC	ARNT, BPHX2, GSTI2, NNMT, NQO2, NRII2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC	MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC	metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
CC	AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC	susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC	used to screen for altered cardiovascular function, in COX2 for altered central
CC	susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC	nervous system function, in FLAP and HNMT for altered pulmonary,
CC	immunological or haematological function, in KLK2 for altered serine
CC	protease activity in the prostate, in LTF for altered immunological or
CC	haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC	peripheral nervous system function. The present sequence represents a PCR
CC	primer used to amplify the sequences of the invention
XX	
XX	Sequence 17 BP; 5 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
SQ	
	Query Match                 9.2%; Score 12.8; DB 1; Length 17;
	Best Local Similarity   87.5%; Pred. No. 2.4e-02;
	Matches      14; Conservative   0; Mismatches   2; Indels     0; Gaps   0;
QY	1670 GCTGGACCGTCGTGT 1685 
Db	17 GCTGGACCGATGCT 2 
RESULT 167	
ABK18660/c	
ID	AEK18660 standard; RNA, 17 BP.
XX	
XX	ABK18660;
XX	

```

RESULT 168
ABK17683/c
ID ABK17683 standard; RNA; 17 BP.
XX
XX
AC ABK17683;
XX
XX 09-APR-2002 (first entry)
DT
DE Human ERG hammerhead ribozyme target sequence, Seq ID No 330.
XX
XX Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulvular; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge-Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
XX Homo sapiens.
OS
XX WO200188124-A2.
XX
XX 22-NOV-2001.
XX
XX 16-MAY-2001; 2001WO-US015866.
XX
XX 16-MAY-2000; 2000US-00572021.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
XX Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
PI WPI; 2002-082995/11.
XX
XX Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
XX Claim 4; Page 64; 149pp; English.
XX
XX The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
XX Sequence 17 BP; 3 A; 3 C; 7 G; 0 T; 4 U; 0 Other;
Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
AC

```

```

Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1674 GAACCTCGAGTCTCC 1689
Db 17 GAACCTCGAGTCTCC 2
RESULT 169
ABK131561/c
ID ABL31561 standard; DNA; 17 BP.
XX
XX ABL31561;
AC
XX 21-MAR-2002 (first entry)
DT
XX Human HLA genotyping oligonucleotide SEQ ID NO 1050.
DE
XX Human; human leukocyte antigen; HLA; genotype; polymorphism;
KW immunogenetic; transplantation; genetic disease; ss.
KW
XX Homo sapiens.
OS
XX WO200192572-A1.
XX
XX 06-DEC-2001.
XX
XX 01-JUN-2001; 2001WO-JP004662.
XX
XX 01-JUN-2000; 2000JP-00164798.
XX
XX (NISN) NISSHINBO IND INC.
PA (SYST-) SYSTEM RES INC.
XX
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
PI WPI; 2002-122074/16.
XX
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
PT individuals e.g. by determining immunogenetic differences when
PT transplanting between them.
XX
XX Claim 10; Page 292; 345pp; Japanese.
XX
XX The invention relates to a typing kit for judging human leukocyte antigen
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of
CC genes e.g. belonging to HLA class I antigens on human genome and
CC containing gene polymorphisms as alloantigens have been immobilised as
CC primers for amplification of cleaved nucleic acids relating to gene
CC polymorphisms. The method is useful for judging HLA genotypes of
CC individuals by determining immunogenetic differences before transplanting
CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
CC pancreas, Langerhans islet in pancreas and cornea, susceptibility
CC diagnosis of genetic diseases and identifying individuals
XX
XX Sequence 17 BP; 4 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1734 GGCTCCCACTCTCC 1749
Db 16 GGCTCCCACTCTCC 1
RESULT 170
ACCS3446
ID ACC53446 standard; DNA; 17 BP.
XX
XX ACC53446;
AC

```

Mon Aug 30 09:26:45 2004

```

XX DT 27-JUN-2003 (first entry)
XX DE Human tumour suppressor sequence #2213.
XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX KW tumour regression; apoptosis; virus resistance; diagnosis;
XX KW cellular degeneration.
XX OS Homo sapiens.
XX FN FR2826373-A1.
XX PD 27-DEC-2002.
XX PF 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX PA (MOLE-) MOLECULAR ENGINEERS LAB SA.
XX PI Tuijnder M, Telerman A, Amson R;
XX DR WPI; 2003-250498/25.
XX PT New nucleic acid sequences associated with tumour suppression, regression,
XX PT apoptosis or virus resistance are useful to diagnose and treat viral
XX PT disease, development of tumour cells and cell degeneration.
XX PS Claim 1; Page 551; 798pp; French.
XX CC This sequence represents an isolated nucleic acid sequence associated
XX CC with tumour suppression or regression, apoptosis or virus resistance. The
XX CC invention relates to these sequences or sequences having at least 80%
XX CC identity to them, and polypeptides encoded by the sequences or
XX CC polypeptides having 80% identity to the polypeptide sequences. The
XX CC invention is used to diagnose or treat viral disease or disease
XX CC characterized by development of tumour cells or cellular degeneration
XX CC
XX CC Sequence 17 BP; 3 A; 1 C; 7 G; 6 T; 0 U; 0 Other;
XX CC
XX CC Query Match 9.2%; Score 12.8; DB 1; Length 17;
XX CC Best Local Similarity 87.5%; Pred. No. 2.4e+02;
XX CC Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX CC
XX QY 1693 AGCGTGGTGAAGTTG 1708
XX DB | ||||| ||||| |||||
XX DB 2 ATCGTGTGGAAGTTG 17
XX
XX RESULT 171
XX ACDS2214
XX ID ACDS2214 standard; RNA; 17 BP.
XX AC ACDS2214;
XX XX
XX DT 24-SEP-2003 (first entry)
XX DE HBV inozyme substrate sequence #293.
XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX KW RNA stability; RNA expression; RNA synthesis; antisense;
XX KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
XX KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
XX KW HBV reverse transcriptase; Enhancer I region; viral replication;
XX KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX KW virucide; antiinflammatory; substrate; ss.
XX OS Hepatitis B virus.
XX XX
XX FN WO200281494-A1.
XX XX

```

---

```

PD 17-OCT-2002.
XX 26-MAR-2002; 2002WO-US009187.
XX 26-MAR-2001; 2001US-00817879.
XX 08-JUN-2001; 2001US-00877478.
XX 08-JUN-2001; 2001US-0293876P.
XX 24-OCT-2001; 2001US-0333059P.
XX 05-DEC-2001; 2001US-0337055P.
XX (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MACE/) MACEJAK D.
XX PA (MCSW/) MCSWIGGEN J.
XX PA (MORE/) MORRISSEY D.
XX PA (PAVC/) PAVCO P.
XX PA (LEEF/) LEE P.
XX PA (DRAP/) DRAPER K.
XX PA (ROBE/) ROBERTS E.
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Favco P, Lee P;
XX Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX DR
XX PT Novel compound useful for treating cirrhosis, liver failure,
XX PT hepatocellular carcinoma, or condition associated with hepatitis C virus
XX PT infection.
XX PS Example 1; Page 155; 387pp; English.
XX CC The present invention relates to nucleic acid molecules which modulate
XX CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,
XX CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
XX CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
XX CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX CC as oligonucleotides that specifically bind the Enhancer I region of HBV
XX CC DNA. The nucleic acids may be used to modulate the expression of HBV
XX CC genes and HBV viral replication. Also disclosed is a method for screening
XX CC compounds and/or potential therapies directed against HBV, and compounds
XX CC that modulate the expression and/or replication of HCV. The compounds and
XX CC methods of the invention are useful for the treatment of degenerative and
XX CC disease states related to HBV and HCV infection, replication and gene
XX CC expression such as cirrhosis, liver failure, and hepatocellular
XX CC carcinoma. The present sequence represents a substrate for one of the HBV
XX CC ribozyme, inozyme, G-cleaver, zinzyme, DNzyme or amberyne sequences
XX CC disclosed in the present invention
XX CC
XX CC Sequence 17 BP; 2 A; 3 C; 5 G; 0 T; 7 U; 0 Other;
XX CC
XX CC Query Match 9.2%; Score 12.8; DB 1; Length 17;
XX CC Best Local Similarity 56.2%; Pred. No. 2.4e+02;
XX CC Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
XX CC
XX QY 1672 TGGAAACCTCGTGTCT 1687
XX DB : ||||| : |||||
XX DB 2 UGGAACCUUUGUCU 17
XX
XX RESULT 172
XX ACDS3479
XX ID ACDS3479 standard; RNA; 17 BP.
XX AC ACDS3479;
XX XX
XX DT 24-SEP-2003 (first entry)
XX DE HBV G-cleaver substrate sequence #167.
XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX KW RNA stability; RNA expression; RNA synthesis; antisense;

```





PT decreased or increased expression or activity of AMLP1.

XX Example 2; SEQ ID NO 63; 172pp; English.

XX The present invention describes the human angiotensin-like protein 1

CC (AMLPI). human AMLPI has cytosolic activity and can be used in gene

CC therapy. The AMLPI protein, nucleic acid molecules, antibodies, and

CC compositions of the present invention can be used for treating or

CC preventing a disorder associated with decreased or increased expression

CC or activity of AMLPI. The present sequence represents a scanning

CC oligonucleotide for human AMLPIa, which is used in an example from the

CC present invention.

XX Sequence 17 BP; 7 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

XX

XX Query Match 9.2%; Score 12.8; DB 1; Length 17;

XX Best Local Similarity 87.5%; Pred. No. 2.4e+02;

XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX

QY 1716 AGTACGGAGATGGAGA 1731

DB 1 AATACGGTATGGAGA 16

RESULT 176

ADD20651

ID ADD20651 standard; DNA; 17 BP.

XX AC ADD20651;

XX

XX 15-JAN-2004 (first entry)

XX Oreochromis niloticus microsatellite primer SEQ ID NO:1286.

DE single nucleotide polymorphism; SNP; fish; Salmo salar;

XX single nucleotide polymorphism; Atlantic halibut; microsatellite; cod;

KW Oreochromis niloticus; Atlantic halibut; microsatellite; cod;

KW polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;

KW detection; primer; ss.

XX

XX Synthetic.

OS Oreochromis niloticus.

XX

XX WO2003060160-A2.

XX

XX 24-JUL-2003.

XX

XX 17-JAN-2003; 2003WO-IB000112.

XX

XX 18-JAN-2002; 2002US-0349950P.

PR 16-AUG-2002; 2002US-0404200P.

XX

XX (GENO-) GENOMAR ASA.

XX

XX Lie O, Slettan A, Hoyum M, Lingaas F;

XX

XX WPI; 2003-627388/59.

DR

XX Novel isolated nucleic acid molecule comprising single nucleotide

PT polymorphism associated with fish, useful for forming PCR primers which

PT are used for detecting single nucleotide polymorphisms in fish nucleic

PT acids.

XX

XX Claim 18; SEQ ID NO 1286; 233pp; English.

PS

XX The present invention describes an isolated nucleic acid (I) comprising

CC single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of

CC Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;

CC and (ii) a nucleic acid having nucleotide sequence that hybridises to

CC (i), or its complement under highly stringent hybridisation conditions.

CC Also described: (1) an isolated oligonucleotide (II) comprising at least

CC 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.

CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod

CC polymorphic sites and seabass polymorphic sites, or their complement; (2)

```

XX WO2003037931-A2.
PN XX
XX 08-MAY-2003 .
XX
XX 01-NOV-2002; 2002WO-US035129.
XX PF
XX PR 01-NOV-2001; 2001US-0334773P.
XX PA
XX (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX PI Shannon M, Phan T;
XX PT WPT; 2003-430501/40.
XX DR
XX New isolated nucleic acid molecule encoding a human angiomotin-like
XX protein, useful for treating or preventing a disorder associated with
XX decreased or increased expression or activity of AMLPL1.
XX PS Example 2; SEQ ID NO 62; 172pp; English.
XX CC The present invention describes the human angiomotin-like protein 1
CC (AMLPL). Human AMLPL has cytostatic activity, and can be used in gene
CC therapy. The AMLPL protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLPL. The present sequence represents a scanning
CC oligonucleotide for human AMLPL $\alpha$ , which is used in an example from the
CC present invention.
XX SQ Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
QY Query Match          9.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches   14; Conservative      0; Mismatches    2; Indels     0; Gaps     0;
Db       1716 AGTACGGAGATGCGAGA 1731
        ||||| |||||||
        2 AATACGGTGATGCGAGA 17

RESULT 175
ADC37714
ID ADC37714 standard; DNA; 17 BP.
XX AC
XX AC ADC37714;
XX DT 18-DEC-2003 (first entry)
XX DE Human AMLPL $\alpha$  scanning 17-mer oligonucleotide SEQ ID NO:63.
XX KW human; angiomotin-like protein 1; AMLPL; cytotstatic; gene therapy;
KW AMLPL $\alpha$ ; ss.
XX OS Synthetic.
OS Homo sapiens.
XX PN WO2003037931-A2.
XX PD 08-MAY-2003 .
XX PF 01-NOV-2002; 2002WO-US035129.
XX PR 01-NOV-2001; 2001US-0334773P.
XX PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX PI Shannon M, Phan T;
XX PT WPT; 2003-430501/40.
XX DR
XX New isolated nucleic acid molecule encoding a human angiomotin-like
XX protein, useful for treating or preventing a disorder associated with
XX decreased or increasing expression or activity of AMLPL1.
XX PS Example 2; SEQ ID NO 62; 172 pp; English.
```

CC a primer pair (III) suitable for use in PCR, comprising two (II) capable  
 CC of amplifying a nucleotide sequence chosen from S. salar SNPs and, O.  
 CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod  
 CC polymorphic sites and seabass polymorphic sites; and determining (M1) the  
 CC origin of fish sample comprising providing a parentage genotype database  
 CC comprising a collection of candidate parent genotypes, where each of the  
 CC candidate parent genotype represents a distinct origin, and comparing a  
 CC sample genotype to the parentage genotype database, where a match between  
 CC the sample genotype and one of the candidate parent genotype identifies  
 CC to the origin of the sample. (M1) is useful for determining the origin of  
 CC a fish sample such as family salmonidae, S. salar, tilapia, O. niloticus,  
 CC rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for  
 CC detecting nucleic acid molecule comprising SNP in a sample, which  
 CC involves contacting the sample containing nucleic acid in a sample, which  
 CC (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus  
 CC SNPs, and identifying nucleic acid that hybridizes to (II). (II) is  
 CC useful for detecting nucleic acid molecule comprising a polymorphic  
 CC sequence in a sample, comprising contacting the sample containing nucleic  
 CC acids with one or more (II) which is derived from O. niloticus  
 CC microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic  
 CC sites or seabass polymorphic sites, and identifying a nucleic acid that  
 CC hybridizes to (II). (III) is useful for detecting nucleic acid molecule  
 CC comprising a microsatellite sequence in sample. The present sequence is  
 CC used in the exemplification of the present invention.

XX  
 SQ Sequence 17 BP; 0 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 9.2%; Score 12.8; DB 1; Length 17;  
 Best Local Similarity 87.5%; Pred. No. 2.4e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1677 CCTGTGTCCTCTCC 1692

DB 1 CCTGTGTCCTCTCC 16

RESULT 177

AAQ91453/c

ID AAQ91453 standard; DNA; 18 BP.

XX AAQ91453;

XX 25-MAR-2003 (revised)

XX 30-AUG-1995 (first entry)

XX Dysprosium (III) texaphyrin (DyTx) DNA conjugate.

XX Dysprosium (III) texaphyrin (DyTx) DNA conjugate; liver disease;  
 XX targeted intracellular mRNA hydrolysis; gene expression inhibition;  
 XX hormone regulation; hydrolysis reagents; alkyl phosphate esters;  
 XX detoxification; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX modified\_base 1

XX /\*tag= a

XX /mod\_base= OTHER

XX /note= "DyTx-NH(CH2)6-PO4-thymine"

XX WO9429316-A2.

XX 22-DEC-1994.

XX 09-JUN-1994; 94WO-US006284.

XX 09-JUN-1993; 93US-00075123.

XX 14-APR-1994; 94US-00227370.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (PHAR-) PHARMACYCLICS INC.

XX Sessler JL, Ross KL, Wright M, Hemmi GW, Dow WC, Smith DA;

PI Kral VA, Iverson B, Mody T, Miller RA, Magda D;

XX WPI; 1995-036382/05.

XX Texaphyrin metal complex mediated ester hydrolysis - esp. useful for  
 XX targeted intracellular hydrolysis of mRNA and for inhibiting gene  
 XX expression.

XX Disclosure; Fig 21; 125pp; English.

XX AAQ91451-091457 are texaphyrin lanthanide metal DNA conjugates, which are  
 XX esp. useful for the targeted intracellular hydrolysis of mRNA; inhibiting  
 XX gene expression. They may also be used for the treatment of liver disease,  
 XX as hormone regulation agents and as hydrolysis reagents for the  
 XX detoxification of alkyl phosphate esters. (Updated on 25-MAR-2003 to  
 XX correct PN field.)

XX Sequence 18 BP; 1 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 9.2%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAG 1670

DB 17 AACACCCGGCTCACAG 2

RESULT 178

AAV07301/c

ID AAV07301 standard; DNA; 18 BP.

XX AAV07301;

XX 14-AUG-1998 (first entry)

XX Metallohexaphyrin-oligonucleotide conjugate #15.

XX Metallohexaphyrin; dysprosium; europium; conjugate; RNase H;  
 XX antisense therapy; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX modified\_base 1

XX /\*tag= a

XX /mod\_base

XX /note= "DyTxNH-(CH2)6-PO4-thymine, where DyTx is  
 XX dysprosium (III) texaphyrin"

XX US5763172-A.

XX 09-JUN-1998.

XX 07-JUN-1995; 95US-00486962.

XX 21-JAN-1992; 92US-00822964.

XX 09-JUN-1993; 93US-00075123.

XX 14-APR-1994; 94US-00227370.

XX 09-JUN-1994; 94WO-US006284.

XX 26-MAY-1995; 95US-00452261.

XX 07-JUN-1995; 95US-00485581.

XX (PHAR-) PHARMACYCLICS INC.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Sessler JL, Wright M, Miller RA, Dow WC, Magda D;

XX WPI; 1998-347306/30.

XX Enhancing therapeutic activity of oligo-nucleotides in cells - using  
 XX conjugate comprising metallohexaphyrin, which hydrolyses phosphate ester  
 XX bonds of RNA, and oligo-nucleotide, which binds to targetted RNA.

XX Example 6; Fig 5; 34pp; English.

XX The invention relates to a method of enhancing the therapeutic activity

XX of oligonucleotides in cells. It comprises contacting a targeted

XX intracellular RNA in a cell with a metallotexaphyrin-oligonucleotide

XX conjugate. The contact is carried out under physiological conditions for

XX a time sufficient to hydrolyse the phosphate ester bond of the targeted

XX RNA. The metallotexaphyrin of the conjugate has catalytic activity for

XX phosphate ester bond hydrolysis. The oligonucleotide of the conjugate has

XX complementary binding affinity to the targeted RNA. The conjugate may be

XX used in antisense therapies for treating, e.g. cancer, viral infections,

XX autoimmune diseases and restenosis. The conjugate may also be used as

XX hydrolysis reagents for the detoxification of di- and trialkyl phosphate

XX esters, which are used in solvents, insecticides and chemical nerve

XX gases. The metallotexaphyrin complex enhances the therapeutic activity of

XX the oligonucleotide, not only by facilitating cellular uptake of the

XX oligonucleotide but also by hydrolysing target RNA within the cell.

XX independent of RNase H. Attachment to the complex may also cause the

XX oligonucleotide to take on some of the pharmacodynamic and biodistribution

XX properties of the texaphyrin, such as selective localisation in tumours.

XX The present sequence represents a metallo- texaphyrin-oligonucleotide

XX conjugate

XX SQ Sequence 18 BP; 1 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 9.2%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 AGCACCAGGCTCACAG 1670

Db 17 AACACCGGCTCACAG 2

RESULT 179

AAA92642

ID AAA92642 standard; DNA; 18 BP.

XX AAA92642;

AC AAA92642;

XX 04-JAN-2001 (first entry)

XX Antisense oligonucleotide ISIS# 30365.

XX Human; SRA; steroid receptor RNA activator; cytostatic; antiinflammatory;

XX SRA inhibitor; cancer; infection; antisense oligonucleotide; ss.

XX Synthetic.

XX US6107092-A.

XX 22-AUG-2000.

XX 29-MAR-1999; 99US-00280409.

XX 29-MAR-1999; 99US-00280409.

XX (ISIS-) ISIS PHARM INC.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Cowsert LM, Bennett CF, O'malley BW;

XX WPI; 2000-586211/55.

XX 22-AUG-2000.

XX 29-MAR-1999; 99US-00280409.

XX 29-MAR-1999; 99US-00280409.

XX (ISIS-) ISIS PHARM INC.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Cowsert LM, Bennett CF, O'malley BW;

XX WPI; 2000-586211/55.

XX Antisense compounds targeted to steroid receptor RNA activator useful for

XX diagnosis, prophylaxis and treatment of diseases associated with the

XX steroid activator, such as infection, inflammation or tumor formation.

XX Claim 3; Col 42; 47pp; English.

XX The present sequence is one of a large number of antisense

XX oligonucleotides which is directed against one of four human steroid

XX receptor RNA activator (SRA) nucleic acid sequences. Two series of

XX antisense oligonucleotides were synthesised. The first series comprised 8

XX -30 oligodeoxynucleotides with a phosphorothioate backbone. The second

XX series comprised chimeric oligonucleotides composed of a central gap

XX region, consisting of ten 2'-deoxynucleotides, which was flanked on both

XX sides by four-nucleotide wings. The wings were composed of 2'-

XX methoxyethyl (2'-MOE) nucleotides. Both series contained the same

XX nucleotide sequences. The antisense compounds are useful for research,

XX diagnosis, treatment and prophylaxis to prevent or delay infection,

XX inflammation or tumour formation. Therapeutically the oligonucleotides

XX are highly safe and are effectively administered to humans

XX SQ Sequence 18 BP; 3 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 9.2%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGAGACCTGGT 1683

Db 2 CTGCTGGAGACCTGGT 17

RESULT 180

AAA92609

ID AAA92609 standard; DNA; 18 BP.

XX AAA92609;

AC AAA92609;

XX 04-JAN-2001 (first entry)

XX Antisense oligonucleotide ISIS# 30428.

XX Human; SRA; steroid receptor RNA activator; cytostatic; antiinflammatory;

XX SRA inhibitor; cancer; infection; antisense oligonucleotide; ss.

XX Synthetic.

XX US6107092-A.

XX 22-AUG-2000.

XX 29-MAR-1999; 99US-00280409.

XX 29-MAR-1999; 99US-00280409.

XX (ISIS-) ISIS PHARM INC.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Cowsert LM, Bennett CF, O'malley BW;

XX WPI; 2000-586211/55.

XX Antisense compounds targeted to steroid receptor RNA activator useful for

XX diagnosis, prophylaxis and treatment of diseases associated with the

XX steroid activator, such as infection, inflammation or tumor formation.

XX Claim 3; Col 42; 47pp; English.

XX The present sequence is one of a large number of antisense

XX oligonucleotides which is directed against one of four human steroid

XX receptor RNA activator (SRA) nucleic acid sequences. Two series of

XX antisense oligonucleotides were synthesised. The first series comprised 8

XX -30 oligodeoxynucleotides with a phosphorothioate backbone. The second

XX series comprised chimeric oligonucleotides composed of a central gap

XX region, consisting of ten 2'-deoxynucleotides, which was flanked on both

XX sides by four-nucleotide wings. The wings were composed of 2'-

XX methoxyethyl (2'-MOE) nucleotides. Both series contained the same

XX nucleotide sequences. The antisense compounds are useful for research,

XX diagnosis, treatment and prophylaxis to prevent or delay infection,

XX inflammation or tumour formation. Therapeutically the oligonucleotides

XX are highly safe and are effectively administered to humans



XX PD 21-MAR-2000.  
 XX PF 10-JAN-1997; 97US-00785247.  
 XX PR 11-JAN-1996; 96US-0009900P.  
 XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 XX PI Zhang Y, Liu J, Kolesnick RN;  
 XX DR WPI; 2000-270133/23.  
 XX PT Novel method of identifying agents capable of inhibiting  
 PT lipopolysaccharide induced threonine phosphorylation by a ceramide-  
 PT activated protein kinase.  
 XX PS Example VI; Col 56; 84pp; English.  
 XX CC The invention relates to a novel method of determining whether an agent  
 CC is capable of specifically inhibiting the ability of a ceramide-activated  
 CC protein (CAP) kinase to phosphorylate the threonine residue in a  
 CC polypeptide containing a Thr-Pro- or Thr-Leu-Pro motif. In particular,  
 CC the peptide substrate that is specifically phosphorylated is Raf-1,  
 CC the epidermal growth factor receptor (EGFR), or suitable fragments thereof.  
 CC The CAP kinase is membrane bound and has an apparent molecular weight of  
 CC 100-110 kD. It is an upstream participant in a sphingomyelin signal  
 CC transduction pathway which uses ceramide as a second messenger. This  
 CC pathway is initiated by tumour necrosis factor-alpha (TNF-alpha) and  
 CC interleukin-beta (IL-beta), causing the hydrolysis of sphingomyelin to  
 CC ceramide. The ceramide in turn stimulates the kinase to phosphorylate  
 CC protein substrates which can then mediate signal transduction. The CAP  
 CC kinase is also stimulated by the bacterial endotoxin lipopolysaccharide  
 CC (LPS), which is thought to mimic the second messenger function of  
 CC ceramide. The methods are useful for identifying agents that inhibit  
 CC lipopolysaccharide-induced Thr phosphorylation by CAP kinase. The agents  
 CC identified using the method are useful for treating disorders associated  
 CC with aberrant phosphorylation of target molecules by CAP kinase, e.g.,  
 CC inflammatory disorders (such as rheumatoid arthritis), ulcerative  
 CC colitis, graft versus host disease, lupus erythematosus, HIV, infection,  
 CC disorders associated with poor stem cell growth, and septic shock.  
 CC Sequences AAA07014-A07015 represent PCR primers used in an  
 CC exemplification of the present invention to introduce DNA encoding the  
 CC Flag epitope (DYKDDDDK) immediately 5' of the Raf-1 start codon in the  
 CC Bluescript KS vector  
 XX SQ Sequence 19 BP; 7 A; 4 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 9.2%; Score 12.8; DB 1; Length 19;  
 Best Local Similarity 87.5%; Pred. No. 2.8e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1648 GAAGGCAAGCAGCAGG 1663  
 Db 1 GAAGGCAAGCTTCAGG 16  
 RESULT 184  
 AAA82742  
 ID AAA82742 standard; DNA; 19 BP.  
 XX AC AAA82742;  
 XX DT 04-DEC-2000 (first entry)  
 XX DE cdk3 ribozyme binding site #27.  
 XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.  
 XX OS Mammalia.  
 XX PN WO200032765-A2.  
 XX PI

PD 08-JUN-2000.  
 XX PF 06-DEC-1999; 99WO-US028772.  
 XX PR 04-DEC-1998; 98US-0110954P.  
 XX PA (IMMU-) IMMUSOL INC.  
 XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;  
 XX DR WPI; 2000-412314/35.  
 XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
 PT PCNA and Cyclin B1.  
 XX PS Disclosure; Page 51; 109pp; English.  
 XX CC The present invention relates to a hairpin or hammerhead ribozyme,  
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
 CC Representative examples of ribozyme recognition sites are given in  
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for  
 CC inhibiting restenosis by introduction of the ribozyme into cells. The  
 CC ribozyme is resistant to endonuclease activity and hence is efficient in  
 CC restenosis treatment  
 XX SQ Sequence 19 BP; 3 A; 10 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 9.2%; Score 12.8; DB 1; Length 19;  
 Best Local Similarity 87.5%; Pred. No. 2.8e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1657 CACCGAGCTCAGAGCT 1672  
 Db 1 CCCAGGCTCAGAGCT 16  
 RESULT 185  
 AAA57904  
 ID AAA57904 standard; DNA; 19 BP.  
 XX AC AAA57904;  
 XX DT 10-SEP-2001 (first entry)  
 XX DE Cell-cycle dependent kinase cdk3 ribozyme binding site SEQ ID NO:328.  
 XX KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
 KW recognition site; target; ribozyme binding site; eye disease; vulneryary;  
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;  
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;  
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;  
 KW antiskilling; ophthalmological; keratolytic; gene therapy; viral wart;  
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;  
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;  
 KW sickle cell retinopathy; ss.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO200130362-A2.  
 XX PD 03-MAY-2001.  
 XX PF 26-OCT-2000; 2000WO-US029500.  
 XX PR 26-OCT-1999; 99US-0161532P.  
 XX PA (IMMU-) IMMUSOL INC.  
 XX PI Robbins JM, Tritz R;

XX WPI; 2001-300427/31.

XX Treating proliferative skin or eye diseases and scarring, using ribozymes

PT that cleave RNA encoding cytokines involved in inflammation, matrix

PT metalloproteinases, growth factors and cell-cycle dependent kinases.

XX

PS Example 1; Page 95; 408pp; English.

XX

XX The present invention describes a method for treating a proliferative

CC skin or eye disease and scarring. The method involves administering a

CC ribozyme (I) which cleaves RNA encoding a cytokine involved in

CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle

CC dependent kinase, growth factor or a reductase, or administering a

CC nucleic acid molecule (II) comprising a promoter operably linked to a

CC nucleic acid segment encoding (I). (I) can have antipsoriatic,

CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,

CC ophthalmological, vulnary, keratolytic and virucide activities, and

CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used

CC in gene therapy. (I) and (II) are useful for treating proliferative skin

CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,

CC squamous or basal cell carcinoma and viral or seborrheic wart. They can

CC also be used for treating proliferative eye diseases such as diabetic

CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of

CC prematurity and retinal detachment, and for treating and preventing

CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn

CC scar. AAH57577 to AAH62099 represent sequences used in the

CC exemplification of the present invention

XX

XX Sequence 19 BP; 3 A; 10 C; 4 G; 2 T; 0 U; 0 Other;

SQ

Query Match 9.2%; Score 12.8; DB 1; Length 19;

Best Local Similarity 87.5%; Pred. No. 2.8e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1657 CACCAGGCTCACAGCT 1672

DB 1 CCCCAGGCTCAGAGCT 16

RESULT 186

ABF35838

ID ABF35838 standard; DNA; 13 BP.

XX

AC ABF35838;

XX

DT 21-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 135835 for detecting SNP TSC0033923.

XX

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR Oligonucleotide SEQ ID NO 135835 for detecting SNP TSC0033923.

XX

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

WPI; 2001-657177/75.

XX

Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

XX Claim 1; SEQ ID NO 135835; 29pp + Sequence Listing; German.

XX

XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 13 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 1 Other;

Query Match 9.1%; Score 12.6; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 1.8e+02;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATT 1733

DB 1 GGAGATGGAGATY 13

RESULT 187

ABF35839/c

ID ABF35839 standard; DNA; 13 BP.

XX

AC ABF35839;

XX

DT 21-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 135836 for detecting SNP TSC0033923.

XX

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

WPI; 2001-657177/75.

XX

Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

XX

Claim 1; SEQ ID NO 135836; 29pp + Sequence Listing; German.

XX

XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

```
CC  was obtained in electronic format from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 13 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 1 Other;
    Query Match          9.1%; Score 12.6; DB 1; Length 13;
    Best Local Similarity 92.3%; Pred. No. 1.8e+02;
    Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1721 GGAGTGGAGATT 1733
    |||||
    13 GGAGTGGAGATT 1
Db

RESULT 188
AAQ84806
ID  AAQ84806 standard; DNA; 19 BP.
XX
AC  AAQ84806;
XX
DT  25-MAR-2003 (revised)
DT  25-SEP-1995 (first entry)
XX
DE  Spinocerebellar ataxia type 1 (SCA 1) PCR primer X2-2 (185-203).
XX
KW  Spinocerebellar ataxia type 1; SCA 1; presymptomatic diagnosis;
KW  PCR primer X2-2 (185-203); ss.
XX
OS  Synthetic.
XX
PN  WO9501437-A2.
XX
PD  12-JAN-1995.
XX
PF  29-JUN-1994; 94WO-US007336.
XX
PR  29-JUN-1993; 93US-00084365.
PR  28-JUN-1994; 94US-00267803.
XX
PA  (MINU ) UNIV MINNESOTA.
PI  Orr HT, Chung M, Zoghbi HV;
XX
XX  WPI; 1995-061001/08.
DR
XX
PT  New autosomal dominant spinocerebellar ataxia type 1 nucleic acid - used
PT  to develop prods. for detection or presymptomatic diagnosis of a SCA1
PT  disorder.
XX
PS  Example II; Page 72; 11pp; English.
XX
CC  AAQ84805 and AAQ84806 are a pair of primers for the PCR amplification of
CC  AAQ84793, a new autosomal dominant spinocerebellar ataxia type 1 (SCA 1)
CC  nucleic acid, which encodes the protein product described in AAR71111.
CC  Both the nucleic acid and the protein can be used to develop products.
CC  for the presymptomatic detection of a SCA 1 disorder. (Updated on 25-MAR-
CC  2003 to correct PN field.)
XX
XX  Sequence 19 BP; 5 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
SQ
    Query Match          9.1%; Score 12.6; DB 1; Length 19;
    Best Local Similarity 78.3%; Pred. No. 3.1e+02;
    Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  1657 CACCAGGCTCACAGCTGGA 1675
    |||||
    1 CACCAGCTCCCTGATGA 19
Db

RESULT 189
AAQ85482
ID  AAQ85482 standard; DNA; 19 BP.
XX
```



XX WPI; 1996-233347/24.  
 XX 18S rRNA oligo:nucleotide(s) for detection and identification of fungi -  
 PT esp. for diagnosis of mycosis including candidiasis and aspergillosis.  
 XX Claim 3; Page 2; 11pp; Japanese.  
 XX The sequences given in AAT27632-42 are primer/probes which were used in a  
 CC method for the detection of pathogenic fungi. They are esp. useful in the  
 CC diagnosis of mycosis including candidiasis and aspergillosis. The  
 CC sequences in AAT27632-36 are oligonucleotides which bind to fungal 18S  
 CC rRNA sequences, whereas the sequences given in AAT27637-42 are species  
 CC specific oligonucleotides. The 18S rRNA sequences are based on sequences  
 CC isolated from *Candida albicans* (see also AAT27643)  
 XX Sequence 19 BP; 7 A; 5 C; 6 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 9.1%; Score 12.6; DB 1; Length 19;  
 Best Local Similarity 78.9%; Pred. No. 3.1e+02;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1646 CAGAGGCGCAGCACCAGGC 1664  
 DB 1 CAGAGGAAAGGTCAGCC 19  
 RESULT 191  
 AAT77561  
 ID AAT77561 standard; DNA; 19 BP.  
 XX AC AAT77561;  
 XX 11-SEP-1997 (first entry)  
 DE Wheat microsatellite WMS122 left primer.  
 XX Microsatellite marker; hypervariable genomic fragment; *Triticum aestivum*;  
 KW wheat; Triticeae; sequence tagged site; STS; primer; PCR; amplify;  
 KW polymorphism; genetic analysis; hexaploid; tetraploid; mapping; ss.  
 OS Synthetic.  
 XX DE19525284-A1.  
 PN 02-JAN-1997.  
 XX 28-JUN-1995; 95DE-01025284.  
 XX 28-JUN-1995; 95DE-01025284.  
 PR (PFLA-) INST PFLANZENGENETIK & KULTURPFLANZENFOR.  
 PA Roeder M, Plaschke J, Ganai M;  
 XX WPI; 1997-053731/06.  
 XX Primers for STS microsatellite markers for wheat and related species -  
 PT useful for genetic mapping, analysis and labelling etc. of wheat.  
 XX Claim 5; Page 7; 8pp; German.  
 XX Microsatellite markers based on hypervariable genomic fragments, from  
 CC *Triticum aestivum* (wheat) or the tribe Triticeae, consist of a sequence  
 CC tagged site (STS), defined by 2 specific primers (of mean size 17-23  
 CC bases) that flank a microsatellite sequence at both ends, which can be  
 CC amplified to polymorphisms (PCR products of different sizes). The  
 CC microsatellites are n-fold tandem repeats (n = 10 or more) of di-, tri-  
 CC or tetra-nucleotide sequences, combination microsatellite sequences or an  
 CC imperfect sequence in which individual bases are mutated. The  
 CC microsatellite markers can be used for genetic analysis of hexaploid and  
 CC tetraploid forms of wheat and for genetic mapping or labelling of  
 CC monogenic and polygenic properties, and for their selection; for

CC analysing relationships and identifying varieties; and for evaluating  
 CC varietal purity, hybrid identification and plant growth. The markers can  
 CC differentiate between almost all European wheat lines and show a higher  
 CC degree of DNA polymorphism than known probes for the wheat genome. They  
 CC can be detected by PCR, so large numbers of samples can be analysed  
 CC easily (e.g. several hundred per day). Microsatellite marker-related  
 CC polymorphisms are stably inherited so can also serve as genetic markers.  
 CC AAT77003-22 and AAT77535-716 are primer pairs that define the  
 CC microsatellite markers. WMS122 has CT and CA type repeats  
 XX Sequence 19 BP; 6 A; 0 C; 11 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 9.1%; Score 12.6; DB 1; Length 19;  
 Best Local Similarity 78.9%; Pred. No. 3.1e+02;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1709 GGTAGGAGTACGAGATG 1727  
 DB 1 GGTGGGAGAAAGGAGATG 19  
 RESULT 192  
 AAA85488  
 ID AAA85488 standard; DNA; 19 BP.  
 XX AC AAA85488;  
 XX 04-DEC-2000 (first entry)  
 DT Cyclin A1 ribozyme binding site #110.  
 DE Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.  
 XX Mammalia.  
 XX WO200032765-A2.  
 PN 08-JUN-2000.  
 PD 06-DEC-1999; 99WO-US028772.  
 PF 04-DEC-1998; 98US-0110954P.  
 PR (IMMU-) IMMUSOL INC.  
 XX Tritz R, Welch PJ, Barber JR, Robbins JM;  
 XX WPI; 2000-412314/35.  
 DR New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
 XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
 XX PCNA and Cyclin B1.  
 PS Disclosure; Page 93; 109pp; English.  
 XX The present invention relates to a hairpin or hammerhead ribozyme,  
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
 CC Representative examples of ribozyme recognition sites are given in  
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for  
 CC inhibiting restenosis by introduction of the ribozyme into cells. The  
 CC ribozyme is resistant to endonuclease activity and hence is efficient in  
 CC restenosis treatment  
 XX Sequence 19 BP; 5 A; 0 C; 11 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 9.1%; Score 12.6; DB 1; Length 19;  
 Best Local Similarity 78.9%; Pred. No. 3.1e+02;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1698 GGTGGAGCTGGTTAGGA 1716  
 DB 1 GGTGGAGTTGGGAGAA 19

```

XX PN WO9954500-A2.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-IB000822.
XX PR 21-APR-1998; 98US-0083614P.
XX PR 23-NOV-1998; 98US-0109732P.
XX PA (GEST ) GENSET.
XX PI Cohen D, Blumenfeld M, Chumakov I;
XX PI WPI; 2000-013267/01.
XX DR Novel biallelic markers used to construct a high density disequilibrium
XX PT map of the human genome.
XX PS Claim 8; Page 1995; 2745pp; English.
XX CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX CC invention, which contain a polymorphic base at position 24 of their
XX CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX CC primers for the biallelic markers. The biallelic markers of the invention
XX CC have a variety of uses: they can be used for high density mapping of the
XX CC human genome, and in complex association studies and haplotyping studies
XX CC which are useful in determining the genetic basis for disease states.
XX CC Compositions and methods of the invention can also be useful for the
XX CC identification of the targets for the development of pharmaceutical
XX CC agents and diagnostic methods, as well as the characterisation of the
XX CC differential efficacious responses to and side effects from
XX CC pharmaceutical agents acting on a disease as well as other treatment.
XX CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX CC 3367, are not actually given a sequence in the Sequence Listing from the
XX CC present invention
XX SQ Sequence 19 BP; 7 A; 10 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 5.1%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1694 GCGTGGTGGAGTTGGGTT 1712
Db ||||| ||||| ||||| |||||
19 GACTTGGGATGTTGGGGT 1

RESULT 195
AAH60650
ID AAH60650 standard; DNA; 19 BP.
XX AC AAH60650;
XX DT 10-SEP-2001 (first entry)
XX DE Cyclin A1 ribozyme binding site SEQ ID NO:3074.
XX KW Human, ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
XX KW recognition site; target; ribozyme binding site; eye disease; vulvar;
XX KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
XX KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
XX KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
XX KW antipsoriatic; dermatological; antiseborrheic; keratolytic; gene therapy; viral wart;
XX KW antiscarring; ophthalmological; actinic keratosis; squamous cell carcinoma;
XX KW atopic dermatitis; actinic keratosis; seboreic wart; vitreoretinopathy; scar;
XX KW basal cell carcinoma; seboreic wart; vitreoretinopathy; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200130362-A2.

RESULT 193
AAA84289
ID AAA84289 standard; DNA; 19 BP.
XX AC AAA84289;
XX DT 04-DEC-2000 (first entry)
XX DE Cyclin D1 ribozyme binding site #56.
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX OS Mammalia.
XX PN WO200032765-A2.
XX PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch FV, Barber JR, Robbins JM;
XX PI WPI; 2000-412314/35.
XX DR New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PT PCNA and Cyclin B1.
XX PS Disclosure; Page 74; 109pp; English.
XX SQ Sequence 19 BP; 5 A; 8 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 9.1%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1739 CCAACTCTCTCCCTATCCTA 1757
Db ||||| ||||| ||||| |||||
1 CCAACAACTTCTCTCTCCTA 19

RESULT 194
AAZ73922/c
ID AAZ73922 standard; DNA; 19 BP.
XX AC AAZ73922;
XX DT 10-SEP-2001 (first entry)
XX DE Human biallelic marker downstream amplification primer SEQ ID NO:8278.
XX KW Human genome; biallelic marker; high density disequilibrium map;
XX KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX KW haplotyping; hybridisation; identification; characterisation;
XX KW amplification; single nucleotide polymorphism; SNP; PCR primer;
XX KW diagnosis; ss.
XX OS Homo sapiens.

```

```

XX PD 03-MAY-2001.
XX PF 26-OCT-2000; 2000WO-US029500.
XX PR 26-OCT-1999; 99US-0161532P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Robbins JM, Tritz R;
XX DR WPI; 2001-300427/31.
XX PT Treating proliferative skin or eye diseases and scarring, using ribozymes
XX PT that cleave RNA encoding cytokines involved in inflammation, matrix
XX PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX PS Example 1; Page 295; 408pp; English.
XX CC The present invention describes a method for treating a proliferative
XX CC skin or eye disease and scarring. The method involves administering a
XX CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
XX CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
XX CC dependent kinase, growth factor or a reductase, or administering a
XX CC nucleic acid molecule (II) comprising a promoter operably linked to a
XX CC nucleic acid segment encoding (I). (I) can have antiposoriatic,
XX CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
XX CC ophthalmological, vulnary, keratolytic and virucide activities, and
XX CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
XX CC in gene therapy. (I) and (II) are useful for treating proliferative skin
XX CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
XX CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
XX CC also be used for treating proliferative eye diseases such as diabetic
XX CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
XX CC prematurity and retinal detachment, and for treating and preventing
XX CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
XX CC scar. AAH57577 to AAH62099 represent sequences used in the
XX CC exemplification of the present invention
XX SQ Sequence 19 BP; 5 A; 0 C; 11 G; 3 T; 0 U; 0 Other;
      Query Match 9.1%; Score 12.6; DB 1; Length 19;
      Best Local Similarity 78.9%; Pred. No. 3.1e+02;
      Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1698 GGTGGAGTTCGGTACGA 1716
Db ||||| ||||| ||||| ||||| |||||
  1 GGTGGAGTTCGGGAAGAA 19

RESULT 196
AAH59451
ID AAH59451 standard; DNA; 19 BP.
XX AC AAH59451;
XX DT 10-SEP-2001 (first entry)
XX DE Cyclin D1 ribozyme binding site SEQ ID NO:1875.
XX KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
XX KW recognition site; target; ribozyme binding site; eye disease; vulnary;
XX KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
XX KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
XX KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
XX KW antiposoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
XX KW antisickling; ophthalmological; keratolytic; antidiabetic; virucide;
XX KW atopic dermatitis; actinic keratosis; gene therapy; viral wart;
XX KW basal cell carcinoma; seborrheic wart; squamous cell carcinoma;
XX KW sickle cell retinopathy; ss.
XX OS Homo sapiens.
XX OS Synthetic.

```

```

XX PN WO200130362-A2.
XX PD 03-MAY-2001.
XX PF 26-OCT-2000; 2000WO-US029500.
XX PR 26-OCT-1999; 99US-0161532P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Robbins JM, Tritz R;
XX DR WPI; 2001-300427/31.
XX PT Treating proliferative skin or eye diseases and scarring, using ribozymes
XX PT that cleave RNA encoding cytokines involved in inflammation, matrix
XX PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX PS Example 1; Page 208; 408pp; English.
XX CC The present invention describes a method for treating a proliferative
XX CC skin or eye disease and scarring. The method involves administering a
XX CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
XX CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
XX CC dependent kinase, growth factor or a reductase, or administering a
XX CC nucleic acid molecule (II) comprising a promoter operably linked to a
XX CC nucleic acid segment encoding (I). (I) can have antiposoriatic,
XX CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
XX CC ophthalmological, vulnary, keratolytic and virucide activities, and
XX CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
XX CC in gene therapy. (I) and (II) are useful for treating proliferative skin
XX CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
XX CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
XX CC also be used for treating proliferative eye diseases such as diabetic
XX CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
XX CC prematurity and retinal detachment, and for treating and preventing
XX CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
XX CC scar. AAH57577 to AAH62099 represent sequences used in the
XX CC exemplification of the present invention
XX SQ Sequence 19 BP; 5 A; 8 C; 1 G; 5 T; 0 U; 0 Other;
      Query Match 9.1%; Score 12.6; DB 1; Length 19;
      Best Local Similarity 78.9%; Pred. No. 3.1e+02;
      Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1739 CCAACTCTCTCCCTATCCTA 1757
Db ||||| ||||| ||||| ||||| |||||
  1 CCAACAACTTCTCTGCTCTA 19

RESULT 197
AAQ34483
ID AAQ34483 standard; DNA; 15 BP.
XX AC AAQ34483;
XX DT 25-MAR-2003 (revised)
XX DT 12-MAY-1993 (first entry)
XX DE Oligo 9, a PCR primer for plant DHK-hydroxylating enzyme clone.
XX KW Dihydrokaempferol; flavonoid; pigmentation; colour; amplification;
XX KW cytochrome P450; ss.
XX OS Synthetic.
XX PN EP522880-A2.
XX PD 13-JAN-1993.
XX PF 10-JUL-1992; 92EP-00306379.

```

```
XX PR 11-JUL-1991; 91AU-00007173.
XX PR 17-FEB-1992; 92AU-00000923.
XX XX (ITFL-) INT FLOWER DEV PTY LTD.
XX XX Holton TA, Cornish EC, Kovacic F, Tanaka Y, Lester DR;
XX DR WPI; 1993-010688/02.
XX XX Nucleic acid sequence encoding a di:hydro:kaempferol-hydroxylating enzyme
XX PT - e.g. cytochrome P450 introduced into transgenic plants for controlling
XX PT flavonoid pigmentation in plants and organisms.
XX PS Disclosure; Page 13; 66pp; English.
XX CC The PCR primer may be used in PCR for amplification of petal cytochrome
XX CC P450 homologues. See also AAQ34475-91. (Updated on 25-MAR-2003 to correct
XX CC PN field.)
XX SQ Sequence 15 BP; 2 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 8.9%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 92.9%; Pred. No. 2.5e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1683 TGTCTCTCTCCAGCG 1696
DB 2 TGTCTCTCTCCAGTG 15
XX
RESULT 199
AAQ56245
ID AAQ56245 standard; cDNA; 15 BP.
XX AC AAQ56245;
XX XX 25-MAR-2003 (revised)
XX DT 08-AUG-1994 (first entry)
XX XX
XX DE PCR primer for amplifying chi-A gene sequence.
XX KW Anthocyanidin-3-glucoside rhamnosyltransferase; glucosyltransferase;
XX KW inflorescence; flowering plants; transgenic plant; Petunia hybrida;
XX KW chi-A; ss.
XX OS Synthetic.
XX XX WO9403591-A1.
XX XX 17-FEB-1994.
XX XX 30-JUL-1993; 93WO-AU000387.
XX XX 30-JUL-1992; 92AU-00003846.
XX XX (ITFL-) INT FLOWER DEV PTY LTD.
XX XX Brugliera F, Holton TA;
XX XX WPI; 1994-065680/08.
XX XX Nucleic acid encoding glycosyltransferase enzymes - used for producing
XX PT transgenic plants with altered inflorescence properties including
XX PT modified petal colours.
XX PS Example 17; Page 21; 76pp; English.
XX CC Two primers (AAQ56245, AAQ56246) were used to amplify the chi-A gene.
XX CC This primer corresponds to nucleotides 6-20 of the published chi-A cDNA
XX CC sequence. chi-A is a previously characterised flavonoid biosynthesis
XX CC gene. (Updated on 25-MAR-2003 to correct PN field.)
XX XX
```

DT 04-NOV-1997 (first entry)  
 XX Haemoglobin G gamma-globin allele B-specific probe.  
 DE  
 XX  
 KW Glycophorin A; sialoglycoprotein; human; erythrocyte; membrane;  
 KW M blood group antigen; N blood group antigen; allele A; B; A'; A''; B';  
 KW polymorphism; detection; sequence-specific oligonucleotide probe;  
 KW genotype; forensic; primer; PCR; polymerase chain reaction; amplify; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX US5643724-A.  
 PN  
 XX  
 PD 01-JUL-1997.  
 XX  
 XX 06-JUN-1994; 94US-00255264.  
 DF  
 XX  
 XX 06-JUN-1994; 94US-00255264.  
 PR  
 XX (HOFF ) ROCHE MOLECULAR SYSTEMS INC.  
 PA  
 XX  
 XX Fildes NJ, Reynolds RL;  
 DI  
 XX  
 XX WPI; 1997-350231/32.  
 DR  
 XX  
 XX  
 PT Detection of glycophorin A allele(s) - by hybridisation assay using  
 PT sequence-specific oligonucleotide probes.  
 XX  
 XX Example 3; Col 15-16; 16pp; English.  
 PS  
 XX Glycophorin A is a major sialoglycoprotein of the human erythrocyte  
 CC membrane. Glycophorin A carries the M or N blood group antigen, which is  
 CC determined by the amino acid at residues 1 and 5. Allele A encodes the  
 CC protein carrying the N blood group antigen and allele B encodes the  
 CC protein carrying the M blood group antigen. Three additional alleles have  
 CC been discovered, designated A', A'', and B'. Detecting an A', A'', or B'  
 CC allele of the Glycophorin A locus in a human nucleic acid sample  
 CC comprises mixing the sample under stringent hybridisation conditions with  
 CC a sequence-specific oligonucleotide probe that distinguishes the A', A'',  
 CC or B' allele from A and B alleles, and detecting any hybridisation. The  
 CC method and probes are used for determining an individual's Glycophorin A  
 CC genotype, especially useful for determining an individual's Glycophorin A  
 CC forensic purposes. AAT70558-67 (and also AAT70582-83) are primers from  
 CC the AmpliType (R) PM kit used in a Glycophorin A typing system developed  
 CC by Hoffmann-La Roche. The primers direct the simultaneous amplification  
 CC of specific regions of the following six genetic loci: Glycophorin A, HLA  
 CC DQA1, low density lipoprotein receptor, Haemoglobin G gamma-globin, D7S8  
 CC and group specific component. Probe strips are also provided in the kit  
 CC (AAT70568-81)  
 XX  
 XX Sequence 16 BP; 4 A; 9 C; 1 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.9%; Score 12.4; DB 1; Length 16;  
 Best Local Similarity 92.9%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1698 GGTGGAGTGGGT 1711  
 DB |||||||  
 16 GGTGGAGTGGGT 3  
 RESULT 201  
 AAC67540  
 ID AAC67540 standard; DNA; 16 BP.  
 XX  
 AC AAC67540;  
 XX  
 XX 14-FEB-2001 (first entry)  
 DT  
 XX Alzheimer's disease-linked mitochondrial SNP PCR primer #240.  
 DE  
 XX Human; mitochondrial genome; single nucleotide polymorphism; SNP;  
 KW Human; mitochondrial genome; single nucleotide polymorphism; SNP;  
 KW Alzheimer's disease; mtDNA; PCR primer; ss.

XX Homo sapiens.  
 OS  
 XX WO200063441-A2.  
 PN  
 XX 26-OCT-2000.  
 PD  
 XX 19-APR-2000; 2000WO-US010906.  
 PF  
 XX 20-APR-1999; 99US-0130447P.  
 PR  
 XX 22-OCT-1999; 99US-0160901P.  
 PR  
 XX (MITO-) MITOKOR.  
 PA  
 XX Hernstadt C, Davis RE;  
 PI  
 XX WPI; 2000-672748/65.  
 DR  
 XX  
 XX Diagnosing a subject at the risk for or having Alzheimer's disease  
 PT comprises determining at least one single nucleotide polymorphism in  
 PT mitochondrial DNA associated with the disease in the sample from the  
 PT subject.  
 XX  
 XX Example 9; Page 53; 89pp; English.  
 PS  
 XX The present invention describes a novel method for determining the risk  
 CC of or diagnosing Alzheimer's disease using single nucleotide  
 CC polymorphisms (SNPs) present in an individual's mitochondrial DNA  
 CC (mtDNA). In addition, the SNPs identified can be used to identify agents  
 CC suitable for use in treating Alzheimer's disease. Sequences AAC67301-  
 CC C67610 are PCR primers used to demonstrate the method of the invention  
 CC  
 XX Sequence 16 BP; 2 A; 3 C; 8 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.9%; Score 12.4; DB 1; Length 16;  
 Best Local Similarity 92.9%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1709 GGTTAGGAGTACGG 1722  
 DB |||||||  
 3 GGTTAGGAGTACGG 16  
 RESULT 202  
 ADD43463  
 ID ADD43463 standard; DNA; 16 BP.  
 XX  
 AC ADD43463;  
 XX  
 XX 15-JAN-2004 (first entry)  
 DT  
 XX Human mitochondrial DNA (mtDNA) PCR primer SEQ ID NO:637.  
 DE  
 XX Mitochondrial haplogroup; mitochondrial DNA; mtDNA;  
 KW single nucleotide polymorphism; SNP; genetic relationship; antidiabetic;  
 KW neotropic; neuroprotective; cytoskeletal; gene therapy; genealogy;  
 KW forensic; Alzheimer's disease; cancer; type 2 diabetes mellitus; human;  
 KW PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS  
 OS Homo sapiens.  
 XX  
 XX WO2003046225-A1.  
 PN  
 XX  
 XX 05-JUN-2003.  
 PD  
 XX  
 XX 25-NOV-2002; 2002WO-US038276.  
 PF  
 XX 26-NOV-2001; 2001US-0333622P.  
 PR  
 XX 28-MAR-2002; 2002US-0369131P.  
 PR  
 XX 01-APR-2002; 2002US-0369539P.  
 PR  
 XX (MITO-) MITOKOR.  
 PA

```

XX PI Herrnstadt C;
XX XX WPI; 2003-505214/47.
XX XX
XX XX Determining single nucleotide polymorphisms in mtDNA or homoplasmic mtDNA
XX PT mutations, useful for diagnosing and treating diseases, such as
XX PT Alzheimer's disease, cancer and type 2 diabetes mellitus.
XX XX
XX PS Example 2; SEQ ID NO 637; 193pp; English.
XX CC
XX CC The present invention describes a method (M1) for determining the
XX CC mitochondrial haplogroup of a subject, comprising determining in a
XX CC biological sample with mitochondrial DNA (mtDNA) from a subject, the
XX CC presence or absence of at least one mitochondrial single nucleotide
XX CC polymorphism (SNP) that is associated with a mitochondrial haplogroup.
XX CC Also described: (1) determining a genetic relationship between two
XX CC subjects; (2) determining a genetic relationship between an unknown
XX CC source or biological subject from which an unidentified sample is
XX CC obtained, and a known source or biological subject from an identified
XX CC sample is obtained; and (3) determining the presence of or the risk of
XX CC having a disease associated with a mtDNA SNP. Mitochondrial DNA can have
XX CC antidiabetic, neurotropic, neuroprotective and cytosolic activities, and
XX CC can be used in gene therapy. M1 and compositions of the present invention
XX CC are useful for detecting the presence or risk of diseases, treating such
XX CC diseases, determining the haplogroup of an individual, and establishing
XX CC genetic relationships between individuals for genealogical and forensic
XX CC purposes. The diseases include Alzheimer's disease, cancer and type 2
XX CC diabetes mellitus. The present sequence represents a PCR primer used in
XX CC the amplification of human mtDNA in an example from the present
XX CC invention.
XX SQ Sequence 16 BP; 2 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 8.9%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1709 GGTAGGACTACGG 1722
DB 3 GGTAGGCGTACGG 16

RESULT 203
AAQ29806/c
ID AAQ29806 standard; DNA; 17 BP.
XX AC AAQ29806;
XX XX
XX XX 25-MAR-2003 (revised)
DT 19-MAR-1993 (first entry)
XX XX
XX XX B allele probe VP08.
XX DE
XX XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;
XX XX paternity; forensic; ss.
XX OS Synthetic.
XX XX
XX XX EP512342-A2.
XX PN
XX XX 11-NOV-1992.
XX PD
XX XX 25-APR-1992; 92EP-00107084.
XX PF
XX PR 07-MAY-1991; 91US-00696793.
XX XX
XX XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PA
XX XX Saiki RK, Nasarabadi SL;
XX PI
XX XX WPI; 1992-374679/46.
XX DR
XX XX

```

---

```

PT Determn. of an individuals genotype at the gamma-globin locus - using
PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.
XX PS Disclosure; Page 17; 29pp; English.
XX XX
XX CC The sequences given in AAQ29787-816 are probes which were used within the
XX CC method of the invention for detecting the presence of a variant sequence
XX CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be
XX CC distinguished from one another by the polymorphic sequence corresponding
XX CC to the HindIII site of the A allele. The sequences of the three alleles
XX CC are given in AAQ29842-44. The methods for determining an individuals
XX CC genotype at the GGG locus with respect to a set of alleles improves the
XX CC discriminatory power of GGG typing methodology compared to previous
XX CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 17 BP; 4 A; 10 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1698 GGTGAAGTTGGGT 1711
DB 17 GGTGAAGCTGGGT 4

RESULT 204
AAT14821
ID AAT14821 standard; DNA; 17 BP.
XX AC AAT14821;
XX XX
XX XX 17-SEP-1996 (first entry)
DT XX
XX DE Histocyte-secreted factor 3' PCR primer.
XX KW Histocyte-secreted factor; HSF; cytokine; antitumour; tumour; therapy;
XX KW polymerase chain reaction; PCR; primer; ss.
XX OS Synthetic.
XX XX
XX XX WO9613586-A2.
XX PN
XX XX 09-MAY-1996.
XX PD
XX XX 26-OCT-1995; 95WO-JPC02200.
XX PF
XX XX 26-OCT-1994; 94JP-00297780.
XX PR
XX XX (SATO/) SATOMI N.
XX PA
XX XX Satomi N;
XX PI
XX XX WPI; 1996-239499/24.
XX XX
XX XX DNA encoding histocyte-secreted factor and its variants - useful as an
XX XX anti-tumour agent and for studying tumour regression, having low
XX XX cytotoxicity compared to TNF.
XX XX
XX XX Example 5; Page 28; 52pp; English.
XX XX
XX CC A 5' PCR primer (AAT14820) and 3' primer (AAT14821) are based on peptides
XX CC derived from rabbit histocyte-secreted factor (HSF). They were used to
XX CC amplify DNA from human TVH histiocytic cells, yielding the PCR product
XX CC given in AAT14819. They were also used to amplify DNA from U-937 (human
XX CC histiocytic lymphoma) cells, which revealed PCR products that led to the
XX CC identification of a genomic clone (AAT14818) coding for human HSF
XX CC (AAR96800), a novel cytokine
XX CC
XX SQ Sequence 17 BP; 6 A; 5 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 8.9%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.9e+02;

```

Matches	13;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1655	AGCACAGGCTCAC	1668						
Db	2	AGAACGAGGCTCAC	15						
RESULT 205									
AAAF02929/c									
ID	AAAF02929	standard; DNA; 17 BP.							
XX	AC	AAAF02929;							
XX	DT	16-FEB-2001 (first entry)							
XX	DE	Hammerhead ribozyme substrate #1224.							
XX	KW	Ribozyme; erythropoietin; granulocyte colony stimulating factor;							
KW	KW	interferon alpha; ss.							
XX	OS	Homo sapiens.							
XX	PN	WO200061729-A2.							
XX	PD	19-OCT-2000.							
XX	PF	11-APR-2000; 2000WO-US009721.							
XX	PR	12-APR-1999; 99US-0129390P.							
XX	PA	(RIBO-) RIBOZYME PHARM INC.							
XX	PI	Blatt L, Zwick M, Pavco P, Mcswiggen J;							
XX	XX	WPI; 2000-647423/62.							
XX	DR	Enzymatic and antisense nucleic acid inhibition of repressor genes,							
PT	PT	useful for producing e.g. granulocyte colony stimulating factor protein,							
PT	PT	interferon alpha and erythropoietin.							
XX	XX	Claim 37; Page 83; 164pp; English.							
XX	XX	The present invention relates to enzymatic and antisense nucleic acid							
CC	CC	molecules that act as inhibitors of the expression of repressor genes							
CC	CC	encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription							
CC	CC	factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).							
CC	CC	Inhibition of the repressors removes prevents inhibition (and							
CC	CC	consequently increases expression of) genes involved in the production of							
CC	CC	erythropoietin, granulocyte colony stimulating factor protein and							
XX	XX	interferon alpha							
XX	XX	Sequence 17 BP; 3 A; 9 C; 0 G; 5 T; 0 U; 0 Other;							
XX	XX	Query Match 8.9%; Score 12.4; DB 1; Length 17;							
XX	XX	Best Local Similarity 92.9%; Pred. No. 2.9e+02;							
XX	XX	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;							
QY	1696	GTGGTGAAGTTGG	1709						
Db	16	GAGGTGAAGTTGG	3						
RESULT 206									
AAAF02930/c									
ID	AAAF02930	standard; DNA; 17 BP.							
XX	AC	AAAF02930;							
XX	DT	16-FEB-2001 (first entry)							
XX	DE	Hammerhead ribozyme substrate #1225.							
XX	KW	Ribozyme; erythropoietin; granulocyte colony stimulating factor;							

```

PR 27-MAR-2000; 2000US-0192176P.
PR 27-MAR-2000; 2000US-0192179P.
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
XX
XX
XX (UYDE ) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC;
XX
XX WPI; 2001-639230/73.
XX
XX Oligonucleotide for targeted alterations of genetic sequences and for
XX treating cystic fibrosis, comprises at least one mismatch and chemical
XX modification.
XX
XX Claim 7; Page 234; 294pp; English.
XX
XX The present invention provides single-stranded oligonucleotides which can
XX be used for the targeted alteration of genomic sequences, where the
XX oligonucleotide has at least one mismatch compared with the genomic
XX sequence to be altered. In particular, these sequences are directed at
XX the following genes: adenosine deaminase, p53, beta-globin,
XX retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
XX (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
XX 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
XX apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
XX (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
XX presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
XX such as cancer, adenosine deaminase deficiency, cystic fibrosis,
XX haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
XX Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
XX various syndromes. The present sequence is one of the gene correcting
XX oligonucleotides of the invention
XX
XX SQ Sequence 17 BP; 5 A; 4 C; 7 G; 1 T; 0 U; 0 Other;
      Query Match      8.9%; Score 12.4; DB 1; Length 17;
      Best Local Similarity 92.9%; Pred No. 2.9e+02;
      Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1686 CTCCTCCAGCGTGG 1699
Db 14 CTCCTCCAGCTTGG 1

RESULT 208
ABA80625
ID ABA80625 standard; DNA; 17 BP.
XX
XX ABA80625;
XX
XX 24-JAN-2002 (first entry)
XX
XX APOE mutation correcting oligonucleotide SEQ ID NO: 3471.
XX
XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
XX retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
XX cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
XX adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
XX haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
XX mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
XX familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
XX UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
XX Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
XX antileptic; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200173002-A2.
XX
XX PD 04-OCT-2001.
XX
XX 27-MAR-2001; 2001WO-US009761.

```

```

XX
XX 27-MAR-2000; 2000US-0192176P.
XX 27-MAR-2000; 2000US-0192179P.
XX 01-JUN-2000; 2000US-0208538P.
XX 30-OCT-2000; 2000US-0244989P.
XX
XX (UYDE ) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC;
XX
XX WPI; 2001-639230/73.
XX
XX Oligonucleotide for targeted alterations of genetic sequences and for
XX treating cystic fibrosis, comprises at least one mismatch and chemical
XX modification.
XX
XX Claim 7; Page 234; 294pp; English.
XX
XX The present invention provides single-stranded oligonucleotides which can
XX be used for the targeted alteration of genomic sequences, where the
XX oligonucleotide has at least one mismatch compared with the genomic
XX sequence to be altered. In particular, these sequences are directed at
XX the following genes: adenosine deaminase, p53, beta-globin,
XX retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
XX (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
XX 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
XX apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
XX (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
XX presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
XX such as cancer, adenosine deaminase deficiency, cystic fibrosis,
XX haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
XX Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
XX various syndromes. The present sequence is one of the gene correcting
XX oligonucleotides of the invention
XX
XX SQ Sequence 17 BP; 1 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
      Query Match      8.9%; Score 12.4; DB 1; Length 17;
      Best Local Similarity 92.9%; Pred No. 2.9e+02;
      Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1686 CTCCTCCAGCGTGG 1699
Db 4 CTCCTCCAGCTTGG 17

RESULT 209
ACD51040/c
ID ACD51040 standard; RNA; 17 BP.
XX
XX ACD51040;
XX
XX 23-SEP-2003 (first entry)
XX
XX HBV hammerhead ribozyme substrate sequence #353.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
XX amzyme; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.
XX
XX OS Hepatitis B virus.
XX
XX PN WO200281494-A1.
XX
XX PD 17-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009187.

```



PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX WPI; 2003-229207/22.  
 DR Novel compound useful for treating cirrhosis, liver failure,  
 XX hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX Example 1; Page 143; 387pp; English.  
 PS The present invention relates to nucleic acid molecules which modulate  
 XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HBV  
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences  
 CC disclosed in the present invention  
 XX Sequence 17 BP; 3 A; 0 C; 12 G; 0 T; 2 U; 0 Other;  
 SQ Query Match 8.9%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1736 CTCCCAACTCCTCC 1749  
 Db 14 CCGCCAACTCCTCC 1  
 RESULT 210  
 ACC68047/c  
 ID ACC68047 standard; DNA; 17 BP.  
 XX AC ACC68047;  
 XX 01-JUL-2003 (first entry)  
 DT Murine oligonucleotide associated with tumour suppression, SEQ ID 5294.  
 DE Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; ss;  
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrenia; ss.  
 XX Mus musculus.

XX WO2003025176-A2.  
 PN 27-MAR-2003.  
 XX 17-SEP-2002; 2002WO-IB004210.  
 PF 17-SEP-2001; 2001FR-00011979.  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 PA Telerman A, Amson R, Tuijnder M;  
 PI WPI; 2003-333167/31.  
 DR New isolated nucleic acid, useful for treating viral diseases associated  
 XX with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 PT Disclosure; Page 649; 738pp; French.  
 PS The present invention relates to murine oligonucleotides (ACC62754-  
 CC ACC68806), which are associated with tumour suppression, tumour  
 CC reversion, apoptosis and virus resistance. The oligonucleotides are  
 CC useful as (1) as probes and primers for detecting, identifying,  
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of  
 CC recombinant polypeptides. The oligonucleotides are useful for preparation  
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia  
 XX Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 8.9%; Score 12.4; DB 1; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 2.9e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1725 ATGGAGATTGGCTC 1738  
 Db 14 ATGGAGATTGGATC 1  
 RESULT 211  
 ADB40159  
 ID ADB40159 standard; DNA; 17 BP.  
 XX AC ADB40159;  
 XX 18-DEC-2003 (revised)  
 DT 04-DEC-2003 (first entry)  
 XX Tumour suppression/reversion associated nucleotide #482.  
 DE Cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;  
 XX primer; probe; tumour suppression; tumour reversion; apoptosis;  
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
 KW diagnosis.  
 XX Homo sapiens.  
 OS WO2003040369-A2.  
 PN 15-MAY-2003.  
 XX 17-SEP-2002; 2002WO-IB004219.  
 PF 17-SEP-2001; 2001FR-00011981.  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 PA Telerman A, Amson R, Tuijnder M;  
 PI Mus musculus.



QY 1718 TACGAGATGAGA 1731  
 Db 1 TACGGTGTGAGA 14

RESULT 214  
 AAQ29798/c  
 ID AAQ29798 standard; DNA; 18 BP.  
 XX AC AAQ29798;  
 XX 25-MAR-2003 (revised)  
 DT 19-MAR-1993 (first entry)  
 XX DE A allele probe VP63.  
 XX G-gamma globulin; GGG; polymorphism; HindIII; A allele; B; C; genotype;  
 KW paternity; forensic; ss.  
 XX Synthetic.  
 OS EP512342-A2.  
 XX 11-NOV-1992.  
 PD 25-APR-1992; 92EP-00107084.  
 FF 07-MAY-1991; 91US-00696793.  
 XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA Saiki RK, Nasarabadi SL;  
 PI WPI; 1992-374679/46.  
 DR Determ. of an individuals genotype at the gamma-globin locus - using  
 PT sequence-specific oligo-nucleotide probes corresp. to 3 alleles.  
 XX Disclosure; Page 15; 29pp; English.  
 CC The sequences given in AAQ29787-816 are probes which were used within the  
 CC method of the invention for detecting the presence of a variant sequence  
 CC in the G-gamma globulin (GGG) locus. The A, B and C alleles can be  
 CC distinguished from one another by the polymorphic sequence corresponding  
 CC to the HindIII site of the A allele. The sequences of the three alleles  
 CC are given in AAQ29842-44. The methods for determining an individuals  
 CC genotype at the GGG locus with respect to a set of alleles improves the  
 CC discriminatory power of GGG typing methodology compared to previous  
 CC methods using two alleles. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 18 BP; 6 A; 10 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 8.9%; Score 12.4; DB 1; Length 18;  
 Best Local Similarity 92.9%; Pred. No. 3.2e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1698 GTTGAAGTTGGGT 1711  
 Db 17 GTTGAAGTTGGT 4

RESULT 215  
 AAT60160/c  
 ID AAT60160 standard; DNA; 18 BP.  
 XX AC AAT60160;  
 XX 01-DEC-1997 (first entry)  
 DT Collagen gene promoter region binding oligomer Oligo 164 AP.  
 DE Triplex; inhibition; collagen gene; promoter; pathological fibrosis;  
 KW myocardial fibrosis; hypertensive heart disease; atherosclerosis;  
 KW restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;  
 XX hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.

KW myocardial fibrosis; hypertensive heart disease; atherosclerosis;  
 KW restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;  
 KW hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT misc\_feature 1..18  
 FT /\*tag= a  
 FT /note= "Phosphorothioate linkages"  
 XX WO9710254-A1.  
 PN 20-MAR-1997.  
 PD 12-SEP-1996; 96WO-US014640.  
 XX 15-SEP-1995; 95US-00528836.  
 PR 11-SEP-1996; 96US-00712357.  
 XX (GUNT/) GUNTAKA R V.  
 PA Guntaka RV, Weber KT, Kovacs A, Kandala J;  
 XX WPI; 1997-202172/18.  
 DR Triplex forming oligomer binds to collagen gene promoter region - used to  
 PT impede pathological fibrosis etc.  
 XX Claim 18; Page 36; 52pp; English.  
 CC An oligomer has been produced which is capable of inhibiting expression  
 CC of a collagen gene. The present sequence represents a specifically  
 CC claimed oligomer Oligo 164 APS, which binds to the polypurine-  
 CC polypyrimidine region of the rat alpha(I) collagen gene promoter region.  
 CC The oligomer may be used to impede pathological fibrosis which is  
 CC associated with myocardial fibrosis in hypertensive heart diseases,  
 CC atherosclerosis, restenosis, liver cirrhosis, lung fibrosis, and skin  
 CC fibrosis found in scleroderma, in hypertrophic scars and in skin  
 CC following burn injury. The oligomer inhibits expression of a collagen  
 CC gene after insertion into a cell by causing an intracellular reaction  
 CC forming oligomer (TFO) which is targeted to a 30-mer polypurine  
 CC oligonucleotide corresponding to the noncoding strand of the promoter  
 CC between -170 and -140. This section was chosen due to its binding  
 CC stability at physiological pH  
 XX Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 8.9%; Score 12.4; DB 1; Length 18;  
 Best Local Similarity 92.9%; Pred. No. 3.2e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756  
 Db 17 CTCCTCCCTTCCT 4

RESULT 216  
 AAT60165/c  
 ID AAT60165 standard; DNA; 18 BP.  
 XX AC AAT60165;  
 XX 01-DEC-1997 (first entry)  
 DT Collagen gene promoter region binding oligomer Oligo 164 AP.  
 DE Triplex; inhibition; collagen gene; promoter; pathological fibrosis;  
 KW myocardial fibrosis; hypertensive heart disease; atherosclerosis;  
 KW restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;  
 KW hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.

```

OS Synthetic.
XX WO9710254-A1.
XX 20-MAR-1997.
XX 12-SEP-1996; 96WO-US014640.
XX 15-SEP-1995; 95US-00528836.
XX 11-SEP-1996; 96US-00712357.
XX (GUNT/) GUNTAKA R V.
XX Guntaka RV, Weber KT, Kovacs A, Kandala J;
XX WPI; 1997-202172/18.
XX Triplex forming oligomer binds to collagen gene promoter region - used to
XX impede pathological fibrosis etc.
XX Example 4; Page 35; 52pp; English.
XX An oligomer has been produced which is capable of inhibiting expression
XX of a collagen gene. The present sequence represents an oligomer Oligo 164
XX AP, which binds to the polypurine-polypyrimidine region of the rat
XX alpha(I) collagen gene promoter region. The oligomer may be used to
XX impede pathological fibrosis which is associated with myocardial fibrosis
XX in hypertensive heart diseases, atherosclerosis, restenosis, liver
XX cirrhosis, lung fibrosis, and skin fibrosis found in scleroderma, in
XX hypertrophic scars and in skin following burn injury. The oligomer
XX inhibits expression of a collagen gene after insertion into a cell by
XX causing an intracellular reaction which inhibits gene expression. The
XX oligomer is preferably a triplex forming oligomer (TFO) which is targeted
XX to a 30-mer polypurine oligonucleotide corresponding to the noncoding
XX strand of the promoter between -170 and -140. This section was chosen due
XX to its binding stability at physiological pH
XX Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

Query Match      8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756
Db |||||
17 CTCCTCCCTATCCT 4

RESULT 217
AAT60158/c
ID AAT60158 standard; DNA; 18 BP.
XX
XX AAT60158;
XX 01-DEC-1997 (first entry)
XX
XX Collagen gene promoter region binding oligomer Oligo 147 P.
XX
XX Triplex; inhibition; collagen gene; promoter; pathological fibrosis;
XX myocardial fibrosis; hypertensive heart disease; atherosclerosis;
XX restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;
XX hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.
XX
XX Synthetic.
XX WO9710254-A1.
XX 20-MAR-1997.
XX 12-SEP-1996; 96WO-US014640.
XX 15-SEP-1995; 95US-00528836.
XX 11-SEP-1996; 96US-00712357.

```

```

XX (GUNT/) GUNTAKA R V.
XX Guntaka RV, Weber KT, Kovacs A, Kandala J;
XX WPI; 1997-202172/18.
XX Triplex forming oligomer binds to collagen gene promoter region - used to
XX impede pathological fibrosis etc.
XX Claim 18; Page 34; 52pp; English.
XX An oligomer has been produced which is capable of inhibiting expression
XX of a collagen gene. The present sequence represents a specifically
XX claimed oligomer Oligo 147 P, which binds to the polypurine-
XX polypyrimidine region of the rat alpha(I) collagen gene promoter region.
XX The oligomer may be used to impede pathological fibrosis which is
XX associated with myocardial fibrosis in hypertensive heart diseases,
XX atherosclerosis, restenosis, liver cirrhosis, lung fibrosis, and skin
XX fibrosis found in scleroderma, in hypertrophic scars and in skin
XX following burn injury. The oligomer inhibits expression of a collagen
XX gene after insertion into a cell by causing an intracellular reaction
XX which inhibits gene expression. The oligomer is preferably a triplex
XX forming oligomer (TFO) which is targeted to a 30-mer polypurine
XX oligonucleotide corresponding to the noncoding strand of the promoter
XX between -170 and -140. This section was chosen due to its binding
XX stability at physiological pH
XX Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

Query Match      8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756
Db |||||
17 CTCCTCCCTATCCT 4

RESULT 218
AAX70290/c
ID AAX70290 standard; RNA; 18 BP.
XX
XX AAX70290;
XX 28-JUL-1999 (first entry)
XX
XX Human flt1 VEGF receptor hairpin ribozyme substrate #58.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX Homo sapiens.
XX
XX WO9715662-A2.
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.

```



```
Best Local Similarity 92.9%; Pred. No. 3.2e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 13; Conservative 0;

QY 1743 CTCCTCCCTATCCT 1756
Db 17 CTCCTCCCTTCTCT 4

RESULT 221
AAZ98715/c
ID AAZ98715 standard; DNA; 18 BP.
XX
AC AAZ98715;
XX
DT 20-JUN-2000 (first entry)
XX
DE Collagen promoter inhibitory oligonucleotide Oligo Col 164 APS.
XX
KW Collagen; inhibit; myocardial fibrosis; hypertensive heart disease;
KW atherosclerosis; restenosis; liver cirrhosis; lung fibrosis; burn injury;
KW peritoneal fibrosis; skin fibrosis; scleroderma; hypertrophic scar; ss.
XX
OS Rattus sp.
XX
PN WO2000082113-A1.
XX
PD 17-FEB-2000.
XX
PF 06-AUG-1999; 99WO-US017824.
XX
PR 07-AUG-1998; 98US-00130888.
XX
PA (GUNT/) GUNTAKA R V.
XX
PI Guntaka RV, Weber KT, Kovacs A, Kandala J;
XX
DR WPI; 2000-205739/18.
XX
PT Inhibitors of collagen gene useful for treating fibrosis associated with
PT atherosclerosis, restenosis, liver cirrhosis, lung and skin fibrosis,
PT comprises oligomers capable of inhibiting collagen gene.
XX
PS Example 4; Fig 8; 77pp; English.
XX
CC This sequence represents an oligomer which is capable of inhibiting the
CC expression of the collagen gene. The oligomer is capable of binding to
CC the promoter region of the collagen gene. Collagen is a family of fibrous
CC proteins, and is the major element of skin, bone, tendon, cartilage,
CC blood vessels and teeth. The oligomers are useful for inhibiting
CC expression of the collagen gene, comprising inserting the oligomers into
CC a cell and causing an intracellular reaction to inhibit the gene
CC expression. The collagen inhibitory oligomers of the invention are useful
CC for treating pathological fibrosis associated with myocardial fibrosis in
CC hypertensive heart disease, atherosclerosis, restenosis, liver cirrhosis,
CC lung fibrosis, peritoneal fibrosis and skin fibrosis found in
CC scleroderma, hypertrophic scars and burn injury
XX
SQ Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756
Db 17 CTCCTCCCTTCTCT 4

RESULT 222
AAZ98708/c
ID AAZ98708 standard; DNA; 18 BP.
XX
AC AAZ98708;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:11223.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
```

```
XX
DT 20-JUN-2000 (first entry)
XX
DE Collagen promoter inhibitory oligonucleotide Oligo Col 164 APS.
XX
KW Collagen; inhibit; myocardial fibrosis; hypertensive heart disease;
KW atherosclerosis; restenosis; liver cirrhosis; lung fibrosis; burn injury;
KW peritoneal fibrosis; skin fibrosis; scleroderma; hypertrophic scar; ss.
XX
OS Rattus sp.
XX
PN WO2000082113-A1.
XX
PD 17-FEB-2000.
XX
PF 06-AUG-1999; 99WO-US017824.
XX
PR 07-AUG-1998; 98US-00130888.
XX
PA (GUNT/) GUNTAKA R V.
XX
PI Guntaka RV, Weber KT, Kovacs A, Kandala J;
XX
DR WPI; 2000-205739/18.
XX
PT Inhibitors of collagen gene useful for treating fibrosis associated with
PT atherosclerosis, restenosis, liver cirrhosis, lung and skin fibrosis,
PT comprises oligomers capable of inhibiting collagen gene.
XX
PS Claim 19; Fig 8; 77pp; English.
XX
CC This sequence represents an oligomer which is capable of inhibiting the
CC expression of the collagen gene. The oligomer is capable of binding to
CC the promoter region of the collagen gene. Collagen is a family of fibrous
CC proteins, and is the major element of skin, bone, tendon, cartilage,
CC blood vessels and teeth. The oligomers are useful for inhibiting
CC expression of the collagen gene, comprising inserting the oligomers into
CC a cell and causing an intracellular reaction to inhibit the gene
CC expression. The collagen inhibitory oligomers of the invention are useful
CC for treating pathological fibrosis associated with myocardial fibrosis in
CC hypertensive heart disease, atherosclerosis, restenosis, liver cirrhosis,
CC lung fibrosis, peritoneal fibrosis and skin fibrosis found in
CC scleroderma, hypertrophic scars and burn injury
XX
SQ Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1743 CTCCTCCCTATCCT 1756
Db 17 CTCCTCCCTTCTCT 4

RESULT 223
AAZ76867
ID AAZ76867 standard; DNA; 18 BP.
XX
AC AAZ76867;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:11223.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
```

PN W09954500-A2.  
XX  
PD 28-OCT-1999.  
XX  
XX 21-APR-1999; 99WO-IB000822.  
XX PF  
XX 21-APR-1998; 98US-0082614P.  
PR PR  
XX 23-NOV-1998; 98US-0109732P.  
XX  
PA (GEST ) GENSET.  
XX  
PI Cohen D, Blumenfeld M, Chumakov I;  
XX WPI; 2000-013267/01.  
XX  
DR Novel biallelic markers used to construct a high density disequilibrium  
XX map of the human genome.  
XX  
PS Claim 9; Page 2623; 2745pp; English.  
XX  
XX AA265654 to AA269578 represent human biallelic markers from the present  
XX invention, which contain a polymorphic base at position 24 of their  
XX nucleotide sequences. AA269579 to AA277440 represent amplification  
XX primers for the biallelic markers. The biallelic markers of the invention  
XX have a variety of uses: they can be used for high density mapping of the  
XX human genome, and in complex association studies and haplotyping studies  
XX which are useful in determining the genetic basis for disease states.  
XX Compositions and methods of the invention can also be useful for the  
XX identification of the targets for the development of pharmaceutical  
XX agents and diagnostic methods, as well as the characterisation of the  
XX differential efficacious responses to and side effects from  
XX pharmaceutical agents acting on a disease as well as other treatment.  
XX N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3157, 3227, 3297 and  
XX 3367, are not actually given a sequence in the Sequence Listing from the  
XX present invention  
XX  
SQ Sequence 18 BP; 8 A; 1 C; 7 G; 2 T; 0 U; 0 Other;  
  
Query Match 8.9%; Score 12.4; DB 1; Length 18;  
Best Local Similarity 92.9%; Pred. No. 3.2e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1722 GAGATGGAGATTGG 1735  
DB ||||| ||||| ||  
5 GAGATGGAGATTAGG 18  
  
RESULT 224  
AAD21095  
ID AAD21095 standard; DNA; 18 BP.  
XX  
AC AAD21095;  
XX  
DT 15-JAN-2002 (first entry)  
XX  
DE Patched-1 RT-PCR primer #2 used in the method for modulating hair growth.  
XX  
XX Signal transduction; Wnt protein; dermal papilla; DP; beta-catenin;  
KW GSK3beta kinase; genetic pattern baldness; hormonal disorder;  
KW chemotherapy; anagen phase; hair growth promoter; RT-PCR primer; ss.  
XX  
OS Unidentified.  
XX  
XX W0200174164-A1.  
PN  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US010164.  
XX  
XX 31-MAR-2000; 2000US-0193771P.  
PR  
XX 12-JAN-2001; 2001US-0261690P.  
XX  
XX (GEHO ) GEN HOSPITAL CORP.  
PA

XX Kishimoto J, Burgeson R, Morgan BA;  
PI WPI; 2001-648492/74.  
XX  
DR Promoting or inhibiting hair growth in a subject by inducing or  
XX mimicking, or inhibiting effect of Wnt-promoted signal transduction,  
XX respectively.  
XX  
PS Disclosure; Page 22; 63pp; English.  
XX  
XX The present invention relates to promoting hair growth in a subject which  
XX involves inducing or mimicking the effect of Wnt-promoted signal  
XX transduction in a subject and inhibiting hair growth in a subject  
XX involves inhibiting level of Wnt protein or inhibiting an effect of Wnt-  
XX promoted signal transduction in a subject. The invention is used for  
XX providing and maintaining dermal papilla (DP) cell graft which involves  
XX culturing a DP cell from a subject under conditions that induce or mimic  
XX the effect of Wnt-promoted signal transduction, thereby providing and  
XX maintaining a DP cell graft. Preferably, the DP cell is cultured in the  
XX presence of Wnt, its fragment or analogue; lithium chloride, beta-catenin  
XX and/or LEF1, an agent which inhibits beta-catenin phosphorylation or  
XX GSK3beta kinase, or an agent which promotes beta-catenin accumulation.  
XX Hair growth is promoted in subject's scalp, or face e.g., beard and/or  
XX mustache, or in conditions where subject suffers from genetic pattern  
XX baldness, suffers from a hormonal disorder which decreases hair growth,  
XX has received a treatment, e.g., radiation or chemotherapy, or a drug  
XX which inhibits hair growth, or has had a surgical procedure, e.g., skin  
XX graft, which is in need of hair growth. Hair growth is inhibited on the  
XX subject's scalp, subject's face, e.g., beard and/or mustache, facial hair  
XX growth, or eyebrow growth, back, legs, chest, armpits. Promoting hair  
XX growth is useful for maintaining or promoting hair inductive activity.  
XX Inhibiting hair growth is useful for maintaining or promoting anagen  
XX phase gene expression in the subject's scalp, face e.g., upper lip and/or  
XX chin. The present sequence is patched-1 RT-PCR primer used in the method  
XX for modulating hair growth  
XX  
SQ Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 U; 0 Other;  
  
Query Match 8.9%; Score 12.4; DB 1; Length 18;  
Best Local Similarity 92.9%; Pred. No. 3.2e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1685 TCTCTCTCAGCGTG 1698  
DB ||||| ||||| ||  
4 TCTCTCTCAGCATG 17  
  
RESULT 225  
ABT06527  
ID ABT06527 standard; DNA; 18 BP.  
XX  
AC ABT06527;  
XX  
DT 07-NOV-2002 (first entry)  
XX  
XX HOXA5 gene promoter sequence methylation specific primer #1.  
DE  
XX Human; methylated gene; methylation; breast cancer; marker; WT-1;  
KW cell proliferative disorder; TWIST; HOXA5; NES-1; RARbeta; cyclin D2;  
KW retinoic acid receptor beta; oestrogen receptor; Wilms' tumour;  
KW 14.3.3 sigma; HIN-1; RASSF1A; tumour suppressor gene; hypermethylation;  
KW PCR; primer; ss.  
XX  
XX Unidentified.  
OS  
XX W0200259347-A2.  
PN  
XX 01-AUG-2002.  
XX  
XX 28-JAN-2002; 2002WO-US002455.  
XX  
XX 26-JAN-2001; 2001US-00771357.  
PR

```
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
PA Sukumar S, Evron E, Dooley WC, Sacchi N, Davidson N, Fackler MJ;
XX WPI; 2002-599803/64.
XX
XX Diagnosing and/or determining a predisposition to a cellular
PT proliferative disorder of breast tissue, in particular breast cancer, by
PT determining the state of methylation of one or more nucleic acids
PT isolated from the subject.
XX
XX Disclosure; Fig 5C; 115pp; English.
XX
XX The present invention relates to a method of diagnosing a cellular
CC proliferative disorder of breast tissue, which involves determining the
CC state of methylation of one or more nucleic acids isolated from the
CC subject, where the state of methylation of the nucleic acids as compared
CC with a state of methylation from a subject not having the cellular
CC proliferative disorder of breast tissue is indicative of a cellular
CC proliferative disorder of breast tissue in the subject. The nucleic acids
CC may be TWIST1, HMXA5, NES-1, retinoic acid receptor beta (RARbeta),
CC oestrogen receptor, cyclin D2, Wilms' tumour gene (WT-1), 14.3.3 sigma,
CC HIN-1 or RASSF1A. The method is useful for diagnosing and/or determining
CC a predisposition to a cellular proliferative disorder, in particular
CC breast cancer including ductal carcinoma in situ, lobular carcinoma,
CC colloid carcinoma, tubular carcinoma, medullary carcinoma, metaplastic
CC carcinoma, intraductal carcinoma in situ, lobular carcinoma in situ and
CC papillary carcinoma in situ. The present sequence is a primer used in the
CC exemplification of the invention
XX
XX Sequence 18 BP; 2 A; 0 C; 9 G; 7 T; 0 U; 0 Other;
SQ
Query Match 8.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 3.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1698 GGTGGAAGTTGGGT 1711
DB 4 GTTGAAGTTGGGT 17
XX
RESULT 226
AAQ25868/c
ID AAQ25868 standard; DNA; 19 BP.
XX
XX AAQ25868;
AC
XX 25-MAR-2003 (revised)
DT 04-JAN-1993 (first entry)
XX
DE 5' Alu primer.
XX
XX PCR; sequence conservation; DNA synthesis; amplification; ss.
XX
XX Synthetic.
XX
XX WO9210566-Al.
XX
XX 25-JUN-1992.
PD
XX 21-NOV-1991; 91WO-US008739.
PF
XX 13-DEC-1990; 90US-00627945.
PR
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX Siciliano MJ, Liu P;
PI
XX WPI; 1992-234623/28.
DR
XX Chromosome-specific DNA probes free of species-specific repeat DNA - used
PT for identification and banding of human chromosomes.
XX
```

```
XX Claim 64; Page 63; 73pp; English.
PS
XX
XX The sequences given in AAQ25868-9 are nucleotide primers which are
CC characterised by binding to a 5' and a 3' Alu terminus, respectively.
CC These Alu primers were based on a current revision of consensus sequence
CC of Alu repeats. This revision is based on nucleotide sequences of 50
CC different, cloned and sequenced human Alu segments. Two regions on the
CC sequence showed a high degree of conservation and these were used as
CC candidate regions for the primer locations. In order to minimize the
CC incorporation of Alu sequence itself in the inter-Alu-PCR, the 5' primer
CC was designed to recognise a specific region and to direct DNA synthesis
CC off the 5' end and away from the middle of the Alu segment to which it is
CC bound. The converse is true for the 3' primer. Amplification using these
CC two primers yields products ranging from a few hundred to several
CC thousand base pairs. The primer design maximizes both the number of Alu
CC segments recruited and the number of inter-Alu unique sequences
CC amplified. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 19 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 2 Other;
SQ
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 3.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1662 GGCTCACAGCTGGAACCC 1679
DB 18 GGCTCAYRCCTGTATCC 1
XX
RESULT 227
AAQ48682/c
ID AAQ48682 standard; cDNA; 19 BP.
XX
XX AAQ48682;
AC
XX 25-MAR-2003 (revised)
DT 25-FEB-1994 (first entry)
XX
DE Human Alu segment consensus sequence PCR primer Alu-1.
XX
XX Abnormality; polymerase chain reaction; amplification; ss.
XX
XX Synthetic.
XX
XX WO9317104-Al.
XX
XX 02-SEP-1993.
PD
XX 19-FEB-1993; 93WO-US001545.
PF
XX 20-FEB-1992; 92US-00839255.
PR
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
PA
XX Brook JD, Housman DE;
PI
XX WPI; 1993-288410/36.
DR
XX
XX DNA sequence of myotonic dystrophy gene - used to produce probes and
PT identify CHR 19 abnormality and protein kinase responsible.
XX
XX Example; Page 32; 64pp; English.
XX
XX The sequence is that of a PCR primer Alu-1 which specifically recognises
CC human consensus sequences located at the 5' and 3' ends of Alu segments.
CC It was used with 2F5 template to amplify human unique sequences. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 19 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 2 Other;
SQ
Query Match 8.9%; Score 12.4; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 3.4e+02;
```



Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCACAGCTGGAACCC 1679  
 |||||::|||  
 18 GGCTCAYRCCTGTAATCC 1

Db

RESULT 228  
 AAQ85676/c  
 ID AAQ85676 standard; DNA; 19 BP.  
 XX AC AAQ85676;  
 XX XX  
 XX 25-MAR-2003 (revised)  
 DT 04-OCT-1995 (first entry)  
 XX XX  
 DE PCR primer alu 1 for inter-Alu region of Wilson's disease gene.  
 XX XX  
 KW Wilson's disease; chromosome 13; Alu; PCR primer; ss.  
 XX XX  
 XX Synthetic.  
 OS OS  
 XX Key Location/Qualifiers  
 PH misc\_difference 1..19 /\*tag= a  
 FT /note= "Std IUPAC codes used"  
 FT XX  
 XX WO9506714-Al.  
 PN XX  
 XX 09-MAR-1995.  
 PD XX  
 XX 01-SEP-1994; 94WO-US009851.  
 PF XX  
 XX 01-SEP-1993; 93US-00118441.  
 XX XX  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA (GEO ) GEN HOSPITAL CORP.  
 XX XX  
 XX Gilliam TC, Tanzi RE;  
 PI WPI; 1995-115430/15.  
 XX XX  
 DR Isolated Wilson's disease nucleic acid mol. - also probes, vectors, etc.,  
 XX useful for diagnosis and gene therapy of Wilson's disease.  
 PT Example; Page 30; 175pp; English.  
 XX XX  
 XX In order to physically map and clone the region of the Wilson's disease  
 CC (WD) gene, a 4.3kb insert from the WD flanking marker D13S31 (probe  
 CC PCR1324) was used to screen a large insert, CEPH II YAC sublibrary. A  
 CC higher resolution YAC map was constructed using inter-Alu PCR product  
 CC from 4 large YAC clones to screen the 1431 colony CEPH I YAC sublibrary.  
 CC A total of 16 mid-size YACs were identified. The pattern of mid-size YACs  
 CC detected by each large YAC clone was used to order the smaller YAC clones  
 CC relative to one another. Inter-Alu PCR "fingerprinting" of YAC clones  
 CC further assisted the ordering process. The data for this are not given in  
 CC the publication. (Updated on 25-MAR-2003 to correct PN field.)  
 XX XX  
 SQ Sequence 19 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 2 Other;  
 Query Match 8.9%; Score 12.4; DB 1; Length 19;  
 Best Local Similarity 72.2%; Pred. No. 3.4e+02;  
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCACAGCTGGAACCC 1679  
 |||||::|||  
 18 GGCTCAYRCCTGTAATCC 1

Db

RESULT 229  
 AAQ76249  
 ID AAQ76249 standard; DNA; 19 BP.  
 XX AC AAQ76249;  
 XX XX  
 XX 25-MAR-2003 (revised)  
 DT 10-AUG-1995 (first entry)  
 XX XX  
 DE Generic Alu consensus sequence used to generate Alu-1 primer set.  
 XX XX  
 KW Primer; PCR; amplification; primer set; probe; Alu sequence; Alu repeat;  
 KW Alu consensus sequence; chromosome; breakpoint; rearrangement;  
 KW chronic myelogenous leukemia; Philadelphia chromosome; translocation; ss.  
 XX XX  
 XX Synthetic.  
 OS OS  
 XX WO9428178-Al.  
 PN XX  
 XX 08-DEC-1994.  
 PD XX  
 XX 01-JUN-1994; 94WO-US006194.  
 PF XX  
 XX 01-JUN-1993; 93US-00070517.  
 PR XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA Siciliano MJ, Liu P;  
 XX WPI; 1995-022844/03.  
 XX XX  
 DR DNA probe specific for Human chromosome region 9q34 - allows detection of  
 PT bcr/abl rearrangement in interphase nuclei.  
 FT Disclosure; Page 22; 81pp; English.  
 XX XX  
 CC The consensus sequence, from bases 13-31, of the 5' end of a 300 bp Alu  
 CC segment. The sequence was used to generate a set of primers, designated  
 CC Alu-1 primers set (AAQ76247). The primers of the set have a reverse  
 CC complementary sequence to the Alu consensus sequence. Thus priming with  
 CC the Alu-1 set directs synthesis towards the 5' end (i.e. away from the  
 CC middle) of the Alu segment. Since the primer set is designed to bind  
 CC close to the edge of an Alu segment, amplification with these primers  
 CC will reduce the amount of Alu segment sequence and increase the amount of  
 CC specific chromosomal DNA present required for probe production. The  
 CC primer set is useful in the production of chromosomal specific probes e.g  
 CC for the detection of chromosomal breakpoints and rearrangements such as a  
 CC probe to detect chronic myelogenous leukemia characterised by the  
 CC Philadelphia chromosome, arising from a reciprocal translocation t(9;22)  
 CC (q34;q11). (Updated on 25-MAR-2003 to correct PN field.)  
 XX XX  
 SQ Sequence 19 BP; 3 A; 6 C; 3 G; 5 T; 0 U; 2 Other;  
 Query Match 8.9%; Score 12.4; DB 1; Length 19;  
 Best Local Similarity 72.2%; Pred. No. 3.4e+02;  
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GGCTCACAGCTGGAACCC 1679  
 |||||::|||  
 2 GGCTCAYRCCTGTAATCC 19

Db

RESULT 230  
 AAQ76247/c  
 ID AAQ76247 standard; DNA; 19 BP.  
 XX AC AAQ76247;  
 XX XX  
 XX 25-MAR-2003 (revised)  
 DT 10-AUG-1995 (first entry)  
 XX XX  
 DE Generic primer from Alu-1 primer set.  
 XX XX  
 KW Primer; PCR; amplification; primer set; probe; Alu sequence; Alu repeat;  
 KW Alu consensus sequence; chromosome; breakpoint; rearrangement;  
 KW chronic myelogenous leukemia; Philadelphia chromosome; translocation; ss.  
 XX XX

OS Synthetic.  
 XX WO9428178-A1.  
 PN  
 XX  
 XX 08-DEC-1994.  
 PD  
 XX  
 XX 01-JUN-1994; 94WO-US006194.  
 PF  
 XX  
 XX 01-JUN-1993; 93US-00070517.  
 PR  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX  
 XX Siciliano MJ, Liu P;  
 PI  
 XX  
 XX WPI; 1995-022844/03.  
 DR  
 XX  
 XX DNA probe specific for Human chromosome region 9q34 - allows detection of  
 PT bcr/abl rearrangement in interphase nuclei.  
 PT  
 XX  
 XX Disclosure; Page 11; 81pp; English.  
 PS  
 XX  
 XX The generic sequence of a primer set designated Alu-1. The primer set was  
 CC based on bases 13-31 of the 5' end of a 300 bp Alu segment (AAQ76249).  
 CC The primers of the set have a reverse complementary sequence to the Alu  
 CC consensus sequence. Thus priming with the Alu-1 set directs synthesis  
 CC towards the 5' end (i.e. away from the middle) of the Alu segment. Since  
 CC the primer set is designed to bind close to the edge of an Alu segment,  
 CC amplification with these primers will reduce the amount of Alu segment  
 CC sequence and increase the amount of specific chromosomal DNA present  
 CC required for probe production. The primer set is useful in the production  
 CC of chromosomal specific probes e.g. for the detection of chromosomal  
 CC breakpoints and rearrangements such as a probe to detect chronic  
 CC myelogenous leukemia characterised by the Philadelphia chromosome,  
 CC arising from a reciprocal translocation t(9;22) (q34;q11). (Updated on 25  
 CC -MAR-2003 to correct PN field.)  
 CC  
 XX Sequence 19 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 2 Other;  
 SQ  
 Query Match 8.9%; Score 12.4; DB 1; Length 19;  
 Best Local Similarity 72.2%; Pred. No. 3.4e+02;  
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 QY 1662 GGCTCACAGCTGGAACCC 1679  
 DB 18 GGCTCAIRCCTGTATCC 1  
 RESULT 231  
 AAV83937/C  
 ID AAV83937 standard; DNA; 19 BP.  
 XX  
 XX AAV83937;  
 AC  
 XX  
 XX 03-MAR-1999 (first entry)  
 DT  
 XX  
 XX PCR primer used to produce a YAC probe.  
 DE  
 XX  
 XX Yeast artificial chromosome; YAC; probe; eukaryotic chromosome;  
 KW neocentromere; replication; extra-chromosomal element; segregation;  
 KW cell division; artificial chromosome; gene therapy;  
 KW human artificial chromosome; transgenic; PCR primer; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX WO9851790-A1.  
 PN  
 XX  
 XX 19-NOV-1998.  
 PD  
 XX  
 XX 13-MAY-1998; 98WO-AU000352.  
 PF  
 XX  
 XX 13-MAY-1997; 97AU-00006784.  
 PR  
 XX  
 XX 26-AUG-1997; 97AU-00008791.  
 PR  
 XX

PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
 XX  
 XX Choo K, Du Sart D, Cancilla MR;  
 PI  
 XX  
 XX WPI; 1999-009773/01.  
 DR  
 XX  
 XX New isolated nucleic acid comprising neocentromere sequences from  
 PT eukaryotic chromosome - used to produce replicable, segregating  
 PT artificial chromosomes that can carry large amounts of DNA for gene  
 PT therapy.  
 PT  
 XX  
 XX Example 1; Page 24; 540pp; English.  
 PS  
 XX  
 XX PCR primers AAV83937-38 were used to amplify total yeast genomic DNA to  
 CC produce yeast artificial chromosome (YAC) probes. The YAC probes are used  
 CC to isolate the nucleic acid sequences of the invention. The specification  
 CC describes nucleic acid sequences derived from a eukaryotic chromosome,  
 CC including a neocentromere or its functional derivative or hybrid, that  
 CC are able, in a compatible cell, of replicating, acting as extra-  
 CC chromosomal element and segregating during cell division. The sequences  
 CC can be used to construct artificial chromosomes for use in gene therapy  
 CC comprising a replicable, segregating nucleic acid that confers a specific  
 CC phenotype on cells. Human artificial chromosomes can propagate in human  
 CC cells and carry large amounts of DNA (e.g. therapeutic genes), and, being  
 CC extra-chromosomal, they are not mutagenic. The artificial chromosomes are  
 CC also useful for generation of transgenic plants and animals, in  
 CC production of proteins and to make diagnostic reagents, e.g. for  
 CC expression of cytokines, receptors and growth factors, or to increase the  
 CC copy number of a gene in a cell. The constructs may also be used for  
 CC functional and structural analysis of chromosomes  
 CC  
 XX Sequence 19 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 2 Other;  
 SQ  
 Query Match 8.9%; Score 12.4; DB 1; Length 19;  
 Best Local Similarity 72.2%; Pred. No. 3.4e+02;  
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 QY 1662 GGCTCACAGCTGGAACCC 1679  
 DB 18 GGCTCAIRCCTGTATCC 1  
 RESULT 232  
 AAZ76552/C  
 ID AAZ76552 standard; DNA; 19 BP.  
 XX  
 XX AAZ76552;  
 AC  
 XX  
 XX 10-SEP-2001 (first entry)  
 DT  
 XX  
 XX Human biallelic marker downstream amplification primer SEQ ID NO:10908.  
 DE  
 XX  
 XX Human genome; biallelic marker; high density disequilibrium map;  
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 KW haplotyping; hybridisation; identification; characterisation;  
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
 KW diagnosis; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO9954500-A2.  
 PN  
 XX  
 XX 28-OCT-1999.  
 PD  
 XX  
 XX 21-APR-1999; 99WO-IB000822.  
 PF  
 XX  
 XX 21-APR-1998; 98US-0082614P.  
 PR  
 XX  
 XX 23-NOV-1998; 98US-0109732P.  
 PR  
 XX  
 XX (GEST ) GENSET.  
 PA  
 XX  
 XX Cohen D, Blumenfeld M, Chumakov I;  
 PI  
 XX



```
PI Boon-Falleur T;
XX
DR WPI; 1995-292948/38.
XX
PT Identification of cells presenting HLA-C-clone 10 or WAGE-1 derived
PT peptide - allows diagnosis and treatment of individuals with cellular
PT abnormalities, e.g. melanoma, also HLA-Cw*1601 derived peptide(s).
XX
XX Claim 20; Page 19; 26pp; English.
XX
CC HLA-C-clone 10 is presented on the surface of certain abnormal cells,
CC MAGS-1 is also expressed by these cells. AAT03827-T03830 are PCR primers
CC for the HLA molecule that may be used in a kit to determine the
CC expression of HLA-C-clone 10. Peptides of such molecules that are
CC expressed and presented on the surface of abnormal cells are useful for
CC the identification of abnormal cells and thus they allow diagnosis and
CC treatment of cellular abnormalities, e.g. melanoma and other cancers. The
CC isolated nucleic acid molecules coding for the peptides are also useful
CC as probes for the determination of HLA-clone-C expression. HLA-C-clone 10
CC is also known as HLA-Cw*1601
XX
SQ Sequence 17 BP; 6 A; 6 C; 5 G; 0 T; 0 U; 0 Other;
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1653 CAAGCACCAGGTCACA 1669
Db 1 CAAGCGCCAGGCACAGA 17
RESULT 235
AAV91297
ID AAV91297 standard; RNA; 17 BP.
XX
AC AAV91297;
XX
DT 18-FEB-1999 (first entry)
XX
DE Human C-raf target site nucleotide position 2318.
XX
DE Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX
OS Homo sapiens.
XX
PN WO9850530-A2.
XX
PD 12-NOV-1998.
XX
PF 05-MAY-1998; 98WO-US009249.
XX
PR 09-MAY-1997; 97US-0046059P.
PR 09-JUN-1997; 97US-0049002P.
PR 03-JUL-1997; 97US-0051718P.
PR 22-AUG-1997; 97US-0056808P.
PR 02-OCT-1997; 97US-0061321P.
PR 02-OCT-1997; 97US-0061324P.
PR 05-NOV-1997; 97US-0064866P.
PR 19-DEC-1997; 97US-0068212P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Beillon L;
PI Parry T, Beigelman L, Meswigen JA, Karpeisky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
DR WPI; 1999-009494/01.
XX
```

```
PT Identifying new catalytic nucleic acid that modulates selected processes
PT - especially ribozymes that cleave Raf RNA for treating cancer,
PT restenosis, and also new ribozymes and modified nucleoside triphosphates
PT used as antiviral agents and synthons.
XX
XX Claim 177; Page 152; 259pp; English.
XX
CC A method has been developed for the identification of a nucleic acid
CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC ascites and infection. They may also be used to detect genetic drift and
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-raf. Introduction
CC of sugar/phosphate modifications increases stability against nuclease and
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene
XX
SQ Sequence 17 BP; 4 A; 8 C; 3 G; 0 T; 2 U; 0 Other;
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 3.2e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1749 CCTATCCTTAAGGCCCA 1765
Db 1 CCCAUGCUCACAGGCCCA 17
RESULT 236
AAV93415/C
ID AAV93415 standard; RNA; 17 BP.
XX
AC AAV93415;
XX
DT 18-FEB-1999 (first entry)
XX
DE Human B-raf substrate nucleotide position 835.
XX
DE Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX
OS Homo sapiens.
XX
PN WO9850530-A2.
XX
PD 12-NOV-1998.
XX
PF 05-MAY-1998; 98WO-US009249.
XX
PR 09-MAY-1997; 97US-0046059P.
PR 09-JUN-1997; 97US-0049002P.
PR 03-JUL-1997; 97US-0051718P.
PR 22-AUG-1997; 97US-0056808P.
PR 02-OCT-1997; 97US-0061321P.
PR 02-OCT-1997; 97US-0061324P.
PR 05-NOV-1997; 97US-0064866P.
PR 19-DEC-1997; 97US-0068212P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Beillon L;
PI Parry T, Beigelman L, Meswigen JA, Karpeisky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
DR WPI; 1999-009494/01.
XX
```

PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;  
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
 DR WPI: 1999-009494/01.  
 XX Identifying new catalytic nucleic acid that modulates selected processes  
 PT - especially ribozymes that cleave Raf RNA for treating cancer,  
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
 PT used as antiviral agents and synthons.  
 XX Claim 177; Page 167; 259pp; English.  
 PS  
 XX A method has been developed for the identification of a nucleic acid  
 CC capable of modulating a process in a biological system. The method  
 CC comprises: (a) introducing into the system a random library of nucleic  
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
 CC in systems where modulation has occurred and/or determining the sequence  
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
 CC endonuclease activity and catalytic activity, from the present invention,  
 CC are used to modulate gene expression in plant and mammalian cells and to  
 CC cleave target nucleic acid, particularly for treating systemic diseases  
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
 CC ascites and infection. They may also be used to detect genetic drift and  
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs  
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
 CC generally any condition associated with the level of c-raf. Introduction  
 CC of sugar/phosphate modifications increases stability against nuclease and  
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the  
 CC method, specifically for modulating the expression of a Raf gene  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 5 G; 0 T; 5 U; 0 Other;  
 Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1665 TCACAGCTGGACCCCTG 1681  
 Db 17 TGACAGCGGAACCCCTG 1  
 RESULT 237  
 AAA55987  
 ID AAA55987 standard; DNA; 17 BP.  
 AC AAA55987;  
 DT 05-SEP-2000 (first entry)  
 DE Murine G713 amplification PCR primer SEQ ID NO:26.  
 XX Human; chromosome 13; G713; chromosome 13q31-q33; schizophrenia;  
 KW biallelic marker; polymorphism; central nervous disease; detection;  
 KW neuroleptic; G713 gene expression inhibitor; genotyping; PCR primer;  
 KW brain disorder; psychiatric disorder; bipolar disorder; ss.  
 OS Mus musculus.  
 XX  
 XX WO200022122-A2.  
 PN 20-APR-2000.  
 PD 12-OCT-1999; 99WO-IB001730.  
 XX 13-OCT-1998; 98US-0103955P.  
 PR 30-OCT-1998; 98US-0106457P.  
 XX (GEST ) GENSET.  
 PA Blumenfeld M, Bougueleret L, Chumakov I, Cohen D, Essieux L;  
 PI

XX  
 DR  
 XX  
 PT  
 PT prophylactic treatment of brain, psychiatric disorders like schizophrenia  
 and bipolar disorders.  
 XX Example 1; Page 144; 271pp; English.  
 PS  
 XX The present invention describes an isolated, purified or recombinant  
 CC polynucleotide (PN) (I) comprising a contiguous span of 8 to 50  
 CC nucleotides, where the span includes a G713 or chromosome 13q31-q33  
 CC related biallelic marker. (I) has neuroleptic activity and can be used as  
 CC a G713 gene expression inhibitor. (I) can be used genotyping to estimate  
 CC the frequency of an allele of a G713 or chromosome 13q31-q33 related  
 CC biallelic marker in a population, and of a haplotype for a set of  
 CC biallelic markers in a population. (I) is also useful in detecting an  
 CC association between a haplotype and a trait. The frequency is used for  
 CC detecting an association between a genotype and a trait being  
 CC schizophrenia. The genotype is used to determine whether an individual is  
 CC at risk of developing schizophrenia. (I) can also be used as a medicament  
 CC against several disorders preferably brain, psychiatric disorders such as  
 CC schizophrenia and bipolar disorder. Early identification of risk of  
 CC developing schizophrenia is possible, which would enable early and/or  
 CC prophylactic treatment. AAA55984 to AAA55966 represent human G713 genomic  
 CC DNA sequences; AAA55967 encodes the human G713 protein AAY90962; AAA55968  
 CC encodes the murine G713 protein AAY90963; AAA55992 to AAA56030 represent  
 CC human chromosome 13q31-q33 locus biallelic markers A12 to A49; AAA55969  
 CC to AAA55991, and AAA56031 and AAA56032 represent PCR primers used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;  
 Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1685 TCTCTCCAGCGTGGTG 1701  
 Db 1 TGTCTCTGAGCGTGGGG 17  
 RESULT 238  
 AAA24962  
 ID AAA24962 standard; DNA; 17 BP.  
 XX  
 AC AAA24962;  
 XX  
 DT 19-JUL-2000 (first entry)  
 XX  
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1460.  
 XX  
 DE Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorothioate; endonuclease;  
 XX anticancer; breast cancer; endometrium cancer; ss.  
 OS Homo sapiens.  
 XX  
 XX WO9954459-A2.  
 PN 28-OCT-1999.  
 PD 19-APR-1999; 99WO-US008547.  
 XX 20-APR-1998; 98US-0082404P.  
 PR 23-JUN-1998; 98US-00103636.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;  
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;  
 PI Matulic-Adamic J;

XX DR WPI; 2000-013248/01.  
 XX PT New nucleic acids that interact, and optionally cleave, target sequences,  
 XX PT used to treat cancer.  
 XX PS Claim 77; Page 64; 148pp; English.  
 XX CC The present invention describes nucleic acids (A) that interact stably  
 CC with a target sequence and contain at least one phosphorodithioate  
 CC link, having endonuclease activity. (A), and more generally any catalytic  
 CC nucleic acid (A') that modulates expression of the oestrogen receptor  
 CC gene, are used to treat cancer (particularly of breast or endometrium),  
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents (for RNA, in the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 XX invention  
 XX SQ Sequence 17 BP; 2 A; 9 C; 1 G; 5 T; 0 U; 0 Other;  
 Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1740 CAACTCCTCCTCCTATCCT 1756  
 Db 1 CAGCTCCTCCTCAFCCT 17  
 RESULT 239  
 AAF01989/C  
 ID AAF01989 standard; DNA; 17 BP.  
 AC AAF01989;  
 XX 16-FEB-2001 (first entry)  
 DT Hammerhead ribozyme substrate #284.  
 XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;  
 KW interferon alpha; ss.  
 XX Homo sapiens.  
 XX WO2000061729-A2.  
 XX 19-OCT-2000.  
 XX 11-APR-2000; 2000WO-US009721.  
 XX 12-APR-1999; 99US-0129390P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX Blatt L, Zwick M, Pavco P, Mcswiggen J;  
 PI WPI; 2000-647423/62.  
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,  
 XX useful for producing e.g. granulocyte colony stimulating factor protein,  
 XX interferon alpha and erythropoietin.  
 PS Claim 88; Page 75; 200pp; English.

PS Claim 37; Page 62; 164pp; English.  
 XX CC The present invention relates to enzymatic and antisense nucleic acid  
 CC molecules that act as inhibitors of the expression of repressor genes  
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription  
 CC factor gene, IRF-2 and/or the CAA/T Displacement Protein (CDP).  
 CC Inhibition of the repressors removes prevents inhibition (and  
 CC consequently increases expression of) genes involved in the production of  
 CC erythropoietin, granulocyte colony stimulating factor protein and  
 CC interferon alpha  
 XX SQ Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1638 GCTTGTAGTAGAGGCCA 1654  
 Db 17 GCTTGTAGTAGAGGCCA 1  
 RESULT 240  
 ABK00576  
 ID ABK00576 standard; RNA; 17 BP.  
 XX AC ABK00576;  
 XX 12-MAR-2002 (first entry)  
 DT Human NOGO Hammerhead Ribozyme #576.  
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; neurotropic; cytoprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNazyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200159103-A2.  
 XX 16-AUG-2001.  
 XX 09-FEB-2001; 2001WO-US004273.  
 XX 11-FEB-2000; 2000US-0191797P.  
 XX 28-FEB-2000; 2000US-0195516P.  
 XX 06-MAR-2000; 2000US-0197128P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX (BLAT/) BLATT L.  
 XX (MCSW/) MCSWIGGEN J.  
 XX (CHOW/) CHOWRIRA B M.  
 XX Blatt L, Mcswiggen J, Chowrira BM;  
 PI WPI; 2001-607195/69.  
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 XX constructs, which down regulate expression of a CD20 gene or neurite  
 XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 XX central nervous system injury.  
 PS Claim 88; Page 75; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an ambezyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NGO-  
 CC targeting nucleic acid is used to cleave RNA of the NGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NGO expression. The present  
 CC sequence is a hammerhead ribozyme of the invention  
 XX  
 SQ Sequence 17 BP; 5 A; 2 C; 5 G; 0 T; 5 U; 0 Other;  
 Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 58.8%; Pred. No. 3.2e+02;  
 Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1704 AGTTGGTTAGGAGNAC 1720  
 Db 1 AGUUGUUCAGAGUAC 17  
 RESULT 241  
 ABN07839  
 ID ABN07839 standard; DNA; 17 BP.  
 AC ABN07839;  
 XX  
 DT 29-MAY-2002 (first entry)  
 XX  
 DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7831.  
 KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 OS Homo sapiens.  
 XX  
 FN WO200192524-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 25-MAY-2001; 2001WO-US016981.  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 03-FEB-2001; 2001US-0266860P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX WPI; 2002-179446/23.  
 XX  
 PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.  
 XX  
 PS Disclosure; SEQ ID NO 7831; 214pp; English.  
 XX  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 17 BP; 5 A; 6 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1661 AGGCTCACAGCTGGAAC 1677  
 Db 1 AGCCTCACAGCTGAAGC 17  
 RESULT 242  
 ABN09666/c  
 ID ABN09666 standard; DNA; 17 BP.  
 XX  
 AC ABN09666;  
 XX  
 DT 29-MAY-2002 (first entry)  
 XX  
 DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9658.  
 KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 OS Homo sapiens.  
 XX  
 FN WO200192524-A2.  
 XX

QY 1645 GCAGAAGGCAAGCACCA 1661



Db 1 GCAGATGACAGCATCA 17  
|||||  
RESULT 244  
ABN00535  
ID ABN00535 standard; DNA; 17 BP.  
XX AC ABN00535;  
XX DT 29-MAY-2002 (first entry)  
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:527.  
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX OS Homo sapiens.  
XX PN WO200192524-A2.  
XX PD 06-DEC-2001.  
XX PF 25-MAY-2001; 2001WO-US016981.  
XX PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX PA (AEOM-) AEOMICA INC.  
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
XX or as specific biomolecule capture probes for surface-enhanced laser  
XX desorption/ionization, comprises human myosin-like protein hGDMPLP-1.  
XX PS Disclosure; SEQ ID NO 527; 214pp; English.  
XX CC The present invention describes a human genome-derived myosin-like  
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
XX nucleic acids can be used as probes to detect, characterise and quantify  
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
XX provide initial substrates for the recombinant engineering of hGDMPLP-1  
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP-  
XX -1 proteins, as standards in assays used to determine the concentration  
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
XX capture probes for surface-enhanced laser desorption/ionisation, as  
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
XX production, and in vaccines or for replacement therapy. The  
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
XX disorder associated with the expression of hGDMPLP-1, in particular heart  
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
XX The present sequence represents an oligomer used in the screening of the  
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.

CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 8.8%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1644 AGCAGAGGCAAGCACC 1660  
Db 1 AGCAGATGACAGCATC 17  
RESULT 245  
ABN01272/c  
ID ABN01272 standard; DNA; 17 BP.  
XX AC ABN01272;  
XX DT 29-MAY-2002 (first entry)  
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1264.  
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX OS Homo sapiens.  
XX PN WO200192524-A2.  
XX PD 06-DEC-2001.  
XX PF 25-MAY-2001; 2001WO-US016981.  
XX PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX PA (AEOM-) AEOMICA INC.  
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
XX or as specific biomolecule capture probes for surface-enhanced laser  
XX desorption/ionization, comprises human myosin-like protein hGDMPLP-1.  
XX PS Disclosure; SEQ ID NO 1264; 214pp; English.  
XX CC The present invention describes a human genome-derived myosin-like  
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
XX nucleic acids can be used as probes to detect, characterise and quantify  
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
XX provide initial substrates for the recombinant engineering of hGDMPLP-1  
XX protein variants having desired phenotypic improvements, and for  
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be

used as immunogens to raise antibodies that specifically recognise hGDMLP  
-1 proteins, as standards in assays used to determine the concentration  
and/or amount specifically of hGDMLP proteins, as specific biomolecule  
capture probes for surface-enhanced laser desorption/ionisation, as  
therapeutic supplement in patients having specific deficiency in hGDMLP-1  
production, and in vaccines or for replacement therapy. The  
polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
disorder associated with the expression of hGDMLP-1, in particular heart  
and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
The present sequence represents an oligomer used in the screening of the  
hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
The sequence data for this patent did not form part of the printed  
specification, but was obtained in electronic format directly from WIPO  
at ftp.wipo.int/pub/published\_pct\_sequence

Sequence 17 BP; 3 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1729 AGATTGGCTCCCAACTC 1745  
Db 17 AGATCGTCCCAACTC 1

RESULT 246  
ABK97683  
ID ABK97683 standard; DNA; 17 BP.  
AC ABK97683;  
XX  
XX 07-OCT-2002 (first entry)  
XX  
XX Cytochrome P450 3A (CYP3A) PCR primer #1.  
XX  
XX Cytochrome P450; CYP3A1; CYP3A2; CYP3A3; CYP3A4; CYP3A5; CYP3A7;  
XX drug metabolism; drug design; drug screening; PCR; primer; ss.  
XX Synthetic.  
XX  
XX WO200244213-A1.  
XX  
XX 06-JUN-2002.  
XX  
XX 28-NOV-2001; 2001WO-SE002631.  
XX  
XX 28-NOV-2000; 2000SE-00004366.  
XX 11-JUN-2001; 2001SE-00002061.  
XX  
XX (ZAPH/) ZAPHIROPOULOS P G.  
XX (FINT/) FINTA C.  
XX  
XX Zaphiropoulos PG, Finta C;  
XX  
XX WPI; 2002-557532/59.  
XX  
XX Novel cytochrome P450 protein in which CYP3A43 exon 1 is joined to sets  
XX of CYP3A4 or CYP3A5 exons, useful as medicament, and in evaluating drug  
XX metabolism, in drug design and drug screening.  
XX  
XX Example 1; Page 22; 131pp; English.  
XX  
XX The invention describes a cytochrome P450 protein (I) in which CYP3A43  
XX exon 1 is joined to sets of CYP3A4 or CYP3A5 exons, as well as sub  
XX fragments, variants and multiples of (I) having essentially the same  
XX characteristics. (I) is useful as a medicament, and for evaluating drug  
XX metabolism, in drug design, and drug screening, and in tests for  
XX adjusting the dose of drugs. This sequence represents a primer used to  
XX isolate DNA encoding the novel cytochrome P450 of the invention  
XX  
XX Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1673 GGAAACCTGGTGTCTCC 1689  
Db 1 GGAAACCTGGTGTCTCC 17

RESULT 247  
ABV79506  
ID ABV79506 standard; DNA; 17 BP.  
XX  
XX ABV79506;  
XX  
XX 03-JAN-2003 (first entry)  
XX  
XX Human HTPL scanning oligonucleotide SEQ ID 752.  
XX  
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
XX human testis expressed Patched like protein; testis; adrenal; liver;  
XX male germ cell development; bone marrow; brain; kidney; lung; placenta;  
XX prostate; skeletal muscle; colon; male infertility; cancer; ss.  
XX  
XX Homo sapiens.  
XX  
XX EP1229046-A2.  
XX  
XX 07-AUG-2002.  
XX  
XX 28-JAN-2002; 2002EP-00001167.  
XX  
XX 30-JAN-2001; 2001WO-US000663.  
XX 30-JAN-2001; 2001WO-US000664.  
XX 30-JAN-2001; 2001WO-US000665.  
XX 30-JAN-2001; 2001WO-US000667.  
XX 30-JAN-2001; 2001WO-US000668.  
XX 30-JAN-2001; 2001WO-US000669.  
XX 23-MAY-2001; 2001US-00364761.  
XX 09-OCT-2001; 2001US-0327898P.  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
XX Zhan J;  
XX  
XX WPI; 2002-676582/73.  
XX  
XX Novel isolated human testis expressed Patched like protein (HTPL), useful  
XX for identifying agonist and antagonist and specific binding partners, and  
XX for treating subjects having defects in HTPL.  
XX  
XX Example 2; Page 162; 718pp; English.  
XX  
XX The present invention relates to human testis expressed Patched like  
XX protein (HTPL, see ABV78759 to ABV78762 and ABV98519 to ABV98520). HTPL  
XX has two isoforms, with a few single base pair differences between the  
XX two. One of the single base pair changes introduces a premature stop  
XX codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
XX shares an overall structure organisation with the Patched protein. The  
XX shared structural features strongly imply that HTPL plays a role similar  
XX to that of Patched, and is a potential tumour suppressor. HTPL is  
XX important in regulating male germ cell development, and the HTPL gene was  
XX mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
XX useful for diagnosing a disorder caused by mutation in HTPL, and in  
XX therapy and manufacture of a medicament for treatment or prevention of  
XX such disorder associated with decreased expression or activity of human  
XX HTPL. Such disorders include disorders of testis, or adrenal, adult and  
XX foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
XX skeletal muscle or colon function. HTPL proteins and nucleic acids are  
XX clinically useful or colon function. HTPL proteins and nucleic acids are  
XX male infertility and cancer. The present oligonucleotide was used in an  
XX example from the invention

used as immunogens to raise antibodies that specifically recognise hGDMLP  
-1 proteins, as standards in assays used to determine the concentration  
and/or amount specifically of hGDMLP proteins, as specific biomolecule  
capture probes for surface-enhanced laser desorption/ionisation, as  
therapeutic supplement in patients having specific deficiency in hGDMLP-1  
production, and in vaccines or for replacement therapy. The  
polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
disorder associated with the expression of hGDMLP-1, in particular heart  
and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
The present sequence represents an oligomer used in the screening of the  
hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
The sequence data for this patent did not form part of the printed  
specification, but was obtained in electronic format directly from WIPO  
at ftp.wipo.int/pub/published\_pct\_sequence

Sequence 17 BP; 3 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1729 AGATTGGCTCCCAACTC 1745  
Db 17 AGATCGTCCCAACTC 1

RESULT 246  
ABK97683  
ID ABK97683 standard; DNA; 17 BP.  
AC ABK97683;  
XX  
XX 07-OCT-2002 (first entry)  
XX  
XX Cytochrome P450 3A (CYP3A) PCR primer #1.  
XX  
XX Cytochrome P450; CYP3A1; CYP3A2; CYP3A3; CYP3A4; CYP3A5; CYP3A7;  
XX drug metabolism; drug design; drug screening; PCR; primer; ss.  
XX Synthetic.  
XX  
XX WO200244213-A1.  
XX  
XX 06-JUN-2002.  
XX  
XX 28-NOV-2001; 2001WO-SE002631.  
XX  
XX 28-NOV-2000; 2000SE-00004366.  
XX 11-JUN-2001; 2001SE-00002061.  
XX  
XX (ZAPH/) ZAPHIROPOULOS P G.  
XX (FINT/) FINTA C.  
XX  
XX Zaphiropoulos PG, Finta C;  
XX  
XX WPI; 2002-557532/59.  
XX  
XX Novel cytochrome P450 protein in which CYP3A43 exon 1 is joined to sets  
XX of CYP3A4 or CYP3A5 exons, useful as medicament, and in evaluating drug  
XX metabolism, in drug design and drug screening.  
XX  
XX Example 1; Page 22; 131pp; English.  
XX  
XX The invention describes a cytochrome P450 protein (I) in which CYP3A43  
XX exon 1 is joined to sets of CYP3A4 or CYP3A5 exons, as well as sub  
XX fragments, variants and multiples of (I) having essentially the same  
XX characteristics. (I) is useful as a medicament, and for evaluating drug  
XX metabolism, in drug design, and drug screening, and in tests for  
XX adjusting the dose of drugs. This sequence represents a primer used to  
XX isolate DNA encoding the novel cytochrome P450 of the invention  
XX  
XX Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1673 GGAAACCTGGTGTCTCC 1689  
Db 1 GGAAACCTGGTGTCTCC 17

RESULT 247  
ABV79506  
ID ABV79506 standard; DNA; 17 BP.  
XX  
XX ABV79506;  
XX  
XX 03-JAN-2003 (first entry)  
XX  
XX Human HTPL scanning oligonucleotide SEQ ID 752.  
XX  
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
XX human testis expressed Patched like protein; testis; adrenal; liver;  
XX male germ cell development; bone marrow; brain; kidney; lung; placenta;  
XX prostate; skeletal muscle; colon; male infertility; cancer; ss.  
XX  
XX Homo sapiens.  
XX  
XX EP1229046-A2.  
XX  
XX 07-AUG-2002.  
XX  
XX 28-JAN-2002; 2002EP-00001167.  
XX  
XX 30-JAN-2001; 2001WO-US000663.  
XX 30-JAN-2001; 2001WO-US000664.  
XX 30-JAN-2001; 2001WO-US000665.  
XX 30-JAN-2001; 2001WO-US000667.  
XX 30-JAN-2001; 2001WO-US000668.  
XX 30-JAN-2001; 2001WO-US000669.  
XX 23-MAY-2001; 2001US-00364761.  
XX 09-OCT-2001; 2001US-0327898P.  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
XX Zhan J;  
XX  
XX WPI; 2002-676582/73.  
XX  
XX Novel isolated human testis expressed Patched like protein (HTPL), useful  
XX for identifying agonist and antagonist and specific binding partners, and  
XX for treating subjects having defects in HTPL.  
XX  
XX Example 2; Page 162; 718pp; English.  
XX  
XX The present invention relates to human testis expressed Patched like  
XX protein (HTPL, see ABV78759 to ABV78762 and ABV98519 to ABV98520). HTPL  
XX has two isoforms, with a few single base pair differences between the  
XX two. One of the single base pair changes introduces a premature stop  
XX codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
XX shares an overall structure organisation with the Patched protein. The  
XX shared structural features strongly imply that HTPL plays a role similar  
XX to that of Patched, and is a potential tumour suppressor. HTPL is  
XX important in regulating male germ cell development, and the HTPL gene was  
XX mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
XX useful for diagnosing a disorder caused by mutation in HTPL, and in  
XX therapy and manufacture of a medicament for treatment or prevention of  
XX such disorder associated with decreased expression or activity of human  
XX HTPL. Such disorders include disorders of testis, or adrenal, adult and  
XX foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
XX skeletal muscle or colon function. HTPL proteins and nucleic acids are  
XX clinically useful or colon function. HTPL proteins and nucleic acids are  
XX male infertility and cancer. The present oligonucleotide was used in an  
XX example from the invention

SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1662 GCTCAGCTGAGACC 1678  
| | | | | | | | | |  
Db 1 GACTCACTGCTGAGACC 17

RESULT 248

ABV90893

ID ABV90893 standard; DNA; 17 BP.

XX AC ABV90893;

DT 23-DEC-2002 (first entry)

XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1606.

XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
KW gene therapy; transgenic; ss.

XX OS Homo sapiens.

XX PN EP1239051-A2.

XX PD 11-SEP-2002.

XX PF 28-JAN-2002; 2002EP-00001165.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 23-MAY-2001; 2001WO-US000670.

XX PR 10-OCT-2001; 2001US-0328205P.

XX PA (ABOM-) ABOMICA INC.

XX PI Shannon M;

XX PT WPI; 2002-684061/74.

XX PS Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL

XX PT -1, useful for treating disorders associated with decreased expression or

XX PT activity of human POSHL1.

XX PS Example 2; SEQ ID NO 1606; 60pp + Sequence Listing; English.

XX CC The invention relates to an isolated SH3 domain (POSH)-like signalling  
XX CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
XX CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),  
XX CC (S1) having 95% deviations, especially conservative substitutions or a  
XX CC fragment of the sequences comprising at least 8 contiguous amino acids.  
XX CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
XX CC adaptor protein that interacts with Rho family small GTPases as well as  
XX CC downstream components of the signal transduction pathway. (I) is useful  
XX CC for identifying a specific binding partner. (I) and nucleic acids (II)  
XX CC encoding (I) are useful for diagnosing, monitoring disease and treating  
XX CC caused by altered expression of human POSHL1 including diagnosing and  
XX CC treating cancer, they are useful in the development of vaccines and (II) is  
XX CC useful in gene therapy. (II) is useful for constructing microarrays which  
XX CC are useful for measuring and for surveying gene expression and creating  
XX CC transgenic non-human animals capable of producing the proteins. The  
XX CC present sequence is that of a scanning oligonucleotide useful in examples  
XX CC of the invention. Note: The present sequence did not form part of the

CC Printed specification, but is based on sequence information supplied to  
CC Derwent by the European Patent Office

XX SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1671 CTGGAACCTGCTGCT 1687

| | | | | | | | | |  
Db 1 CCGAGCCCTGCTCTCT 17

RESULT 249

ABV90895

ID ABV90895 standard; DNA; 17 BP.

XX AC ABV90895;

XX DT 23-DEC-2002 (first entry)

XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1608.

XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
KW gene therapy; transgenic; ss.

XX OS Homo sapiens.

XX PN EP1239051-A2.

XX PD 11-SEP-2002.

XX PF 28-JAN-2002; 2002EP-00001165.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 23-MAY-2001; 2001WO-US000670.

XX PR 10-OCT-2001; 2001US-0328205P.

XX PA (ABOM-) ABOMICA INC.

XX PI Shannon M;

XX PT WPI; 2002-684061/74.

XX PT Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL

XX PT -1, useful for treating disorders associated with decreased expression or

XX PT activity of human POSHL1.

XX PS Example 2; SEQ ID NO 1608; 60pp + Sequence Listing; English.

XX CC The invention relates to an isolated SH3 domain (POSH)-like signalling  
XX CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
XX CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),  
XX CC (S1) having 95% deviations, especially conservative substitutions or a  
XX CC fragment of the sequences comprising at least 8 contiguous amino acids.  
XX CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
XX CC adaptor protein that interacts with Rho family small GTPases as well as  
XX CC downstream components of the signal transduction pathway. (I) is useful  
XX CC for identifying a specific binding partner. (I) and nucleic acids (II)  
XX CC encoding (I) are useful for diagnosing, monitoring disease and treating  
XX CC caused by altered expression of human POSHL1 including diagnosing and  
XX CC treating cancer, they are useful in the development of vaccines and (II) is  
XX CC useful in gene therapy. (II) is useful for constructing microarrays which  
XX CC are useful for measuring and for surveying gene expression and creating

CC transgenic non-human animals capable of producing the proteins. The  
 CC present sequence is that of a scanning oligonucleotide useful in examples  
 CC of the invention. Note: The present sequence did not form part of the  
 CC printed specification, but is based on sequence information supplied to  
 CC Derwent by the European Patent Office  
 XX  
 SQ Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1673 GGAACCGCTGGTCTCC 1689  
 ||| ||||| |||  
 Db 1 GGAGCCCTGGTCTCTAC 17

RESULT 250  
 ABV91050/c  
 ID ABV91050 standard; DNA; 17 BP.

XX  
 AC ABV91050;  
 XX  
 DT 23-DEC-2002 (first entry)

XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1763.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
 KW gene therapy; transgenic; ss.

XX Homo sapiens.

XX EP1239051-A2.

XX 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 30-JAN-2001; 2001WO-US000670.

XX 23-MAY-2001; 2001US-00864761.

XX 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.

XX Shannon M;

XX WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
 PT -1, useful for treating disorders associated with decreased expression or  
 PT activity of human POSHL1.

XX Example 2; SEQ ID NO 1763; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling  
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
 CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),  
 CC (SI) having 95% deviations, especially conservative substitutions or a  
 CC fragment of the sequences comprising at least 8 contiguous amino acids.  
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
 CC adaptor protein that interacts with Rho family small GTPases as well as  
 CC downstream components of the signal transduction pathway. (I) is useful  
 CC for identifying a specific binding partner. (I) and nucleic acids (II)  
 CC encoding (I) are useful for diagnosing, monitoring disease and treating  
 CC caused by altered expression of human POSHL1 including diagnosing and

CC treating cancer, they useful in the development of vaccines and (II) is  
 CC useful in gene therapy. (II) is useful for constructing microarrays which  
 CC are useful for measuring and for surveying gene expression and creating  
 CC transgenic non-human animals capable of producing the proteins. The  
 CC present sequence is that of a scanning oligonucleotide useful in examples  
 CC of the invention. Note: The present sequence did not form part of the  
 CC printed specification, but is based on sequence information supplied to  
 CC Derwent by the European Patent Office  
 XX  
 SQ Sequence 17 BP; 5 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1748 CCTATCTCTAAGGCC 1764  
 ||| ||||| |||  
 Db 17 CCTGTCTCTAAGTCCC 1

RESULT 251

ABV90899

ID ABV90899 standard; DNA; 17 BP.

XX  
 AC ABV90899;

XX 23-DEC-2002 (first entry)

XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1612.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
 KW gene therapy; transgenic; ss.

XX Homo sapiens.

XX EP1239051-A2.

XX 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 23-MAY-2001; 2001US-00864761.

XX 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.

XX Shannon M;

XX WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
 PT -1, useful for treating disorders associated with decreased expression or  
 PT activity of human POSHL1.

XX Example 2; SEQ ID NO 1512; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling  
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
 CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),  
 CC (SI) having 95% deviations, especially conservative substitutions or a  
 CC fragment of the sequences comprising at least 8 contiguous amino acids.  
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
 CC adaptor protein that interacts with Rho family small GTPases as well as  
 CC downstream components of the signal transduction pathway. (I) is useful

CC for identifying a specific binding partner. (I) and nucleic acids (II)  
 CC caused by altered expression of human POSHL1 including diagnosing and treating  
 CC treating cancer, they are useful in the development of vaccines and (II) is  
 CC useful in gene therapy. (II) is useful for constructing microarrays which  
 CC are useful for measuring and for surveying gene expression and creating  
 CC transgenic non-human animals capable of producing the proteins. The  
 CC present sequence is that of a scanning oligonucleotide useful in examples  
 CC of the invention. Note: The present sequence did not form part of the  
 CC printed specification, but is based on sequence information supplied to  
 CC Derwent by the European Patent Office  
 XX  
 SQ Sequence 17 BP; 3 A; 8 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1677 CCTGTGCTCTCTCCCA 1693  
 Db 1 CCTGTGCTCTACACCA 17  
 RESULT 252  
 ABV91049/c  
 ID ABV91049 standard; DNA; 17 BP.  
 XX AC ABV91049;  
 XX DT 23-DEC-2002 (first entry)  
 XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1762.  
 XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
 KW gene therapy; transgenic; ss.  
 XX OS Homo sapiens.  
 XX EW EP1239051-A2.  
 XX PD 11-SEP-2002.  
 XX PF 28-JAN-2002; 2002EP-00001165.  
 XX PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 10-OCT-2001; 2001US-0328205P.  
 PA (AEOM-) AEOMICA INC.  
 XX PI Shannon M;  
 XX DR WPI; 2002-684061/74.  
 XX PT Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
 PT -1, useful for treating disorders associated with decreased expression or  
 PT activity of human POSHL1.  
 XX PS Example 2; SEQ ID NO 1762; 60pp + Sequence Listing; English.  
 XX CC The invention relates to an isolated SH3 domain (POSH)-like signalling  
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
 CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),  
 CC (S1) having 95% deviations, especially conservative substitutions or a  
 CC fragment of the sequences comprising at least 8 contiguous amino acids.

CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
 CC adaptor protein that interacts with Rho family small GTPases as well as  
 CC downstream components of the signal transduction pathway. (I) is useful  
 CC for identifying a specific binding partner. (I) and nucleic acids (II)  
 CC encoding (I) are useful for diagnosing, monitoring disease and treating  
 CC caused by altered expression of human POSHL1 including diagnosing and  
 CC treating cancer, they are useful in the development of vaccines and (II) is  
 CC useful in gene therapy. (II) is useful for constructing microarrays which  
 CC are useful for measuring and for surveying gene expression and creating  
 CC transgenic non-human animals capable of producing the proteins. The  
 CC present sequence is that of a scanning oligonucleotide useful in examples  
 CC of the invention. Note: The present sequence did not form part of the  
 CC printed specification, but is based on sequence information supplied to  
 CC Derwent by the European Patent Office  
 XX  
 SQ Sequence 17 BP; 5 A; 2 C; 6 G; 4 T; 0 U; 0 Other;  
 Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1749 CCTATCCTAAAGGCCCA 1765  
 Db 17 CTGTCTTAAGTCCCA 1  
 RESULT 253  
 ABT34389/c  
 ID ABT34389 standard; DNA; 17 BP.  
 XX AC ABT34389;  
 XX DT 12-JUN-2003 (first entry)  
 XX DE Tumour suppression related human fukutin oligo SEQ ID No 26.  
 XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrenia; protein chip; gene therapy; tumour suppression;  
 KW human fukutin; ds.  
 XX OS Homo sapiens.  
 XX PN WO2003025175-A2.  
 XX PD 27-MAR-2003.  
 XX PF 17-SEP-2002; 2002WO-IB004208.  
 XX PR 17-SEP-2001; 2001FR-00011978.  
 XX PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX PI Telerman A, Amson R, Tuijnder M;  
 XX DR WPI; 2003-313353/30.  
 XX PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX PS Disclosure; Page 37; 720pp; French.  
 XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,  
 CC given in the specification, a sequence containing at least 15 consecutive  
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
 CC hybridizes to them under highly stringent conditions, or the complement  
 CC of any of them, or the corresponding RNA. The novel isolated nucleic  
 CC acids of the invention are useful as probes and primers for detecting,  
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
 CC component of a gene chip, in vitro as (anti)sense reagents, and for  
 CC production of recombinant polypeptides. Any of the nucleic acids,

CC polypeptides, vectors containing the nucleic acids, cells containing the  
CC vector or antibodies directed against the polypeptides are useful for  
CC preparation of pharmaceuticals for prevention and/or treatment of viral  
CC diseases that are characterised by development of tumours or cell  
CC degeneration, specifically cancer but also Alzheimer's disease and  
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
CC patient samples is useful for diagnosis and/or prognosis of these  
CC diseases. The polypeptides can also be used to generate antibodies, and  
CC both the polypeptide and antibodies are useful as components of protein  
CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
CC related human fukutin oligonucleotide of the invention  
CC  
XX  
SQ Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1641 TGTAGCAGAGGCAAGC 1657  
|||||  
DB 17 TGTAGCAGATGGCGATC 1

RESULT 254  
ABT40165  
ID ABT40165 standard; DNA; 17 BP.  
XX  
AC ABT40165;  
XX  
DT 13-JUN-2003 (first entry)  
XX  
DE Tumour suppression related human fukutin oligo SEQ ID No 5802.  
XX  
KW Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; gene chip;  
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; protein chip; gene therapy; tumour suppression;  
KW human fukutin; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2003025175-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 17-SEP-2002; 2002WO-IB004208.  
XX  
PR 17-SEP-2001; 2001FR-00011978.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
PI Telerman A, Amson R, Tuijnder M;  
XX  
PP WPI; 2003-313353/30.  
XX  
PT New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
PS Disclosure; Page 712; 720pp; French.  
XX  
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,  
CC given in the specification, a sequence containing at least 15 consecutive  
CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
CC hybridizes to them under highly stringent conditions, or the complement  
CC of any of them, or the corresponding RNA. The novel isolated nucleic  
CC acids of the invention are useful as probes and primers for detecting,  
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
CC component of a gene chip, in vitro as (anti)sense reagents, and for  
CC production of recombinant polypeptides. Any of the nucleic acids,  
CC polypeptides, vectors containing the nucleic acids, cells containing the  
CC vector or antibodies directed against the polypeptides are useful for

CC	preparation of pharmaceuticals for prevention and/or treatment of viral
CC	diseases that are characterised by development of tumours or cell
CC	degeneration, specifically cancer but also Alzheimer's disease and
CC	schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC	patient samples is useful for diagnosis and/or prognosis of these
CC	diseases. The polypeptides can also be used to generate antibodies, and
CC	both the polypeptide and antibodies are useful as components of protein
CC	chips. The nucleic acid sequences of the invention can be used in gene
CC	therapy. This polynucleotide sequence represents a tumour suppression
CC	related human fukutin oligonucleotide of the invention
XX	
SQ	Sequence 17 BP; 3 A; 7 C; 2 G; 5 T; 0 U; 0 Other;
	Query Match 8.8%; Score 12.2; DB 1; Length 17;
	Best Local Similarity 82.4%; Pred.No. 3.2e+02;
	Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1735 GCTCCCAACTCTCCCT 1751
Db	1 GATCCCAACTGCTCTT 17
RESULT 255	
ACA07738	
ID	ACA07738 standard; RNA; 17 BP.
XX	
AC	ACA07738;
XX	
DT	03-JUN-2003 (first entry)
XX	
DE	NFKB sub-unit modulating zinzyme substrate #137.
XX	
KW	Enzymatic nucleic acid, nuclear factor kappa B; NFKB; inozyme; zinzyme;
KW	G-cleaver; amberyne; cancer; REL-A activity; breast cancer; human;
KW	lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW	oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW	cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW	lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW	chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW	cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW	gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW	rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW	gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW	transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW	allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX	
OS	Homo sapiens.
XX	
PN	US2002177568-A1.
XX	
PD	28-NOV-2002.
XX	
PF	23-MAY-2001; 2001US-00864785.
XX	
PR	07-DEC-1992; 92US-00987132.
PR	18-MAY-1994; 94US-00245466.
PR	15-AUG-1994; 94US-00291932.
PR	23-DEC-1996; 96US-00779916.
XX	
PA	(STIN/) STINCHOMB D T.
PA	(MCSW/) MCSWIGGEN J.
PA	(DRAP/) DRAPER K G.
XX	
PI	Stinchcomb DT, Mcswiggen J, Draper KG;
XX	
DR	WPI; 2003-340953/32.
XX	
PT	Novel enzymatic nucleic acid molecules which down regulates expression of
PT	a sequence encoding a subunit of nuclear factor kappa B useful for
PT	treating cancer, inflammatory disorders and autoimmune diseases.
XX	
XX	Claim 3; Page 39; 72pp; English.
XX	

CC The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,  
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule

SQ Sequence 17 BP; 2 A; 5 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 52.9%; Pred. No. 3.2e+02;  
 Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1676 ACCCTGCTGTCTCTCC 1692

Db 1 ACCAUGGUGUUCUUC 17

RESULT 256

ACA09103/c

ID ACA09103 standard; RNA; 17 BP.

AC ACA09103;

DT 03-JUN-2003 (first entry)

DE NFKB sub-unit modulating amberzyme substrate #266.

Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;  
 G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;  
 lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;  
 gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 allergic airway inflammation; inflammatory bowel disease; infection; ss.

OS Homo sapiens.

XX US2002177568-A1.

XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

XX 18-MAY-1994; 94US-00245466.

XX 15-AUG-1994; 94US-00291932.

XX 23-DEC-1996; 96US-00777916.

PA (STIN/) STINCHOMB D T.  
 PA (MCSW/) MCSWIGGEN J.  
 XX (DRAP/) DRAPER K G.

PI Stinchcomb DT, Mcswiggen J, Draper KG;

XX WPI; 2003-340953/32.

XX Novel enzymatic nucleic acid molecules which down regulates expression of  
 PT a sequence encoding a subunit of nuclear factor kappa B useful for  
 PT treating cancer, inflammatory disorders and autoimmune diseases.

XX Claim 3; Page 56; 72pp; English.

CC The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,  
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule

SQ Sequence 17 BP; 4 A; 1 C; 11 G; 0 T; 1 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1738 CCCCAACTCTCTCCCTATC 1754

Db 17 CCCAGCTCCCCCTTTC 1

RESULT 257

ACA09102/c

ID ACA09102 standard; RNA; 17 BP.

XX ACA09102;

DT 03-JUN-2003 (first entry)

DE NFKB sub-unit modulating amberzyme substrate #265.

Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;  
 G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;  
 lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;  
 gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 allergic airway inflammation; inflammatory bowel disease; infection; ss.

```

XX OS Homo sapiens.
XX KW US200217568-A1.
XX PD 28-NOV-2002.
XX PF 23-MAY-2001; 2001US-00864785.
XX PR 07-DEC-1992; 92US-00987132.
XX PR 18-MAY-1994; 94US-00245466.
XX PR 15-AUG-1994; 94US-00291932.
XX PR 23-DEC-1996; 96US-00777916.
XX XX (STIN/) STINCHOMB D T.
XX PA (MCSW/) MCSWIGGEN J.
XX PA (DRAP/) DRAPER K G.
XX PI Stinchcomb DT, Mcswiggen J, Draper KG;
XX WPI; 2003-340953/32.
XX DR Novel enzymatic nucleic acid molecules which down regulates expression of
XX PT a sequence encoding a subunit of nuclear factor kappa B useful for
XX PT treating cancer, inflammatory disorders and autoimmune diseases.
XX PS Claim 3; Page 56; 72pp; English.
XX CC The invention describes an enzymatic nucleic acid molecule (I) which down
XX CC regulates expression of a sequence encoding a subunit of nuclear factor
XX CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
XX CC configuration. The enzymatic nucleic acid molecule is adapted to treat
XX CC cancer and is useful for down-regulating REL-A activity in a cell, for
XX CC treating a patient having a condition associated with the level of REL-A.
XX CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
XX CC the presence of a divalent cation, especially Mg2+. The enzymatic and
XX CC antisense nucleic acid molecules are useful for treating breast, lung,
XX CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
XX CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
XX CC multidrug resistant cancer. The method involves use of other drug
XX CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
XX CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
XX CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
XX CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
XX CC acid molecules are also useful for treating inflammatory disease such as
XX CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
XX CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
XX CC rejection, gene therapy applications, ischaemia/reperfusion injury
XX CC (central nervous system (CNS) and myocardial), glomerulonephritis
XX CC sepsis, allergic airway inflammation, inflammatory bowel disease or
XX CC infection. This sequence represents the substrate of a novel enzymatic
XX CC nucleic acid molecule
XX SQ Sequence 17 BP; 4 A; 1 C; 11 G; 0 T; 1 U; 0 Other;
Query Match 8.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1739 CCAACTCTCTCCCTATCC 1755
Db 17 CCAGCTCCCCCTTTC 1
RESULT 258
ADA99593/C
ID ADA99593 standard; DNA; 17 BP.
XX AC ADA99593;
XX XX 20-NOV-2003 (first entry)
XX DT Human MDZ3 scanning oligonucleotide SEQ ID 582.
XX DE

XX OS Homo sapiens.
XX KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX KW developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX XX (AEOM-) AEOMICA INC.
XX PA Shannon M, Gu Y, Nguyen C;
XX PI WPI; 2003-423107/40.
XX DR New zinc finger-containing proteins and nucleic acids, useful in
XX PT manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MDZ3,
XX PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX PS Example 8; SEQ ID NO 582; 103pp; English.
XX CC The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX CC or in manufacturing a medicament for treating or preventing a disorder
XX CC associated with decreased or increased expression or activity of MDZ3,
XX CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX CC acids and proteins are also useful for diagnosing or monitoring a disease
XX CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX CC acids can also be used as probes to detect and characterize gross
XX CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX CC useful in constructing microarrays for measuring gene expression. The
XX CC proteins are useful as therapeutic agents for gene therapy or as
XX CC vaccines. The present sequence was used to illustrate the invention.
XX SQ Sequence 17 BP; 3 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 3.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 83.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1666 CACAGCTGGACCTGG 1682
Db 17 CCCAGCTGGATGCTGG 1
RESULT 259
ADA99410
ID ADA99410 standard; DNA; 17 BP.
XX AC ADA99410;
XX XX 20-NOV-2003 (first entry)
XX DT Human MDZ3 scanning oligonucleotide SEQ ID 399.
XX DE
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX KW developmental disorder; ss.
XX OS Homo sapiens.
XX XX

```



PN EP1281758-A2.  
 PD 05-FEB-2003.  
 XX 30-JUL-2002; 2002EP-00016874.  
 XX 02-AUG-2001; 2001US-00922181.  
 XX (AEOM-) AEOMICA INC.  
 XX Shannon M, Gu Y, Nguyen C;  
 XX WPI; 2003-423107/40.  
 XX  
 XX New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MDZ3,  
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
 XX  
 PS Example 8; SEQ ID NO 399; 103pp; English.  
 XX  
 CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences; MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MDZ3,  
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 17 BP; 3 A; 7 C; 1 G; 6 T; 0 U; 0 Other;  
 Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1740 CAATCTCTCCCTATCCT 1756  
 || ||||| |||||  
 Db 1 CAGTTCCTCACTATCCT 17  
 RESULT 260  
 ABZ65014  
 ID ABZ65014 standard; RNA; 17 BP.  
 XX  
 AC ABZ65014;  
 XX  
 DT 21-MAR-2003 (first entry)  
 XX  
 DE Human HER2 DNazyme substrate #471.  
 XX  
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
 KW anti-rheumatic; cancer; AIDS; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200297114-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 XX 29-MAY-2002; 2002WO-US016840.  
 PF 29-MAY-2001; 2001US-0294140P.  
 PR 06-JUN-2001; 2001US-0296249P.  
 PR 10-SEP-2001; 2001US-0318471P.

XX (RIBO-) RIBOZYME PHARM INC.  
 XX Mcswiggen J;  
 XX WPI; 2003-140484/13.  
 XX  
 PT Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
 XX  
 PS Claim 4; Page 142; 185pp; English.  
 XX  
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
 CC rheumatic activity. The nucleic acid molecules are useful for reducing  
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
 CC also useful for treating breast, ovarian, colorectal, lung, prostate, and  
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
 CC ABZ66530 - ABZ66595 represent substrate/target sequences for the human  
 CC ribozymes of the invention  
 XX  
 SQ Sequence 17 BP; 3 A; 9 C; 1 G; 0 T; 4 U; 0 Other;  
 Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 64.7%; Pred. No. 3.2e+02;  
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1749 CCTATCTCTAAAGGCCCA 1765  
 ||: ||||| |||||  
 Db 1 CCUCUCCUACAUGCCCA 17  
 RESULT 261  
 ACD55654/c  
 ID ACD55654 standard; RNA; 17 BP.  
 XX  
 AC ACD55654;  
 XX  
 DT 23-SEP-2003 (first entry)  
 XX  
 DE HBV amberyze substrate sequence #164.  
 XX  
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberyze; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis B virus.  
 XX  
 PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 XX 26-MAR-2002; 2002WO-US009187.  
 PF 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLAT L.  
 PA (MACE/) MACEJAK D.

Mon Aug 30 09:26:45 2004

(MCSW/) MCSWIGGEN J.  
 (MORR/) MORRISSEY D.  
 (PAVC/) PAVCO P.  
 (LEEP/) LEE P.  
 (DRAP/) DRAPER K.  
 (ROBE/) ROBERTS E.  
 Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 Draper K, Roberts E;  
 WPI; 2003-229207/22.  
 Novel compound useful for treating cirrhosis, liver failure,  
 hepatocellular carcinoma, or condition associated with hepatitis C virus  
 infection.  
 Example 1; Page 206; 387pp; English.  
 The present invention relates to nucleic acid molecules which modulate  
 the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 as oligonucleotides that specifically bind the Enhancer I region of HBV  
 DNA. The nucleic acids may be used to modulate the expression of HBV  
 genes and HBV viral replication. Also disclosed is a method for screening  
 compounds and/or potential therapies directed against HBV, and compounds  
 that modulate the expression and/or replication of HCV. The compounds and  
 methods of the invention are useful for the treatment of degenerative and  
 disease states related to HBV and HCV infection, replication and gene  
 expression such as cirrhosis, liver failure, and hepatocellular  
 carcinoma. The present sequence represents a substrate for one of the HBV  
 carboxyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences  
 disclosed in the present invention  
 Sequence 17 BP; 4 A; 0 C; 9 G; 0 T; 4 U; 0 Other;  
 Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1740 CAACCTCTCCCTATCCT 1756  
 DB 17 CAACCTCTCCCTATCAT 1  
 RESULT 262  
 ACC67113/C  
 ID ACC67113 standard; DNA; 17 BP.  
 XX ACC67113;  
 XX 01-JUL-2003 (first entry)  
 XX Murine oligonucleotide associated with tumour suppression, SEQ ID 4360.  
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrania; ss.  
 XX Mus musculus.  
 OS  
 XX WO2003025176-A2.  
 PN 27-MAR-2003.  
 XX 17-SEP-2002; 2002WO-IB004210.  
 PF 17-SEP-2001; 2001FR-00011979.  
 PR 17-SEP-2001; 2001FR-00011979.  
 XX

(MOLE-) MOLECULAR ENGINES LAB.  
 Telerman A, Amson R, Tuijnder M;  
 WPI; 2003-333167/31.  
 New isolated nucleic acid, useful for treating viral diseases associated  
 with tumors and cell degeneration, also related polypeptides, antibodies  
 and transfected cells.  
 Disclosure; Page 540; 738pp; French.  
 The present invention relates to murine oligonucleotides (ACC62754-  
 ACC6806), which are associated with tumour suppression, tumour  
 reversion, apoptosis and virus resistance. The oligonucleotides are  
 useful as (1) as probes and primers for detecting, identifying,  
 quantifying and/or amplifying nucleic acid, e.g. as one component of a  
 gene chip; in vitro as (anti)sense reagents; and (2) for production of  
 recombinant polypeptides. The oligonucleotides are useful for preparation  
 of pharmaceuticals for prevention and/or treatment of viral diseases that  
 are characterised by development of tumours or cell degeneration,  
 specifically cancer but also Alzheimer's disease and schizophrania  
 Sequence 17 BP; 1 A; 5 C; 3 G; 8 T; 0 U; 0 Other;  
 Query Match 8.8%; Score 12.2; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1650 AGGCAAGCACCAGGCTC 1666  
 DB 17 AGGCAAGCACCAGGATC 1  
 RESULT 263  
 ADB45561/C  
 ID ADB45561 standard; DNA; 17 BP.  
 XX ADB45561;  
 XX 18-DEC-2003 (first entry)  
 XX Tumour suppression/reversion associated nucleotide #5884.  
 DE cytosatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrania;  
 KW diagnosis.  
 XX Homo sapiens.  
 OS  
 XX WO2003040369-A2.  
 PN 15-MAY-2003.  
 XX 17-SEP-2002; 2002WO-IB004219.  
 PF 17-SEP-2001; 2001FR-00011981.  
 PR (MOLE-) MOLECULAR ENGINES LAB.  
 Telerman A, Amson R, Tuijnder M;  
 WPI; 2003-441574/41.  
 New nucleic acid encoding human prostate membrane-specific antigen,  
 useful e.g. for treatment of tumors and viral infection, also related  
 polypeptide and antibodies.  
 Disclosure; Page 719; 771pp; French.  
 The invention relates to the isolation of 6327 nucleotide sequences,  
 fragments of at least 15 consecutive nucleotides of these nucleotides, a

sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia). Analysis of the expression of the nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides and polypeptides can also be used to screen for their specific interactive molecules, potentially useful for treating diseases associated with abnormal expression of the nucleotides.

XX  
SQ Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1641 TGTAGCAGAGGCAAGC 1657  
Db 17 TGTAGCAGATGGCGATC 1

RESULT 264  
ADE30685  
ID ADE30685 standard; DNA; 17 BP.  
XX  
AC ADE30685;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Cholesterol homeostasis/adipogenesis related DNA seq id 72.  
XX  
KW expression vector; anorectic; antiarteriosclerotic; cardiant;  
XX antidiabetic; elevated cholesterol; elevated lipid; adipogenesis;  
KW obesity; atherosclerosis; diabetes mellitus;  
KW coronary artery heart disease; cholesterol homeostasis; ss;  
XX differential expression.

OS Homo sapiens.  
XX  
PN US2003180764-A1.  
XX  
PD 25-SEP-2003.  
XX  
PF 08-JAN-2003; 2003US-00339793.  
XX  
PR 09-JAN-2002; 2002US-0347286P.  
XX  
PA (LYNX-) LYNX THERAPEUTICS INC.  
XX  
PI Shang J, Bowen B;  
XX  
PT WPI; 2003-830986/77.  
XX  
DR Polynucleotides differentially regulated in response to cholesterol and  
XX adipogenesis are useful to detect and treat associated conditions such as  
PT obesity, atherosclerosis, diabetes mellitus and coronary artery heart  
PT disease.  
XX  
PS Claim 8; SEQ ID NO 72; 59pp; English.

XX  
CC The invention describes a composition comprising at least one expression  
CC vector comprising a polynucleotide of the invention. The composition has  
CC anorectic, antiarteriosclerotic, cardiant and antidiabetic properties.  
CC The invention is used to detect and treat conditions associated with

CC elevated cholesterol and lipid or during adipogenesis, particularly  
CC obesity, atherosclerosis, diabetes mellitus or coronary artery heart  
CC disease. This sequence represents a polynucleotide differentially  
CC expressed during cholesterol homeostasis and adipogenesis.

XX  
SQ Sequence 17 BP; 3 A; 7 C; 2 G; 5 T; 0 U; 0 Other;  
Query Match 8.8%; Score 12.2; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1735 GCTCCCAACTCTCCCT 1751  
Db 1 GATCCCAACTCTCCTT 17

RESULT 265  
AAA92642/C  
ID AAA92642 standard; DNA; 18 BP.  
XX  
AC AAA92642;  
XX  
DT 04-JAN-2001 (first entry)  
XX  
DE Antisense oligonucleotide ISIS# 30365.  
XX  
KW Human; SRA; steroid receptor RNA activator; cytostatic; antiinflammatory;  
KW SRA inhibitor; cancer; infection; antisense oligonucleotide; ss.  
XX  
OS Synthetic.

XX  
PN US6107092-A.  
XX  
PD 22-AUG-2000.  
XX  
PF 29-MAR-1999; 99US-00280409.  
XX  
PR 29-MAR-1999; 99US-00280409.

XX  
PA (ISIS-) ISIS PHARM INC.  
XX (BAYU) BAYLOR COLLEGE MEDICINE.  
XX  
PI Cowsert LM, Bennett CF, O'malley BW;  
XX  
DR WPI; 2000-586211/55.  
XX

XX  
PT Antisense compounds targeted to steroid receptor RNA activator useful for  
PT diagnosis, prophylaxis and treatment of diseases associated with the  
PT steroid activator, such as infection, inflammation or tumor formation.  
XX  
PS Claim 3; Col 42; 47pp; English.

XX  
CC The present sequence is one of a large number of antisense  
CC oligonucleotides which is directed against one of four human steroid  
CC receptor RNA activator (SRA) nucleic acid sequences. Two series of  
CC antisense oligonucleotides were synthesized. The first series comprised 8  
CC -30 oligodeoxynucleotides with a phosphorothioate backbone. The second  
CC series comprised chimeric oligonucleotides composed of a central gap  
CC region, consisting of ten 2'-deoxynucleotides, which was flanked on both  
CC sides by four-nucleotide wings. The wings were composed of 2'-  
CC methoxyethyl (2'-MOE) nucleotides. Both series contained the same  
CC nucleotide sequences. The antisense compounds are useful for research,  
CC diagnosis, treatment and prophylaxis to prevent or delay infection,  
CC inflammation or tumor formation. Therapeutically the oligonucleotides  
CC are highly safe and are effectively administered to humans

XX  
SQ Sequence 18 BP; 3 A; 5 C; 6 G; 4 T; 0 U; 0 Other;  
Query Match 8.8%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 3.5e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1658 ACCAGGCTCAGCTGG 1674

Immunoglobulin heavy chain E (enhancer) region oligonucleotide.  
 DE  
 XX  
 XX  
 Immunoglobulin heavy chain; IgH: immuno-response; antisense; leukaemia;  
 KW  
 KW  
 neoplasia; tumour; cancer; lymphoma; lymphocyte; J region; E region;  
 XX  
 enhancer; J6 region; ss.  
 XX  
 XX

PT Activation of polypeptides - by interaction with activating peptide,  
XX resulting in refolding of the polypeptides to give active form.  
PS Example 2; Col 19; 29pp; English.  
XX  
XX  
CC PCR primers AAV16094-95 are used in a random mutagenesis reaction in the  
CC presence of an error prone polymerase to introduce mutations into the  
CC prosequence of subtilisin E of Bacillus subtilis (see AAW45599). The  
CC prosequence is essential for the production of active, correctly folded  
CC subtilisin. When certain amino acid substitutions are made, no mature,  
CC biochemically active subtilisin protein is produced. The mutations  
CC inhibited folding. The mutations have been observed to occur with high  
CC frequency within the hydrophobic region of the propeptide. It appears  
CC that the propeptide contains select functional domains which interact  
CC with specific regions of the mature region of the polypeptide to promote  
CC the refolding process. An in vitro method to restore or increase the  
CC natural biological activity of a target polypeptide (inactive or with  
CC decreased activity due to improper folding), which is normally expressed  
CC containing a prosequence forms the basis of the invention. An exogenous  
CC activating peptide used to promote refolding of the target polypeptide to  
CC give its active form. The activating peptide comprises the prosequence of  
CC the target or other proteins with a similar sequence and function to the  
CC target polypeptide. The method is used to produce biologically, correctly  
CC folded proteins from their inactive, incorrectly folded forms. Suitable  
CC target polypeptides include members of the serine protease or subtilisin  
CC families  
XX  
XX  
SQ Sequence 18 BP; 3 A; 1 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 3.5e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1636 GGGCTGTAGCAGAGG 1652  
Db 2 GGGTTGTTTCAGAGG 18

RESULT 269  
AAV08683  
ID AAV08683 standard; DNA; 18 BP.  
XX  
XX AAV08683;  
AC  
XX  
XX 15-FEB-1999 (first entry)  
DE  
XX  
XX Primer ATP/20RT for human ACE gene.  
DE  
XX  
XX PCR primer; human; ACE; angiotensin converting enzyme; angiotensinogen;  
KW cardiovascular status; AGT; AT1; type 1 angiotensin II receptor; stroke;  
KW polymorphic pattern; blood pressure; electrocardiographic profile;  
KW cardiac condition diagnosis; myocardial infarction; atherosclerosis;  
KW hypertension; cardiovascular disease; ss.  
XX  
XX Synthetic.  
OS  
XX Homo sapiens.  
XX  
XX WO9845477-A2.  
XX  
XX 15-OCT-1998.  
XX  
XX 01-APR-1998; 98WO-IB000475.  
XX  
XX 04-APR-1997; 97US-0042930P.  
XX  
XX (EURO-) EURONA MEDICAL AB.  
XX  
XX Norberg LT, Andersson MK, Lindstroem PHR;  
XX  
XX WPI; 1998-568361/48.  
XX  
XX  
XX Assessing cardiovascular status in humans by polymorphic analysis - of  
PT Genes for angiotensin converting enzyme, angiotensinogen and angiotensin

PT II receptor, used to diagnose predisposition to disease and to predict  
XX effect of therapy.

XX Example 1; Page 32; 71pp; English.

XX This sequence represents a PCR primer for the human ACE (angiotensin  
CC converting enzyme) gene, and can be used in the method of the invention.  
CC The method is for assessing cardiovascular status in humans by  
CC determining the sequence of at least one polymorphic site in the ACE  
CC (angiotensin converting enzyme), AGT (angiotensinogen) and/or AT1 (type 1  
CC angiotensin II receptor) genes, and comparing the polymorphic pattern  
CC with that in patients with predetermined markers of status. The method is  
CC used to assess blood pressure or electrocardiographic profile, to  
CC diagnose a cardiac condition such as (silent) myocardial infarction (MI),  
CC hypertension, atherosclerosis or stroke. They can also be used to predict  
CC response to treatments with ACE inhibitors, angiotensin II receptor  
CC antagonists, diuretics, alpha- or beta-adrenergic receptor antagonists,  
CC etc. It is also used to identify susceptibility to cardiovascular  
CC disease. Libraries of nucleic acids containing polymorphic positions in  
CC the 3 genes, and libraries of targets corresponding to the peptides from  
CC the genes are used to screen for cardiovascular agents. The nucleic acids  
CC contained in the library can be used as source of probes  
XX

SQ Sequence 18 BP; 2 A; 12 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 3.5e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1738 CCCAACTCTCTCCTATC 1754  
Db 2 CCAACTCTCTCCTCTC 18

RESULT 270  
AAV24515/c  
ID AAV24515 standard; DNA; 18 BP.  
XX  
XX AAV24515;  
AC  
XX  
XX 20-MAR-2003 (revised)  
DT 21-JUN-1999 (first entry)  
XX  
XX Human SR-BI gene exon 3 primer 3e30srbl.  
DE  
XX  
XX SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;  
KW restenosis; congestive heart failure; atherosclerosis; cholesterol;  
KW low density lipoprotein; LDL; high density lipoprotein; HDL; diagnosis;  
KW body mass index; obesity; cachexia; gallstone; PCR; primer; ss.  
XX  
XX Synthetic.  
OS  
XX Homo sapiens.  
XX  
XX WO9902735-A2.  
XX  
XX 21-JAN-1999.  
XX  
XX 10-JUL-1998; 98WO-US014354.  
XX  
XX 10-JUL-1997; 97US-00890979.  
XX  
XX 27-FEB-1998; 98US-00031626.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX (TUFT) UNIV TUFTS.  
XX  
XX Acton SL, Ordovas JM;  
XX  
XX WPI; 1999-120935/10.  
XX  
XX  
XX Detecting genetic predisposition for body mass disorders - by identifying  
PT allelic variants of a polymorphic region of the SR-BI gene.  
XX  
XX Example 2; Page 67; 102pp; English.

XX Primer 3e30srbl is used with primer 5e30srbl (see AAX24514) in the PCR  
CC amplification of exon 3 (see AAX24500) of the human SR-BI gene. The  
CC invention is based on the discovery of the genomic structure of the human  
CC SR-BI gene (see AAX24498-509) and on the identification of polymorphic  
CC regions within the gene which are associated with abnormal body mass  
CC index (BMI) and abnormal lipoprotein levels and hence with disorders such  
CC as obesity, cachexia, cardiovascular disorders and gallstone formation.  
CC primers (see AAX24510-35) are provided for amplification of the exons,  
CC introns and promoter region of the SR-BI gene for detection of  
CC polymorphisms and mutations. The invention provides methods for  
CC determining whether a subject has, or is at risk of developing, a disease  
CC associated with a specific allele of a polymorphic region of an SR-BI  
CC gene. Kits comprising the relevant probe or primer are claimed. (Updated  
CC on 20-MAR-2003 to correct PA field.)  
XX Sequence 18 BP; 6 A; 3 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 3.5e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1682 GTGTCCTCCAGCGTG 1698  
DB 17 GTCTCTCTCCCGCTG 1

RESULT 272  
AAX24607/C  
ID AAX24607 standard; DNA; 18 BP.  
XX AAX24607;  
XX 21-JUN-1999 (first entry)  
XX Human SR-BI gene exon 3 primer 3e30srbl.  
XX SR-BI; human; polymorphism; cardiovascular disorder; ischaemia;  
XX restenosis; congestive heart failure; atherosclerosis; cholesterol;  
XX low density lipoprotein; LDL; high density lipoprotein; HDL; diagnosis;  
XX body mass index; obesity; cachexia; gallstone; PCR; primer; ss.  
XX Synthetic.  
XX Homo sapiens.  
XX WO9902736-A2.  
XX 21-JAN-1999.  
XX 10-JUL-1998; 98WO-US014359.  
XX 10-JUL-1997; 97US-00890980.  
XX 27-FEB-1998; 98US-00032894.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Acton SL;  
XX WPI; 1999-120936/10.  
XX New nucleic acids comprising intronic sequence of a human scavenger  
XX receptor-BI (SR-BI) gene - useful for prognosis, diagnosis and treatment  
XX of SR-BI associated diseases or conditions.  
XX Claim 10; Page 66; 103pp; English.

XX Primer 3e30srbl is used with primer 5e30srbl (see AAX24606) in the PCR  
CC amplification of exon 3 (see AAX24592) of the human SR-BI gene. The  
CC invention is based on the discovery of the genomic structure of the human  
CC SR-BI gene (see AAX24590-601) and on the identification of polymorphic  
CC regions within the gene which are associated with abnormal body mass  
CC index (BMI) and abnormal lipoprotein levels and hence with disorders such  
CC as obesity, cachexia, cardiovascular disorders and gallstone formation.

CC Claimed primers (see AAX24602-25) are used for the amplification of the  
CC exons, introns and promoter region of the SR-BI gene for detection of  
CC polymorphisms and mutations. The invention provides methods for  
CC determining whether a subject has, or is at risk of developing, a disease  
CC associated with a specific allele of a polymorphic region of an SR-BI  
CC gene. Kits comprising the relevant probe or primer are claimed

QY 1682 GTGTCCTCCAGCGTG 1698  
DB 17 GTCTCTCTCCCGCTG 1

Query Match 8.8%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 3.5e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1682 GTGTCCTCCAGCGTG 1698  
DB 17 GTCTCTCTCCCGCTG 1

RESULT 272  
AAX38311  
ID AAX38311 standard; DNA; 18 BP.  
XX AAX38311;  
XX 21-AUG-2000 (first entry)  
XX Human AT1 regulatory region PCR primer, SEQ ID NO:111.  
XX Angiotensin II receptor: type 1 gene; AT1; regulatory region;  
XX polymorphism; polymorphic marker; cardiovascular disease;  
XX myocardial infarction; unstable angina; hypertension; atherosclerosis;  
XX stroke; prognosis; drug screening; treatment outcome; human; PCR primer;  
XX ss.  
XX Homo sapiens.  
XX WO200022166-A2.  
XX 20-APR-2000.  
XX 13-OCT-1999; 99WO-IB001678.  
XX 14-OCT-1998; 98US-0104286P.  
XX 14-OCT-1998; 98US-0104302P.  
XX (EURO-) EURONA MEDICAL AB.  
XX Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;  
XX WPI; 2000-318010/27.  
XX Assessing cardiovascular status in humans involves comparing test  
XX polymorphic pattern comprising polymorphic positions within genes  
XX encoding specific proteins, with reference polymorphic pattern.  
XX Example 1; Page 54; 126pp; English.

XX The invention relates to a novel method of assessing the cardiovascular  
CC status in an individual and to newly identified polymorphisms in the  
CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II  
CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,  
CC aldosterone synthase, endothelin receptor type A and beta-adrenergic  
CC receptors 1 and 2. The method comprises determining the sequence at one  
CC or more polymorphic positions within these genes, and comparing the  
CC pattern of polymorphisms from the individual with a reference polymorphic  
CC pattern obtained from a population of individuals exhibiting a  
CC predetermined cardiovascular disease status. The polymorphic markers are  
CC useful for determining the predisposition of an individual to  
CC cardiovascular disorders such as myocardial infarction, unstable angina,  
CC hypertension, atherosclerosis and stroke. They are also useful for  
CC predicting the likely cardiovascular status of a patient given a  
CC treatment regimen comprising administration of cardiovascular drugs  
CC (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-







CC neuroprotective, disorder and vasotropic activity. The antisense  
CC oligonucleotides are useful for inhibiting the expression of inducible  
CC nitric oxide synthase in cells or tissues. In particular, the antisense  
CC oligonucleotides are useful for treating diseases or disorders associated  
CC with inducible nitric oxide synthase, e.g. diabetes, immunological  
CC ischaemia, cardiovascular disorder, neurological disorder or  
CC useful for research and diagnostics. The antisense oligonucleotides are also  
CC antisense 2'-O-methoxyethyl gapper oligonucleotide with a  
CC phosphorothioate backbone, a central "gap" region of ten nucleotides  
CC flanked by four nucleotide 2'-MOE (2'-methoxyethyl) wings and 5-  
CC methylcytidine residues throughout the oligonucleotide. The antisense  
CC oligonucleotide is targeted to human inducible nitric oxide synthase  
CC mRNA (AAH47973)  
XX  
SQ Sequence 18 BP; 5 A; 5 C; 3 G; 5 T; 0 U; 0 Other;  
Query Match 8.8%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 3.5e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1723 AGATGGAGATTGGCTCC 1739  
Db 18 AGTTTGAGATGGCTCC 2  
RESULT 277  
AAH4080/c  
ID AAS14080 standard; DNA; 18 BP.  
XX AC AAS14080;  
XX DT 18-DEC-2001 (first entry)  
XX DE Forward PCR primer used in prevention of SMN2 exon 7 skipping.  
XX KW Survival motor neuron gene; SMN1; SMN2; spinal muscular atrophy; SMA; ss;  
XX KW chromosome 5q13; exonic splicing enhancer; ESE; pre-mRNA processing;  
XX KW human; mammal; exon skipping; PCR primer.  
XX OS Homo sapiens.  
XX PN WO200166129-A1.  
XX PD 13-SEP-2001.  
XX PF 07-MAR-2001; 2001WO-EP002567.  
XX PR 10-MAR-2000; 2000EP-00105081.  
XX PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
XX PI Stamm S, Wirth B, Hofmann V, Androphy E, Lorson C;  
XX DR WPI; 2001-589914/66.  
XX PT Substances capable of preventing skipping of exon 7 of survival motor  
XX neuron gene 2 are useful for treating spinal muscular atrophy.  
XX PS Example 4; Page 25; 49pp; English.  
XX CC The invention relates to a substance capable of preventing the skipping  
XX of exon 7 of the survival motor neuron gene 2 (SMN2). This is the spinal  
XX muscular atrophy (SMA) determining gene, present on chromosome 5q13, and  
XX can be used as a therapeutic agent. SMN2 expresses reduced full-length  
XX and abundant levels of transcripts lacking exon 7, encoding a less stable  
XX protein than that encoded by SMN1, with a reduced self-oligomerisation  
XX capacity. SMN1 and SMN2 differ by a nucleotide exchange in exon 7 that  
XX disrupts an exonic splicing enhancer (ESE) and causes exon 7 skipping in  
XX SMN2 transcripts. Substances of the invention are useful for treating  
XX spinal muscular atrophy (SMA) and for changing the pre-mRNA processing  
XX relating to the SMN gene of mammalian cells. Control of exon 7 inclusion  
XX can be determined by monitoring the ratio between exon 7 exclusion and

CC skipping in cells exposed to possible therapeutic agents. This sequence  
CC represents a PCR primer used in prevention of skipping of exon 7 of the  
CC SMN2 gene  
XX  
SQ Sequence 18 BP; 6 A; 2 C; 8 G; 2 T; 0 U; 0 Other;  
Query Match 8.8%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 3.5e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1731 ATTGGTCCCAACTCCT 1747  
Db 18 ATGGCCTCCCATCTCCT 2  
RESULT 278  
AAH25354/c  
ID AAH25354 standard; DNA; 18 BP.  
XX AC AAH25354;  
XX DT 22-AUG-2001 (first entry)  
XX DE Antisense oligonucleotide targeted to human Her-4 coding region.  
XX KW Antisense oligonucleotide; Her-4; receptor kinase; tyrosine kinase;  
XX KW infection; inflammation; tumour; phosphorothioate; ss.  
XX OS Homo sapiens.  
XX PH Key  
FT modified\_base 1..18  
FT /tag= b  
FT /note= "all cytidine residues are 5-methylcytidines"  
FT modified\_base 1..18  
FT /tag= c  
FT /note= "all internucleoside linkages are phosphorothioate  
FT linkages"  
FT modified\_base 1..4  
FT /tag= a  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
FT modified\_base 5..14  
FT /tag= d  
FT /note= "2'-deoxynucleotides"  
FT modified\_base 15..18  
FT /tag= e  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
XX US6255111-B1.  
XX PD 03-JUL-2001.  
XX PF 31-JUL-2000; 2000US-00632580.  
XX PR 31-JUL-2000; 2000US-00632580.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Bennett CF, Cowser LM;  
XX DR WPI; 2001-388929/41.  
XX PT Compound for inhibiting the expression of Her-4 (a receptor/tyrosine  
XX kinase) e.g. in preventing tumor formation, comprises an antisense  
XX oligonucleotide that hybridizes to a nucleic acid encoding Her-4.  
XX PS Claim 1; Col 43-44; 44pp; English.  
XX CC The specification describes antisense oligonucleotides which are targeted  
XX to a nucleic acid encoding Her-4 (a receptor/tyrosine kinase). The  
XX antisense oligonucleotides are used to inhibit the expression of Her-4 in  
XX cells or tissues in vitro. They can be used in diagnostics, therapeutics,  
XX prophylaxis and as a probe in research reagents. The antisense

CC oligonucleotides can be used to prevent or delay infection, inflammation  
 CC or tumour formation. AAH25315-AAH25398 represent antisense  
 CC oligonucleotides which are targeted to different regions of the human Her  
 CC -4 gene  
 XX  
 XX Sequence 18 BP; 5 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 18;  
 Best Local Similarity 82.4%; Pred. No. 3.5e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1723 AGATGAGATGGCTCC 1739  
 ||| ||||| |||||  
 Db 18 AGTTTGAGATGGCTCC 2

RESULT 279  
 AAS95242  
 ID AAS95242 standard; DNA; 18 BP.  
 XX  
 AC AAS95242;  
 XX  
 XX 14-FEB-2002 (first entry)  
 DT  
 XX Otoferlin exon PCR primer #31.  
 DE  
 XX Human; mouse; otoferlin; OTOF; brain; auditory function; PCR primer;  
 KW autosomal nonsyndromic prelingual deafness; DFNB9; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WC200170972-A2.  
 PN  
 XX 27-SEP-2001.  
 PD  
 XX 23-MAR-2001; 2001WO-IB000578.  
 PF  
 XX 24-MAR-2000; 2000US-0191738P.  
 PR  
 XX (INSP ) INST PASTEUR.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX Yasunaga S, Grati M, Cohen-Salmon M, El Amraoui A, Petit C;  
 PI Weil D;  
 PI  
 XX WPI; 2001-611499/70.  
 DR  
 XX Novel human gene Otoferlin, underlying an autosomal recessive  
 PT nonsyndromic prelingual deafness, DFNB9, and proteins encoded by the  
 PT gene, implicated in deafness.  
 PT  
 XX Claim 25; Page 31; 99pp; English.

PS The invention relates to a purified polynucleotide (I) encoding a protein  
 CC sequence (II) encoded by a novel human gene, otoferlin (OTOF) or the long  
 CC human otoferlin isoform in brain. (I) was identified as underlying an  
 CC autosomal nonsyndromic prelingual deafness DFNB9, and is thus useful for  
 CC detecting deafness disease in humans and for characterising the functions  
 CC of proteins and genes encoding them in auditory function. AAS95022-  
 CC AAS95248 represent human and mouse otoferlin coding sequences, PCR  
 CC primers and related sequences of the invention  
 XX  
 XX Sequence 18 BP; 3 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 8.8%; Score 12.2; DB 1; Length 18;  
 Best Local Similarity 82.4%; Pred. No. 3.5e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1671 CTGGAAACCCCTGGTGCT 1687  
 ||||| ||||| |||||  
 Db 2 CTGGGACCCAGGTGACT 18

RESULT 280  
 AAF79532/c  
 ID AAF79532 standard; DNA; 18 BP.  
 XX  
 AC AAF79532;  
 XX  
 XX 29-MAY-2001 (first entry)  
 DT  
 XX Caspase-4 protease cleavage signal nucleotide sequence.  
 DE  
 XX Caspase-4; protease; cleavage signal; transgene expression;  
 KW transgene localisation; sodium iodide symporter; NIS; ds.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200113106-A1.  
 PN  
 XX 22-FEB-2001.  
 PD  
 XX 17-AUG-2000; 2000WO-US022566.  
 PF  
 XX 17-AUG-1999; 99US-0149168P.  
 PR 16-AUG-2000; 2000US-00639667.  
 PR 16-AUG-2000; 2000US-00640198.  
 XX  
 XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
 PA  
 XX Russell SJ, Morris J, Peng K;  
 PI  
 XX WPI; 2001-257548/26.  
 DR  
 XX P-PSDB; AAB73916.

PT Monitoring transgene expression and therapeutic peptide production in  
 PT mammals by detecting marker polypeptides linked to transgenes or  
 PT therapeutic genes released from cells into extracellular body fluid.  
 XX  
 XX Example 11; Page 48; 79pp; English.

PS The present sequence is a self-cleaving linker. It may be used in a  
 CC method for monitoring expression and/or localisation of a transgene, and  
 CC production of therapeutic peptide in a mammal. The method involves  
 CC quantifying or detecting the amount of marker polypeptide and/or sodium  
 CC iodide symporter (NIS) linked to the product of the transgene or  
 CC therapeutic gene released from cells into extracellular body fluid, or  
 CC determining the location of labelled molecules which are transported into  
 CC the cells bearing the marker peptide. The method provides convenient and  
 CC effective monitoring of the level and kinetics of expression of  
 CC transgenes and the tissue-specific distribution of expressed transgenes  
 CC in cells, tissues, animals or humans without the need for disruptive and  
 CC expensive sampling methods including surgery. The transgene location can  
 CC be monitored without adversely affecting the mammal or the cell. The NIS  
 CC is a self protein and as such does not stimulate a host immune reaction.  
 CC Furthermore, the NIS functions solely to sequester iodine into a cell,  
 CC which does not adversely affect normal cellular function or overall cell  
 CC biology

SQ Sequence 18 BP; 4 A; 7 C; 1 G; 6 T; 0 U; 0 Other;  
 Query Match 8.8%; Score 12.2; DB 1; Length 18;  
 Best Local Similarity 82.4%; Pred. No. 3.5e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1717 GTACGGAGATGGAGATT 1733  
 ||||| ||||| |||||  
 Db 17 GTACGGAGATGGAGATT 1  
 RESULT 281  
 ABZ80661/c  
 ID ABZ80661 standard; DNA; 18 BP.  
 XX  
 XX ABZ80661;  
 XX

DT 13-JUN-2003 (first entry)  
 XX Magnaporthe grisea plsl gene PCR primer 39+ for expression construct.  
 DE plsl; rice blast fungus; ss; fungicide; tetraspanin; pathogenicity;  
 XX appressorium; PCR; primer; amplification.  
 KW Magnaporthe grisea.  
 OS WO200077036-A2.  
 XX  
 XX 21-DEC-2000.  
 XX  
 XX 16-JUN-2000; 2000WO-FR001666.  
 XX  
 XX 16-JUN-1999; 99FR-00007867.  
 PR 31-MAR-2000; 2000FR-00004102.  
 XX  
 XX (AVET ) AVENTIS CROPS SCIENCE SA.  
 XX  
 XX Cots J, Gourgues M, Latorse M, Lebrun M;  
 XX WPI; 2001-080679/09.  
 XX  
 XX Novel nucleic acid essential for pathogenicity of fungi, useful for  
 PT identifying agricultural fungicides, also related proteins and  
 PT transformants.  
 XX  
 XX Example 4; Page 42; 72pp; French.  
 PS  
 XX  
 XX The invention relates to the isolation of the rice blast fungus  
 CC (Magnaporthe grisea) plsl gene (also known as gene 421). The gene encodes  
 CC a tetraspanin that is essential for fungal pathogenicity. The plsl  
 CC protein is essential for controlling biological functions of the  
 CC appressorium such as differentiation of the penetrative hyphal tip in  
 CC this pathogenic fungus. The gene, host cells that express it and/or the  
 CC polypeptide encoded by it are used to identify genes involved in fungal  
 CC pathogenicity and to identify compounds that inhibit fungal  
 CC pathogenicity, potentially useful as plant-protection agents. The gene is  
 CC also useful for isolating homologous genes from other fungi and as  
 CC antisense sequences (antifungal agents). This sequence represents a  
 CC primer used to PCR amplify a Magnaporthe grisea plsl gene to generate an  
 CC expression construct  
 XX  
 XX Sequence 18 BP; 1 A; 6 C; 5 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.8%; Score 12.2; DB 1; Length 18;  
 Best Local Similarity 82.4%; Pred. No. 3.5e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1647 AGAAGGCAAGCACCAGG 1663  
 ||||| ||||| |||||  
 Db 17 AGAAGCCAGCATCAGG 1  
 RESULT 282  
 ABS98053/c  
 ID ABS98053 standard; DNA; 18 BP.  
 XX  
 XX ABS98053;  
 AC  
 XX  
 XX 23-DEC-2002 (first entry)  
 DT  
 XX Human multidrug resistance gene PCR primer #17.  
 DE  
 XX Human; ss; primer: cytochrome P450 A1; CYP450A1; UGT2B4; MDR1; PCR;  
 KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;  
 KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;  
 KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;  
 KW cyclooxigenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
 KW epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;  
 KW glutathione-S-transferase 12; GSTI2; histamine-N-methyl transferase;  
 KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;

KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;  
 KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; UPA;  
 KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;  
 KW multidrug resistance associated protein 3; cancer; prostate;  
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;  
 KW altered drug metabolism; cardiovascular function; colorectal tumour;  
 KW central nervous system; pulmonary; immunological.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200257410-A2.  
 XX  
 XX 25-JUL-2002.  
 XX  
 XX 28-NOV-2001; 2001WO-US044838.  
 XX  
 XX 28-NOV-2000; 2000US-00724389.  
 XX  
 XX (DNAS-) DNA SCI LAB INC.  
 PA  
 XX Guida M, Hall J;  
 PI  
 XX WPI; 2002-698522/75.  
 DR  
 XX Isolated nucleic acid molecules having polymorphisms in known human genes  
 PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers  
 PT for locating, identifying and characterizing the genes responsible for  
 PT disorder-related traits.  
 XX  
 XX Example 22; Page 141; 714pp; English.  
 PS  
 XX This invention relates to the sequence of an isolated nucleic acid  
 CC molecule comprising at least one base variation from that of a known  
 CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),  
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),  
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
 CC (ARNT), cathepsin S (CTSS), cyclooxigenase 2 (COX2), diazepam binding  
 CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating  
 CC protein (FLAP), glutathione-S-transferase 12 (GSTI2), histamine-N-methyl  
 CC transferase (HNMT), kallikrein 2 (KLK2), nicotinamide -N-methyl  
 CC sulfotransferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),  
 CC sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4  
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl  
 CC transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance 1  
 CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3  
 CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic  
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.  
 CC The polymorphisms in the human genes cited in the invention are useful as  
 CC genetic linkage markers for locating and characterizing the genes that  
 CC are responsible for specific traits within the genome and eventually  
 CC identifying the genes responsible for a variety of disorder-related  
 CC traits as a result of their e.g., overexpression, constitutive  
 CC expression, mutation or underexpression, which may be used in diagnosing  
 CC and/or treating the disorders. The nucleic acid molecules comprising the  
 CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP45002E1,  
 CC ARNT, EPHX2, GSTI2, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,  
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug  
 CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,  
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for  
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are  
 CC used to screen for altered cardiovascular function, in COX2 or CHMR2 are  
 CC susceptible to colorectal tumours, in DBI or CHMR1 for altered central  
 CC nervous system function, in FLAP and HNMT for altered pulmonary,  
 CC immunological or haematological function, in KLK2 for altered serine  
 CC protease activity in the prostate, in LTF for altered immunological or  
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and  
 CC peripheral nervous system function. The present sequence represents a PCR  
 CC primer used to amplify the sequences of the invention  
 XX  
 SQ Sequence 18 BP; 4 A; 2 C; 8 G; 4 T; 0 U; 0 Other;  
 Query Match 8.8%; Score 12.2; DB 1; Length 18;

[illegible]

QY 1682 GTGTCCTCCAGCGTG 1698  
 Db 17 GTCTCTCTCCGCGTG 1

RESULT 285  
 ADC24242  
 ID ADC24242 standard; DNA; 18 BP.  
 AC ADC24242;  
 XX  
 XX 18-DEC-2003 (first entry)  
 DE Human NOV1b reverse PCR primer SEQ ID NO:49.  
 XX  
 XX human; NOVX; cardiact; antiarteriosclerotic; hypotensive; vasotropic;  
 KW dermatological; anorectic; immunosuppressive; cytostatic;  
 KW antiinfertility; haemostatic; anti-HIV; antiasthmatic; antiinflammatory;  
 KW neuroprotective; anabolic; nootropic; antiparkinsonian; gene therapy;  
 KW cardiomyopathy; atherosclerosis; hypertension; congenital heart defect;  
 KW pulmonary stenosis; scleroderma; obesity; metabolic disturbance; obesity;  
 KW transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia;  
 KW prostate cancer; diabetes; metabolic disorder; neoplasm; adenocarcinoma;  
 KW fertility; haemophilia; graft versus host disease; AIDS;  
 KW bronchial asthma; Crohn's disease; multiple sclerosis;  
 KW infectious disease; anorexia; neurodegenerative disorder;  
 KW Alzheimer's disease; Parkinson's disease; immune disorder;  
 KW haematopoietic disorder; dyslipidaemia; wasting disorder; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO2003076584-A2.  
 XX  
 XX 18-SEP-2003.  
 XX  
 XX 06-MAR-2003; 2003WO-US006951.  
 XX  
 XX 06-MAR-2002; 2002US-0361974P.  
 XX  
 XX 19-MAR-2002; 2002US-0365477P.  
 XX  
 XX 22-MAR-2002; 2002US-0366928P.  
 XX  
 XX 06-AUG-2002; 2002US-0401661P.  
 XX  
 XX 05-MAR-2003; 2003US-00401661.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Alsobrook JP, Burgess CE, Bainger SR, Gerlach VL, Ji W, Kekuda R;  
 XX Li L, Macdougall JR, Miller CE, Millet I, Patturajan M, Pena CEA;  
 XX Rieger DK, Sciore P, Shenoy SG, Smithson G, Spytek KA, Stone DJ;  
 XX Voss Ez, Zhong M;  
 XX  
 XX WPI; 2003-722330/68.  
 XX  
 XX New NOVX polypeptides and nucleic acids, useful for diagnosing or  
 XX treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma,  
 XX obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or  
 XX multiple sclerosis.  
 XX  
 XX Example C; SEQ ID NO 49; 229pp; English.  
 XX  
 XX The present invention describes novel human proteins, designated NOVX  
 XX proteins. The NOVX sequences have cardiant, antiarteriosclerotic,  
 XX hypotensive, vasotropic, dermatological, anorectic, immunosuppressive,  
 XX cytostatic, antiinfertility, haemostatic, anti-HIV, antiasthmatic,  
 XX antiinflammatory, neuroprotective, anabolic, nootropic and  
 XX antiparkinsonian activities, and can be used in gene therapy. The NOVX  
 XX sequences can be used as a therapeutic in the manufacture of a medicament  
 XX for treating a syndrome associated with a human disease, such as a  
 XX pathology associated with NOVX. The NOVX proteins and nucleic acids  
 XX encoding them are useful for diagnosing or treating pathologies, diseases  
 XX or conditions associated with NOVX sequences, including cardiomyopathy,  
 XX atherosclerosis, hypertension, congenital heart defects, pulmonary

CC stenosis, scleroderma, obesity, metabolic disturbances associated with  
 CC obesity, transplantation, adrenoleukodystrophy, congenital adrenal  
 CC hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm,  
 CC adenocarcinoma, fertility, haemophilia, graft versus host disease, AIDS,  
 CC bronchial asthma, Crohn's disease, multiple sclerosis, infectious  
 CC disease, anorexia, neurodegenerative disorders (e.g. Alzheimer's disease,  
 CC or Parkinson's disease), immune disorders, haematopoietic disorders,  
 CC dyslipidaemias, and wasting disorders associated with chronic diseases.  
 CC The proteins can also be used as immunogens to produce antibodies and as  
 CC vaccines. The sequences may further be used in chromosome mapping,  
 CC identifying individual from minute biological samples (tissue typing),  
 CC and in forensic identification of a biological sample. The present  
 CC sequence represents a PCR primer for a human NOVX sequence, which is used  
 CC in an example from the present invention.  
 XX  
 XX Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;  
 SQ

Query Match 8.8%; Score 12.2; DB 1; Length 18;  
 Best Local Similarity 82.4%; Pred. No. 3.5e+02;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1682 GTGTCCTCCAGCGTG 1698  
 Db 2 GTGGCTCTGCGAGCTTG 18

RESULT 286  
 ADC98350  
 ID ADC98350 standard; DNA; 18 BP.  
 XX  
 XX AC ADC98350;  
 XX  
 XX 01-JAN-2004 (first entry)  
 XX  
 XX ACLP06 polymorphism marker PCR primer B primer seq.  
 XX  
 XX low bone mineral density; BMD; bone damage; polymorphism; osteoporosis;  
 KW single nucleotide polymorphism; SNP; PCR primer; ss; human.  
 KW  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO2003054218-A2.  
 XX  
 XX 03-JUL-2003.  
 XX  
 XX 19-DEC-2002; 2002WO-US040948.  
 XX  
 XX 20-DEC-2001; 2001US-0342711P.  
 XX  
 XX 04-NOV-2002; 2002US-0423559P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX  
 XX Jones KA, Valdes A, Townley DJ, Mangion J, Galwey N, Bennett S;  
 XX McKay I, Schafer A;  
 XX  
 XX WPI; 2003-559156/52.  
 XX  
 XX Determining whether an individual is predisposed to susceptibility to low  
 XX bone mineral density (BMD) and/or bone damage, involves identifying  
 XX polymorphisms in associated genes.  
 XX  
 XX Example 8; Page 237; 246pp; English.  
 XX  
 XX The present invention describes a method of determining whether an  
 XX individual is predisposed to susceptibility to low bone mineral density  
 XX (BMD) and/or bone damage comprising identifying whether the individual  
 XX has at least one polymorphism in a polynucleotide encoding a protein,  
 XX where the polynucleotide is one of 81 200-500 nucleotide sequences (S1,  
 XX see ADC98235 to ADC98315). An agent identified in an method from the  
 XX present invention which can be used for the prevention or treatment of a  
 XX disease resulting in susceptibility to low BMD and/or bone damage is  
 XX useful in the manufacture of a medicament for use in modulating the



OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 293464; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 PS Sequence 12 BP; 3 A; 5 C; 1 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 8.6%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1711 TTAGGAGTACGG 1722  
 Db 12 TTAGGAGTACGG 1  
 RESULT 290  
 ABH80452  
 ID ABH80452 standard; DNA; 12 BP.  
 XX  
 AC ABH80452;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide primer SEQ ID NO 280445 for detecting SNP TSC0008642.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 293464; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 PS Sequence 12 BP; 3 A; 5 C; 1 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 8.6%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1711 TTAGGAGTACGG 1722  
 Db 12 TTAGGAGTACGG 1  
 RESULT 290  
 ABH80452  
 ID ABH80452 standard; DNA; 12 BP.  
 XX  
 AC ABH80452;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide primer SEQ ID NO 280445 for detecting SNP TSC0008642.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 312150; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 280445; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 PS Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 8.6%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1703 AAGTTGGGTTAG 1714  
 Db 1 AAGTTGGGTTAG 12  
 RESULT 291  
 ABI12177/c  
 ID ABI12177 standard; DNA; 12 BP.  
 XX  
 AC ABI12177;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide primer SEQ ID NO 312150 for detecting SNP TSC0024874.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 312150; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 CC SQ Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 8.6%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1747 TCCCTATCCTAA 1758

Db 12 TCCCTATCCTAA 1

RESULT 292  
 ABC63273/c  
 ID ABC63273 standard; DNA; 13 BP.

XX AC ABC63273;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 63290 for detecting SNP TSC0016721.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PS WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.

XX PS Claim 1; SEQ ID NO 63290; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 1 Other;

Query Match 8.6%; Score 12; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1697 TGGTGGAGTTG 1708  
 Db 13 TGGTGGAGTTG 2

RESULT 293  
 ABF24345/c  
 ID ABF24345 standard; DNA; 13 BP.

XX AC ABF24345;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 124342 for detecting SNP TSC0031088.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PS WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.

XX PS Claim 1; SEQ ID NO 124342; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 8.6%; Score 12; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1723 AGATGGAGATTG 1734

Db 13 AGATGGAGATTG 2

RESULT 294  
 ABH00388  
 ID ABH00388 standard; DNA; 13 BP.

XX AC ABH00388;

XX XX



DT 22-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 200365 for detecting SNP TSC0049306.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 DE peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 KW Homo sapiens.  
 OS  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 200365; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 13 BP; 4 A; 0 C; 7 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.6%; Score 12; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1721 GGAGATGGAGAT 1732  
 Db 1 GGAGATGGAGAT 12  
 RESULT 295  
 ABH00389/c  
 ID ABH00389 standard; DNA; 13 BP.  
 AC ABH00389;  
 XX  
 XX 22-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 200366 for detecting SNP TSC0049306.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 200366; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 13 BP; 4 A; 0 C; 7 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.6%; Score 12; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1721 GGAGATGGAGAT 1732  
 Db 1 GGAGATGGAGAT 12  
 RESULT 295  
 ABH00389/c  
 ID ABH00389 standard; DNA; 13 BP.  
 AC ABH00389;  
 XX  
 XX 22-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 200365 for detecting SNP TSC0049306.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 200366; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 13 BP; 2 A; 7 C; 0 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.6%; Score 12; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1721 GGAGATGGAGAT 1732  
 Db 13 GGAGATGGAGAT 2  
 RESULT 296  
 ABH47625/c  
 ID ABH47625 standard; DNA; 13 BP.  
 XX  
 XX ABH47625;  
 XX  
 XX 22-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 247602 for detecting SNP TSC0060506.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

PT methylation status.

XX Claim 1; SEQ ID NO 247602; 29pp + Sequence Listing; German.

PS

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABF99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 8.6%; Score 12; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1705 GTTGGGTAGGA 1716  
12 GTTGGGTAGGA 1

Db

RESULT 297  
ABF95704  
ID ABF95704 standard; DNA; 13 BP.  
XX AC ABF95704;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 195701 for detecting SNP TSC0009428.  
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.  
XX PS Claim 1; SEQ ID NO 195701; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 8.6%; Score 12; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1705 GTTGGGTAGGA 1716  
12 GTTGGGTAGGA 1

Db

RESULT 297  
ABF95704  
ID ABF95704 standard; DNA; 13 BP.  
XX AC ABF95704;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 195701 for detecting SNP TSC0009428.  
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.  
XX PS Claim 1; SEQ ID NO 195701; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 5 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 8.6%; Score 12; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1705 GTTGGGTAGGA 1716  
12 GTTGGGTAGGA 1

Db

RESULT 298  
ABC84321/C  
ID ABC84321 standard; DNA; 13 BP.  
XX AC ABC84321;  
XX DT 21-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 84338 for detecting SNP TSC0021205.  
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.  
XX PS Claim 1; SEQ ID NO 84338; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 1 Other;

Query Match 8.6%; Score 12; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1722 GAGATGGAGATT 1733  
13 GAGATGGAGATT 2

Db

```

RESULT 299
ABC05018
ID ABC05018 standard; DNA; 13 BP.
AC ABC05018;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 5009 for detecting SNP TSC0001740.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 5009; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 8.6%; Score 12; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1721 GGAGATGGAGAT 1732
DB 2 GGAGATGGAGAT 13
RESULT 300
ABC05019/c
ID ABC05019 standard; DNA; 13 BP.
XX
AC ABC05019;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 5010 for detecting SNP TSC0001740.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

```

```

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 5010; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 13 BP; 2 A; 6 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 8.6%; Score 12; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1721 GGAGATGGAGAT 1732
DB 12 GGAGATGGAGAT 1
RESULT 301
ABC63272
ID ABC63272 standard; DNA; 13 BP.
XX
AC ABC63272;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 63289 for detecting SNP TSC0016721.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX

```

```
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 63389; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 1 Other;
XX
Query Match 8.6%; Score 12; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1697 TGGTGGAGATTG 1708
Db 1 TGGTGGAGATTG 12
XXXXXXXXXXXXXXXXXXXX
RESULT 302
ABF24344
ID ABF24344 standard; DNA; 13 BP.
XX
AC ABF24344;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 124341 for detecting SNP TSC0031088.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 124341; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 1 Other;
XX
Query Match 8.6%; Score 12; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1697 TGGTGGAGATTG 1708
Db 1 TGGTGGAGATTG 12
XXXXXXXXXXXXXXXXXXXX
RESULT 302
ABF24344
ID ABF24344 standard; DNA; 13 BP.
XX
AC ABF24344;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 124341 for detecting SNP TSC0021205.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 84337; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 8.6%; Score 12; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1723 AGATGGAGATTG 1734
Db 1 AGATGGAGATTG 12
XXXXXXXXXXXXXXXXXXXX
RESULT 303
ABC84320
ID ABC84320 standard; DNA; 13 BP.
XX
AC ABC84320;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 84337 for detecting SNP TSC0021205.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 84337; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 1 Other;
```

```

Query Match      8.6%; Score 12; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1722 GAGATGGAGATT 1733
   |||||
Db 1 GAGATGGAGATT 12

RESULT 304
ABH47624
ID ABH47624 standard; DNA; 13 BP.
XX AC
XX ABH47624;
XX DT
XX 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide SEQ ID NO 247601 for detecting SNP TSC0060506.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX Homo sapiens.
XX PN
XX WO200177384-A2.
XX PD
XX 18-OCT-2001.
XX PF
XX 06-APR-2000; 2000DE-01019173.
XX PR
XX Oligonucleotide SEQ ID NO 247601 for detecting SNP TSC0060506.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX Homo sapiens.
XX PN
XX WO200177384-A2.
XX PD
XX 18-OCT-2001.
XX PF
XX 06-APR-2000; 2000DE-01019173.
XX PR
XX 07-APR-2000; 2000DE-01019173.
XX PA
XX (EPIG-) EPIGENOMICS AG.
XX PI
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 247601; 29pp + Sequence Listing; German.
XX CC
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ
XX Sequence 13 BP; 2 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
XX
XX Query Match      8.6%; Score 12; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1705 GTTGGGTTAGGA 1716
XX |||||
XX Db 2 GTTGGGTTAGGA 13

RESULT 305
ABF95705/c
ID ABF95705 standard; DNA; 13 BP.
XX AC
XX ABF95705;
XX DT
XX 25-MAR-2002 (first entry)
XX DE
XX Human apolipoprotein E (APOE) gene polymorphism detecting ASO primer #12.
XX Human; antilipaeamic; neuroprotective; nootropic; genetic variant; APOE;
XX apolipoprotein E; haplotyping; familial dysbetalipoproteinemia; therapy;
XX genotyping; type III hyperlipoproteinemia; Alzheimer's disease;
XX atherosclerosis; polymorphism; allele specific oligonucleotide;
XX ASO primer; ss.
XX ASO
```

```

XX ABF95705;
XX AC
XX 22-FEB-2002 (first entry)
XX DT
XX Oligonucleotide SEQ ID NO 195702 for detecting SNP TSC0009428.
XX DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX Homo sapiens.
XX PN
XX WO200177384-A2.
XX PD
XX 18-OCT-2001.
XX PF
XX 06-APR-2001; 2001WO-IB000713.
XX PR
XX 07-APR-2000; 2000DE-01019173.
XX PA
XX (EPIG-) EPIGENOMICS AG.
XX PI
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 195702; 29pp + Sequence Listing; German.
XX CC
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ
XX Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match      8.6%; Score 12; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1702 GAAGTTGGGTTA 1713
XX |||||
XX Db 13 GAAGTTGGGTTA 2

RESULT 306
AAD26061/c
ID AAD26061 standard; DNA; 15 BP.
XX AC
XX AAD26061;
XX DT
XX 25-MAR-2002 (first entry)
XX DE
XX Human apolipoprotein E (APOE) gene polymorphism detecting ASO primer #12.
XX Human; antilipaeamic; neuroprotective; nootropic; genetic variant; APOE;
XX apolipoprotein E; haplotyping; familial dysbetalipoproteinemia; therapy;
XX genotyping; type III hyperlipoproteinemia; Alzheimer's disease;
XX atherosclerosis; polymorphism; allele specific oligonucleotide;
XX ASO primer; ss.
XX ASO
```

12-APR-2000; 2000US-0196411P.	12-APR-2000; 2000US-0196411P.	12-APR-2000; 2000US-0197188P.	12-APR-2000; 2000US-0197188P.
(GENA-) GENAISSANCE PHARM INC.	(GENA-) GENAISSANCE PHARM INC.	(GENA-) GENAISSANCE PHARM INC.	(GENA-) GENAISSANCE PHARM INC.
Chew A, Choi JY, Koshy B;	Chew A, Choi JY, Koshy B;	Choi JY, Kliem SE, Koshy B, Lee HH;	Choi JY, Kliem SE, Koshy B, Lee HH;
WPI; 2002-075058/10.	WPI; 2002-075058/10.	WPI; 2002-075064/10.	WPI; 2002-075064/10.
Novel polymorphic variants of colony stimulating factor 1 receptor useful in studying expression and function of the protein, useful for screening candidate drugs to treat diseases e.g. inflammatory disorders.	Novel polymorphic variants of colony stimulating factor 1 receptor useful in studying expression and function of the protein, useful for screening candidate drugs to treat diseases e.g. inflammatory disorders.	Genotyping human apolipoprotein gene of individual for determining haplotype of individual, involves determining identity of nucleotide pair at specific polymorphic sites for two copies of gene.	Genotyping human apolipoprotein gene of individual for determining haplotype of individual, involves determining identity of nucleotide pair at specific polymorphic sites for two copies of gene.
Claim 15; Page 16; 164pp; English.	Claim 15; Page 16; 164pp; English.	Claim 16; Page 14; 78pp; English.	Claim 16; Page 14; 78pp; English.
The invention describes a novel isolated polynucleotide (I) comprising a sequence which is a polymorphic variant (PV) of a reference sequence for colony stimulating factor 1 receptor (CSF1R) gene, found on the polypeptide are useful for improving the discovery and development of drugs for treating diseases associated with CSF1R activity, e.g., malignant histiocytosis, myeloid malignancies and inflammatory disorders and the haplotypes can be used to validate CSF1R as a candidate target for treating a specific condition or disease predicted to be associated with CSF1R activity. Genotyping the CSF1R gene of an individual can also be used in developing diagnostic tests and therapeutic treatments. (I) is useful in studying the expression and function of CSF1R, and in expressing CSF1R protein for use in screening for candidate drugs to treat diseases related to CSF1R activity and in studying the effect of the variation on the biological activity of CSF1R as well as on the binding affinity of candidate drugs targeting CSF1R. Antibodies are useful in a variety of diagnostic and prognostic formats and therapeutic methods. A transgenic animal is useful in studying expression of the CSF1R isogenes in vivo, for in vivo screening and testing of drugs targeted against CSF1R protein, and for testing the efficacy of therapeutic agents and compounds. Allele specific oligonucleotides (ASO) are useful as probes and primers, and for assaying a polymorphism in the target region. Without requiring any a priori knowledge of the phenotypic effect of any particular CSF1R or haplotype the invention provides a method for identifying lead compounds that are more likely to show efficacy in clinical trials. This sequence is an allele specific oligonucleotide primer used for detecting CSF1R gene polymorphisms, described in the method of the invention	The patent discloses novel genetic variants of human apolipoprotein E (APOE) gene. The invention also relates to compositions and methods for haplotyping and/or genotyping the APOE gene. The haplotyping methods of the invention are useful for improving the efficacy and reliability of several steps in the discovery and development of drugs for treating diseases associated with APOE activity, e.g. familial dysbetalipoproteinemia, type III hyperlipoproteinemia, atherosclerosis, and Alzheimer's disease. They are useful to validate APOE as a candidate agent for treating a specific condition or disease predicted to be associated with APOE activity and in the design of clinical trials of candidate drugs for treating a specific condition or disease predicted to be associated with APOE activity. Genotyping or haplotyping methods are useful to screen for compounds targeting APOE to treat a specific condition or disease associated with APOE activity. The present DNA sequence is an allele specific oligonucleotide (ASO) primer which is used for detecting human APOE gene polymorphisms		
Sequence 15 BP; 2 A; 3 C; 6 G; 3 T; 0 U; 1 Other;	Sequence 15 BP; 2 A; 3 C; 6 G; 3 T; 0 U; 1 Other;	Sequence 15 BP; 1 A; 5 C; 3 G; 5 T; 0 U; 1 Other;	Sequence 15 BP; 1 A; 5 C; 3 G; 5 T; 0 U; 1 Other;
Query Match 8.6%; Score 12; DB 1; Length 15;	Query Match 8.6%; Score 12; DB 1; Length 15;	Query Match 8.6%; Score 12; DB 1; Length 15;	Query Match 8.6%; Score 12; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 3e+02;	Best Local Similarity 85.7%; Pred. No. 3e+02;	Best Local Similarity 85.7%; Pred. No. 3e+02;	Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
1726 TGGAGATTGGCTCC 1739	1726 TGGAGATTGGCTCC 1739	1649 AAGGCAAGCAGCAG 1662	1649 AAGGCAAGCAGCAG 1662
2 TGGAGAGTGGCTYC 15	2 TGGAGAGTGGCTYC 15	14 RAGGCAAGCAGCAG 1	14 RAGGCAAGCAGCAG 1
RESULT 308	RESULT 308	RESULT 307	RESULT 307
ABL52231	ABL52231	AAS98750	AAS98750
ID ABL52231 standard; DNA; 15 BP.	ID ABL52231 standard; DNA; 15 BP.	ID AAS98750 standard; DNA; 15 BP.	ID AAS98750 standard; DNA; 15 BP.
XX ABL52231;	XX ABL52231;	XX AAS98750;	XX AAS98750;
XX 15-JUL-2002 (first entry)	XX 15-JUL-2002 (first entry)	XX 26-MAR-2002 (first entry)	XX 26-MAR-2002 (first entry)
XX Human PHKG2 allele specific oligonucleotide primer SEQ ID NO:18.	XX Human PHKG2 allele specific oligonucleotide primer SEQ ID NO:18.	XX Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #116.	XX Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #116.
XX Human, phosphorylase kinase gamma 2 (testis); PHKG2; enzyme; SNP;	XX Human, phosphorylase kinase gamma 2 (testis); PHKG2; enzyme; SNP;	XX Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;	XX Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
XX phosphorylase kinase gamma 2; single nucleotide polymorphism;	XX phosphorylase kinase gamma 2; single nucleotide polymorphism;	XX cytostatic; gene therapy; malignant histiocytosis; isogene;	XX cytostatic; gene therapy; malignant histiocytosis; isogene;
XX polymorphic; hepatotropic; gene therapy; glycogen storage disease;	XX polymorphic; hepatotropic; gene therapy; glycogen storage disease;	XX myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;	XX myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;
XX liver cirrhosis; allele specific oligonucleotide; ASO; primer; ss.	XX liver cirrhosis; allele specific oligonucleotide; ASO; primer; ss.	XX genotype; human; allele specific oligonucleotide; ASO; primer; ss.	XX genotype; human; allele specific oligonucleotide; ASO; primer; ss.
XX Homo sapiens.	XX Homo sapiens.	XX Homo sapiens.	XX Homo sapiens.
XX W0200179225-A2.	XX W0200179225-A2.	XX W0200179225-A2.	XX W0200179225-A2.
XX 25-OCT-2001.	XX 25-OCT-2001.	XX 25-OCT-2001.	XX 25-OCT-2001.
XX 12-APR-2001; 2001WO-US012044.	XX 12-APR-2001; 2001WO-US012044.	XX 12-APR-2001; 2001WO-US012044.	XX 12-APR-2001; 2001WO-US012044.

FT XX /note= "polymorphic site indicated by an ambiguity base"  
 PN WO200194365-A2.  
 XX  
 PD 13-DEC-2001.  
 XX  
 PF 11-JUN-2001; 2001WO-US018814.  
 XX  
 PR 09-JUN-2000; 2000US-0210568P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Choi JY, Koshy B, Sanchis A, Sausker EA;  
 XX WPI; 2002-404359/43.  
 DR  
 XX New variants of phosphorylase kinase gamma 2 isogenes, useful for  
 PT improving efficiency and reliability in the development of drugs for  
 PT treating diseases e.g. liver cirrhosis.  
 XX  
 PS Claim 16; Page 13; 76pp; English.  
 XX  
 CC The present invention describes an isolated polynucleotide (I) comprising  
 CC a nucleotide sequence which is a polymorphic variant of a reference  
 CC sequence for human phosphorylase kinase gamma2 (testis) (PHKG2) gene or  
 CC its fragment, or a polymorphic variant of a reference sequence for a  
 CC PHKG2 cDNA or its fragment. Also described is an isolated polypeptide  
 CC (II) comprising an amino acid sequence which is a polymorphic variant of  
 CC a reference sequence for PHKG2 protein or its fragment, where the  
 CC reference sequence comprises a sequence (see ABB09290) of 406 amino  
 CC acids, and the polymorphic variant comprises one or more variant amino  
 CC acids selected from glutamic acid at a position corresponding to amino  
 CC acid position 153 and tryptophan at position corresponding to amino acid  
 CC position 329. (I) has hepatotropic activity and can be used in gene  
 CC therapy. (II) is useful in screening for drugs targeting (II), by  
 CC contacting a PHKG2 polymorphic variant with a candidate agent and  
 CC assaying for binding activity. The identified candidate agents targeting  
 CC PHKG2, are useful for treating liver cirrhosis and glycogen storage  
 CC diseases. The present sequence represents an allele specific  
 CC oligonucleotide (ASO) primer for the PHKG2 gene, which is used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 15 BP; 1 A; 10 C; 0 G; 3 T; 0 U; 1 Other;  
 Query Match 8.6%; Score 12; DB 1; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 3e+02;  
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1736 CTCCTCACTCTCTCC 1749  
 Db ||||| |||||  
 2 CTCCTCACTCTCTSC 15  
 RESULT 309  
 AAL44022  
 ID AAL44022 standard; DNA; 16 BP.  
 XX  
 AC AAL44022;  
 XX  
 DT 27-SEP-2002 (first entry)  
 XX  
 DE Human cytochrome P450A6 (CYP450A6 or CYP2A6) gene sequencing primer 3.  
 XX  
 KW Human; PCR; sequencing; primer; ss; single nucleotide polymorphism; SNP;  
 KW cytochrome; P450A6; CYP450A6; CYP2A6; chromosome 19;  
 KW steroid metabolism; drug detoxification; xenobiotic detoxification;  
 KW procarcinogen activation; inflammation; asthma; habitual smoking.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200194633-A1.  
 XX  
 PD 13-DEC-2001.

XX 01-JUN-2001; 2001WO-US017781.  
 XX  
 XX 02-JUN-2000; 2000US-00586376.  
 XX  
 PA (DNAS-) DNA SCI INC.  
 XX  
 PI Guida M, Hall J;  
 XX WPI; 2002-566448/60.  
 DR  
 XX New isolated polynucleotide, useful to screen individuals for asthma,  
 PT inflammation and susceptibility to habitual smoking, comprises base  
 PT variation from that of known human cytochrome P450A6 sequence.  
 XX  
 PS Example 1; Page 26; 48pp; English.  
 XX  
 CC The invention comprises the identification of genetic polymorphisms in  
 CC the human cytochrome P450A6 (CYP450A6 or CYP2A6) gene. The human  
 CC cytochrome P450A6 gene is located on chromosome 19 and encodes an enzyme  
 CC that plays a role in the metabolism of steroids, the detoxification of  
 CC drugs and xenobiotics, and the activation of procarcinogens. The P450A6  
 CC polymorphisms identified in the invention are useful for evaluating an  
 CC individual's risk of developing asthma or an individual's propensity for  
 CC cigarette consumption. The P450A6 DNA sequences of the invention are  
 CC useful for identifying individuals having a polymorphic genotype and to  
 CC screen individuals for altered metabolism for cytochrome P450A6  
 CC substrates. The P450A6 DNA sequences of the invention are also useful  
 CC for identifying individuals who are at risk from inflammation or  
 CC habitual smoking and diseases that result from environmental or  
 CC occupational exposures to dangerous substances. The present DNA sequence  
 CC represents a human cytochrome P450A6 sequencing primer  
 XX  
 SQ Sequence 16 BP; 1 A; 1 C; 8 G; 6 T; 0 U; 0 Other;  
 Query Match 8.6%; Score 12; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1634 TGGGGCTTGAG 1645  
 Db ||||| |||||  
 1 TGGGGCTTGAG 12  
 RESULT 310  
 AAF02799/c  
 ID AAF02799 standard; DNA; 17 BP.  
 XX  
 AC AAF02799;  
 XX  
 DT 16-FEB-2001 (first entry)  
 XX  
 DE Hammerhead ribozyme substrate #1094.  
 XX  
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;  
 KW interferon alpha; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200061729-A2.  
 XX  
 PD 19-OCT-2000.  
 XX  
 PF 11-APR-2000; 2000WO-US009721.  
 XX  
 PR 12-APR-1999; 99US-0129390P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;  
 XX WPI; 2000-647423/62.

Enzymatic and antisense nucleic acid inhibition of repressor genes,  
useful for producing e.g. granulocyte colony stimulating factor protein,  
interferon alpha and erythropoietin.  
Claim 37; Page 80; 164pp; English.  
The present invention relates to enzymatic and antisense nucleic acid  
molecules that act as inhibitors of the expression of repressor genes  
encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription  
factor gene, IRF-2 and/or the CCAAT Displacement Protein (CDP).  
Inhibition of the repressors removes prevents inhibition (and  
consequently increases expression of) genes involved in the production of  
erythropoietin, granulocyte colony stimulating factor protein and  
interferon alpha  
Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 8.6%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1651 GGCAGCACCAG 1662  
DB 12 GGCAGCACCAG 1

RESULT 311  
ABV90232  
ID ABV90232 standard; DNA; 17 BP.  
AC ABV90232;  
DT 23-DEC-2002 (first entry)  
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 945.  
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
XW gene therapy; transgenic; ss.  
XX Homo sapiens.  
OS EF1239051-A2.  
XX 11-SEP-2002.  
XX 28-JAN-2002; 2002EP-00001165.  
XX 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-00864761.  
PR 10-OCT-2001; 2001US-0328205P.  
(AEOM-) AEOMICA INC.  
Shannon M;  
WPI; 2002-684061/74.  
Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
-1, useful for treating disorders associated with decreased expression or  
activity of human POSHL1.  
Example 2; SEQ ID NO 945; 60pp + Sequence Listing; English.  
The invention relates to an isolated SH3 domain (POSH)-like signalling  
protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino

acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),  
(S1) having 95% deviations, especially conservative substitutions or a  
fragment of the sequences comprising at least 8 contiguous amino acids.  
Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
adaptor protein that interacts with Rho family small GTPases as well as  
downstream components of the signal transduction pathway. (I) is useful  
for identifying a specific binding partner. (I) and nucleic acids (II)  
encoding (I) are useful for diagnosing, monitoring disease and treating  
caused by altered expression of human POSHL1 including diagnosing and  
treating cancer, they are useful in the development of vaccines and (II) is  
useful in gene therapy. (II) is useful for constructing microarrays which  
are useful for measuring and for surveying gene expression and creating  
transgenic non-human animals capable of producing the proteins. The  
present sequence is that of a scanning oligonucleotide useful in examples  
of the invention. Note: The present sequence did not form part of the  
printed specification, but is based on sequence information supplied to  
Derwent by the European Patent Office

Sequence 17 BP; 6 A; 3 C; 7 G; 1 T; 0 U; 0 Other;  
Query Match 8.6%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1645 GCAGAAGGCAAG 1656  
DB 6 GCAGAAGGCAAG 17

RESULT 312  
ABV90236  
ID ABV90236 standard; DNA; 17 BP.  
XX AC ABV90236;  
XX 23-DEC-2002 (first entry)  
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 949.  
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
XW gene therapy; transgenic; ss.  
XX Homo sapiens.  
OS EF1239051-A2.  
XX 11-SEP-2002.  
XX 28-JAN-2002; 2002EP-00001165.  
XX 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-00864761.  
PR 10-OCT-2001; 2001US-0328205P.  
(AEOM-) AEOMICA INC.  
Shannon M;  
WPI; 2002-684061/74.  
Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
-1, useful for treating disorders associated with decreased expression or  
activity of human POSHL1.  
Example 2; SEQ ID NO 949; 60pp + Sequence Listing; English.



XX The invention relates to an isolated SH3 domain (POSH)-like signalling  
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
 CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),  
 CC (S1) having 95% deviations, especially conservative substitutions or a  
 CC fragment of the sequences comprising at least 8 contiguous amino acids.  
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
 CC adaptor protein that interacts with Rho family small GTPases as well as  
 CC downstream components of the signal transduction pathway. (I) is useful  
 CC for identifying a specific binding partner. (I) and nucleic acids (II)  
 CC encoding (I) are useful for diagnosing, monitoring disease and treating  
 CC caused by altered expression of human POSHL1 including diagnosing and  
 CC treating cancer, they are useful in the development of vaccines and (II) is  
 CC useful in gene therapy. (II) is useful for constructing microarrays which  
 CC are useful for measuring and for surveying gene expression and creating  
 CC transgenic non-human animals capable of producing the proteins. The  
 CC present sequence is that of a scanning oligonucleotide useful in examples  
 CC of the invention. Note: The present sequence did not form part of the  
 CC printed specification, but is based on sequence information supplied to  
 CC Derwent by the European Patent Office  
 XX  
 XX Sequence 17 BP; 6 A; 2 C; 7 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.6%; Score 12; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1645 GCAGAAGGCAAG 1656  
 Db 2 GCAGAAGGCAAG 13  
 |||||  
 |||||  
 RESULT 313  
 ABV90234  
 ID ABV90234 standard; DNA; 17 BP.  
 XX  
 AC ABV90234;  
 XX  
 DT 23-DEC-2002 (first entry)  
 XX  
 DE Human POSHL1 scanning oligonucleotide SEQ ID NO 947.  
 XX  
 KW Human: POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
 KW gene therapy; transgenic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1239051-A2.  
 XX  
 PD 11-SEP-2002.  
 XX  
 PF 28-JAN-2002; 2002EP-00001165.  
 XX  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 10-OCT-2001; 2001US-0328205P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Shannon M;  
 XX  
 XX WPI; 2002-684061/74.  
 DR  
 Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL  
 PT -1, useful for treating disorders associated with decreased expression or

PT activity of human POSHL1.  
 XX  
 PS Example 2; SEQ ID NO 947; 60pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated SH3 domain (POSH)-like signalling  
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
 CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),  
 CC (S1) having 95% deviations, especially conservative substitutions or a  
 CC fragment of the sequences comprising at least 8 contiguous amino acids.  
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
 CC adaptor protein that interacts with Rho family small GTPases as well as  
 CC downstream components of the signal transduction pathway. (I) is useful  
 CC for identifying a specific binding partner. (I) and nucleic acids (II)  
 CC encoding (I) are useful for diagnosing, monitoring disease and treating  
 CC caused by altered expression of human POSHL1 including diagnosing and  
 CC treating cancer, they are useful in the development of vaccines and (II) is  
 CC useful in gene therapy. (II) is useful for constructing microarrays which  
 CC are useful for measuring and for surveying gene expression and creating  
 CC transgenic non-human animals capable of producing the proteins. The  
 CC present sequence is that of a scanning oligonucleotide useful in examples  
 CC of the invention. Note: The present sequence did not form part of the  
 CC printed specification, but is based on sequence information supplied to  
 CC Derwent by the European Patent Office  
 XX  
 XX Sequence 17 BP; 5 A; 2 C; 7 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.6%; Score 12; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1645 GCAGAAGGCAAG 1656  
 Db 4 GCAGAAGGCAAG 15  
 |||||  
 |||||  
 RESULT 314  
 ABV90235  
 ID ABV90235 standard; DNA; 17 BP.  
 XX  
 AC ABV90235;  
 XX  
 DT 23-DEC-2002 (first entry)  
 XX  
 DE Human POSHL1 scanning oligonucleotide SEQ ID NO 948.  
 XX  
 KW Human: POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
 KW gene therapy; transgenic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1239051-A2.  
 XX  
 PD 11-SEP-2002.  
 XX  
 PF 28-JAN-2002; 2002EP-00001165.  
 XX  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 10-OCT-2001; 2001US-0328205P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Shannon M;  
 XX  
 XX WPI; 2002-684061/74.  
 DR

Mon Aug 30 09:26:45 2004

```

XX  Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT  -1, useful for treating disorders associated with decreased expression or
PT  activity of human POSHL1.
XX
XX  Example 2; SEQ ID NO 948; 60pp + Sequence Listing; English.
XX
XX  The invention relates to an isolated SH3 domain (POSH)-like signalling
CC  protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC  acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),
CC  (SI) having 95% deviations, especially conservative substitutions or a
CC  fragment of the sequences comprising at least 8 contiguous amino acids.
CC  Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC  adaptor protein that interacts with Rho family small GTPases as well as
CC  downstream components of the signal transduction pathway. (I) is useful
CC  for identifying a specific binding partner. (I) and nucleic acids (II)
CC  encoding (I) are useful for diagnosing, monitoring disease and treating
CC  caused by altered expression of human POSHL1 including diagnosing and
CC  useful in gene therapy. (II) is useful for constructing microarrays which
CC  are useful for measuring and for surveying gene expression and creating
CC  transgenic non-human animals capable of producing the proteins. The
CC  present sequence is that of a scanning oligonucleotide useful in examples
CC  of the invention. Note: The present sequence did not form part of the
CC  printed specification, but is based on sequence information supplied to
CC  Derwent by the European Patent Office
XX
XX  Sequence 17 BP; 5 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
SQ  Query Match 8.6%; Score 12; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 3.6e+02;
    Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1645 GCAGAGGCGCAAG 1656
DB  3 GCAGAGGCGCAAG 14

RESULT 315
ABV90233
ID  ABV90233 standard; DNA; 17 BP.
AC  ABV90233;
DT  23-DEC-2002 (first entry)
XX  Human POSHL1 scanning oligonucleotide SEQ ID NO 946.
DE
XX  Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW  Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW  gene therapy; transgenic; ss.
XX  Homo sapiens.
XX  OS
XX  EP1239051-A2.
XX  11-SEP-2002.
XX  28-JAN-2002; 2002EP-00001165.
XX  30-JAN-2001; 2001WO-US000663.
XX  30-JAN-2001; 2001WO-US000664.
XX  30-JAN-2001; 2001WO-US000665.
XX  30-JAN-2001; 2001WO-US000666.
XX  30-JAN-2001; 2001WO-US000667.
XX  30-JAN-2001; 2001WO-US000668.
XX  30-JAN-2001; 2001WO-US000669.
XX  30-JAN-2001; 2001WO-US000670.
XX  23-MAY-2001; 2001US-00864761.
XX  10-OCT-2001; 2001US-0328205P.
XX  (AEOM-) ABONICA INC.
XX

PI  Shannon M;
XX  WPI; 2002-684061/74.
XX  Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT  -1, useful for treating disorders associated with decreased expression or
PT  activity of human POSHL1.
XX
XX  Example 2; SEQ ID NO 946; 60pp + Sequence Listing; English.
XX
XX  The invention relates to an isolated SH3 domain (POSH)-like signalling
CC  protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC  acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),
CC  (SI) having 95% deviations, especially conservative substitutions or a
CC  fragment of the sequences comprising at least 8 contiguous amino acids.
CC  Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC  adaptor protein that interacts with Rho family small GTPases as well as
CC  downstream components of the signal transduction pathway. (I) is useful
CC  for identifying a specific binding partner. (I) and nucleic acids (II)
CC  encoding (I) are useful for diagnosing, monitoring disease and treating
CC  caused by altered expression of human POSHL1 including diagnosing and
CC  useful in gene therapy. (II) is useful for constructing microarrays which
CC  are useful for measuring and for surveying gene expression and creating
CC  transgenic non-human animals capable of producing the proteins. The
CC  present sequence is that of a scanning oligonucleotide useful in examples
CC  of the invention. Note: The present sequence did not form part of the
CC  printed specification, but is based on sequence information supplied to
CC  Derwent by the European Patent Office
XX
XX  Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;
SQ  Query Match 8.6%; Score 12; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 3.6e+02;
    Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1645 GCAGAGGCGCAAG 1656
DB  5 GCAGAGGCGCAAG 16

RESULT 316
ABV90237
ID  ABV90237 standard; DNA; 17 BP.
AC  ABV90237;
DT  23-DEC-2002 (first entry)
XX  Human POSHL1 scanning oligonucleotide SEQ ID NO 950.
DE
XX  Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW  Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW  gene therapy; transgenic; ss.
XX  Homo sapiens.
XX  OS
XX  EP1239051-A2.
XX  11-SEP-2002.
XX  28-JAN-2002; 2002EP-00001165.
XX  30-JAN-2001; 2001WO-US000663.
XX  30-JAN-2001; 2001WO-US000664.
XX  30-JAN-2001; 2001WO-US000665.
XX  30-JAN-2001; 2001WO-US000666.
XX  30-JAN-2001; 2001WO-US000667.
XX  30-JAN-2001; 2001WO-US000668.
XX  30-JAN-2001; 2001WO-US000669.
XX  30-JAN-2001; 2001WO-US000670.
XX  23-MAY-2001; 2001US-00864761.
XX  10-OCT-2001; 2001US-0328205P.
XX  (AEOM-) ABONICA INC.
XX

```

XX (AEOM-) AEOMICA INC.  
 XX Shannon M;  
 XX WPI; 2002-684061/74.  
 XX  
 XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL  
 PT -1, useful for treating disorders associated with decreased expression or  
 PT activity of human POSHL.  
 XX  
 XX Example 2; SEQ ID NO 950; 60pp + Sequence Listing; English.  
 XX  
 XX The invention relates to an isolated SH3 domain (POSH)-like signalling  
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
 CC acids (S1, ABP83999), a sequence having 65% sequence identity to (S1),  
 CC (S1) having 95% deviations, especially conservative substitutions or a  
 CC fragment of the sequences comprising at least 8 contiguous amino acids.  
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
 CC adaptor protein that interacts with Rho family small GTPases as well as  
 CC downstream components of the signal transduction pathway. (I) is useful  
 CC for identifying a specific binding partner. (I) and nucleic acids (II)  
 CC encoding (I) are useful for diagnosing, monitoring disease and treating  
 CC caused by altered expression of human POSHL1 including diagnosing and  
 CC treating cancer, they are useful in the development of vaccines and (II) is  
 CC useful in gene therapy. (II) is useful for constructing microarrays which  
 CC are useful for measuring and for surveying gene expression and creating  
 CC transgenic non-human animals capable of producing the proteins. The  
 CC present sequence is that of a scanning oligonucleotide useful in examples  
 CC of the invention. Note: The present sequence did not form part of the  
 CC printed specification, but is based on sequence information supplied to  
 CC Derwent by the European Patent Office  
 XX  
 XX Sequence 17 BP; 6 A; 2 C; 7 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.6%; Score 12; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1645 GCAGAGGCGAAG 1656  
 Db 1 GCAGAGGCGAAG 12  
 RESULT 317  
 ACC64298  
 ID ACC64298 standard; DNA; 17 BP.  
 XX ACC64298;  
 XX 01-JUL-2003 (first entry)  
 XX Murine oligonucleotide associated with tumour suppression, SEQ ID 1545.  
 DE Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; murine;  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrenia; ss.  
 XX Mus musculus.  
 XX WO2003025176-A2.  
 XX 27-MAR-2003.  
 XX 17-SEP-2002; 2002WO-IB004210.  
 XX 17-SEP-2001; 2001FR-00011979.  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 XX Telerman A, Amson R, Tuijnder M;  
 XX

DR WPI; 2003-333167/31.  
 XX  
 XX New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 XX Disclosure; Page 211; 738pp; French.  
 XX  
 XX The present invention relates to murine oligonucleotides (ACC62754-  
 CC ACC68806), which are associated with tumour suppression, tumour  
 CC reversion, apoptosis and virus resistance. The oligonucleotides are  
 CC useful as (1) as probes and primers for detecting, identifying,  
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a  
 CC recombinant polypeptides. The oligonucleotides are useful for preparation  
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia  
 XX  
 XX Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.6%; Score 12; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1659 CCAGGCTCACAG 1670  
 Db 4 CCAGGCTCACAG 15  
 RESULT 318  
 AAX28111  
 ID AAX28111 standard; DNA; 18 BP.  
 XX AAX28111;  
 XX 11-JUN-1999 (first entry)  
 DT PCR primer for M. kansasii KATS2 sequence.  
 XX  
 XX KATS2 sequence; Mycobacterium kansasii detection; probe; primer;  
 KW microorganism detection; ds.  
 XX Synthetic.  
 OS Mycobacterium kansasii.  
 XX EP905259-A1.  
 XX 31-MAR-1999.  
 XX 23-SEP-1998; 98EP-00118036.  
 XX 25-SEP-1997; 97US-00937580.  
 XX (BECT ) BECTON DICKINSON & CO.  
 XX Harris JM, You Q;  
 XX WPI; 1999-192672/17.  
 XX  
 XX New Mycobacterium kansasii specific DNA fragment (KATS2) useful for  
 PT designing oligonucleotides which are useful for detecting M. kansasii  
 PT nucleic acid in clinical samples.  
 XX  
 XX Claim 2; Page 11; 36pp; English.  
 XX  
 XX This sequence is a primer for a Mycobacterium kansasii KATS2 sequence of  
 CC the invention. The KATS2 oligonucleotide is useful as a probe and a  
 CC primer for detection of M. kansasii microorganisms or nucleic acids in  
 CC veterinary and human clinical samples by hybridisation and amplification  
 CC respectively. The KATS2 fragment was hybridized to genomic DNA from M.  
 CC kansasii and non-M. kansasii species, and was found to hybridise to all  
 CC six M. kansasii strains tested, and none of the 17 non-M. kansasii

CC strains. The new oligonucleotides allows rapid, accurate and sensitive  
 CC identification of all strains of M. kansasii, compared to prior art  
 CC probes which only identify 73 % of M. kansasii strains (e.g. ACCU-PROBE),  
 CC or fail to detect one distinct M. kansasii subgroup (e.g. pMK1-9)

XX SQ Sequence 18 BP; 4 A; 0 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 8.6%; Score 12; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1721 CGAGATGGAGAT 1732  
 Db 4 CGAGATGGAGAT 15  
 |||||

RESULT 319  
 AAX82250  
 ID AAX82250 standard; DNA; 18 BP.  
 XX AC AAX82250;  
 XX DT 18-AUG-1999 (first entry)  
 XX DE Influenza virus PA gene specific primer.  
 XX KW Cold-adapted influenza virus; passage culture; PB2 protein; PB1 protein;  
 KW PA protein; NP protein; M protein; NS protein; temperature sensitivity;  
 KW vaccine; flu; influenza; PCR primer; ss.  
 XX OS Synthetic.  
 OS Influenza virus.  
 OS WO9928445-A1.  
 PN 10-JUN-1999.  
 XX PF 30-NOV-1998; 98WO-KR000384.  
 XX PR 29-NOV-1997; 97KR-00064854.  
 XX PA (CHEI-) CHEIL JEDANG CORP.  
 XX PI Seong BL, Lee KH, Youn JW, Kim SJ, Cheoun KH, Kim J, Kim HG;  
 XX WPI; 1999-385377/32.  
 XX DR Cold-adapted influenza viruses useful for the production of protective  
 PT vaccines against flu.  
 XX PS Example 4; Page 15; 62pp; English.  
 XX CC The invention relates to cold-adapted influenza viruses prepared by  
 CC passage culture of A/X-31, B/Yamagata/16/88 or B/Lee/40 viruses at low  
 CC temperatures. A cDNA gene of cold-adapted influenza virus HTCA-A101 can  
 CC be selected from a group consisting of PB2 protein gene, PB1 protein  
 CC gene, PA protein gene, NP protein gene, M protein gene and NS protein  
 CC gene (AAX82192-X82197). The method is useful for the production of cold-  
 CC adapted influenza virus that exhibit temperature sensitivity and can be  
 CC actively grown in fertilized eggs. The virus is useful for vaccines for  
 CC protection against 'flu. Live vaccines containing cold-adapted viruses  
 CC have several advantages over killed vaccines. It can prevent reduction of  
 CC immunogenicity, which may occur in the killed vaccine where antigenic  
 CC proteins would be denatured at its inactivation. It can also avoid  
 CC hypersensitivity due to the prolonged administration of heterologous  
 CC proteins. It promotes the immunity by inducing IgA and it can be  
 CC administered into a spray formulation via nasal cavity and thus its  
 CC application is convenient for children. It is able to inhibit the growth  
 CC of the wild-type virus and thus its therapeutic effect can be expected.  
 CC Sequences AAX82222-X82257 represent PCR primers specific for the various  
 CC genes of influenza virus  
 XX SQ Sequence 18 BP; 2 A; 7 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 8.6%; Score 12; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1683 TGTCTCTCCAG 1694  
 Db 2 TGTCTCTCCAG 13  
 |||||

RESULT 320  
 AAZ46979/C  
 ID AAZ46979 standard; DNA; 18 BP.  
 XX AC AAZ46979;  
 XX DT 14-APR-2000 (first entry)  
 XX DE Bcl-XL mRNA specific antisense oligo I.  
 XX KW Anti-apoptotic protein; bcl-xL; tumour; cancer; epithelial; prostate;  
 KW lung; bladder; bcl-2; vascular lesion; antisense; ss.  
 XX OS Homo sapiens.  
 OS WO200001393-A2.  
 PN 13-JAN-2000.  
 XX PF 02-JUL-1999; 99WO-US015250.  
 XX PR 02-JUL-1998; 98US-00109614.  
 XX PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX PI Stein CA;  
 XX WPI; 2000-137140/12.  
 XX DR New antisense oligonucleotides inhibiting the anti-apoptotic protein bcl-  
 PT xL, useful for reducing bcl-xL production in tumor cells to treat cancer  
 PT or in vascular cells to promote the regression of vascular lesions.  
 XX PS Claim 1; Fig 1; 69pp; English.  
 XX CC The invention provides antisense oligonucleotides or their derivatives  
 CC which reduce or eliminate expression of the anti-apoptotic protein bcl-  
 CC xL. The oligonucleotides can be introduced into tumor cells to reduce  
 CC bcl-xL production to treat cancer, especially epithelial cancer, e.g.  
 CC prostate, lung or bladder cancer. Oligonucleotides comprising one or more  
 CC bases with a C-5 propylpyrrolidine modification may especially be used  
 CC to reduce levels of bcl-2 family proteins (to which bcl-xL belongs) in  
 CC such treatment. The oligonucleotides can be introduced into vascular  
 CC cells to reduce bcl-xL production to promote the regression of vascular  
 CC lesions. They can also be included with a carrier (and optionally tetra  
 CC meso-(4-methylpyridyl)porphine and/or tetra meso- (anilinium)porphine; in  
 CC pharmaceutical compositions, useful as above. Sequences AAZ46971-983  
 CC represent antisense oligos specific for the bcl-XL mRNA  
 XX SQ Sequence 18 BP; 2 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 8.6%; Score 12; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1720 CGAGATGGAGA :731  
 Db 14 CGAGATGGAGA :3  
 |||||

RESULT 321  
 ABZ10839  
 ID ABZ10839 standard; DNA; 18 BP.

```
XX AC ABZ10839;
XX DT 16-JAN-2003 (first entry)
XX DE Haematopoietic cell proliferation disorder related oligonucleotide #979.
XX KW Human; haematopoietic cell proliferation disorder; cytostatic;
XX KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
XX KW cytosine methylation state; probe; primer; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200277272-A2.
XX PD 03-OCT-2002.
XX PF 26-MAR-2002; 2002WO-EP003401.
XX PR 26-MAR-2001; 2001US-0278333P.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
XX PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E,
XX PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
XX PI Schwöbe I, Ziebarth H;
XX DR WPI; 2003-018942/01.
XX PT Detecting and differentiating between hematopoietic cell proliferative
XX PT disorders, comprises contacting a target nucleic acid with a reagent that
XX PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX PS Claim 15; Page 65; 117pp; English.
XX CC The present invention describes a method for detecting and
XX CC differentiating between haematopoietic cell proliferative disorders
XX CC associated with at least 1 gene and/or their regulatory regions in a
XX CC subject. The method comprises contacting a target nucleic acid in a
XX CC biological sample obtained from the subject with at least 1 reagent,
XX CC which distinguishes between methylated and non-methylated CpG
XX CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
XX CC represent specifically claimed nucleotide sequences from the present
XX CC invention. Oligonucleotides from the present invention can be used: for
XX CC differentiating between healthy haematopoietic cells and proliferative
XX CC disorder haematopoietic cells; for differentiating between acute
XX CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
XX CC determining the cytosine methylation state and/or single nucleotide
XX CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
XX CC related sequences and their complements; and as primers for the
XX CC amplification of haematopoietic cell proliferation disorder related
XX CC sequences. The nucleotide sequences from the present invention can also
XX CC be used for detecting a predisposition to, differentiation between
XX CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
XX CC haematopoietic cell proliferative disorders. The present method enables a
XX CC highly specific classification of haematopoietic cell proliferative
XX CC disorders allowing for improved and informed treatment of patients
XX SQ Sequence 18 BP; 5 A; 1 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 8.6%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1712 TAGGAGTACCGA 1723
Db 1 TAGGAGTACCGA 12

RESULT 322
AAQ50548/c
```

```
ID AAQ50548 standard; DNA; 15 BP.
XX AC AAQ50548;
XX DT 24-MAY-1994 (first entry)
XX DE Human chromosome 6 cCI6-111 VNTR consensus sequence.
XX KW Variable Number of Tandem Repeats; human VNTR; satellite sequence;
XX KW DNA fingerprint; Southern hybridisation; probe; ss.
XX OS Homo sapiens.
XX PN JP05276949-A.
XX PD 26-OCT-1993.
XX PF 27-DEC-1991; 91JP-00359482.
XX PR 27-DEC-1991; 91JP-00359482.
XX PA (GANK-) ZH GAN KENYUKAI.
XX DR WPI; 1993-373584/47.
XX PT Human VNTR sequence - used to discriminate individual, esp. parent and
XX PT child.
XX PS Disclosure; Fig 12; 11pp; Japanese.
XX CC The degenerate probe sequence AAQ50544 corresponds to VNTRs found in
XX CC human chromosome 6. See AAQ61882-3 for the repeat region sequence and
XX CC AAQ50548 for the consensus sequence
XX SQ Sequence 15 BP; 2 A; 2 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 GGCTCCCAACTCCTC 1748
Db 15 GGCCCCCACCCTCTC 1

RESULT 323
AAT89133/c
ID AAT89133 standard; RNA; 15 BP.
XX AC AAT89133;
XX DT 04-MAR-1998 (first entry)
XX DE Lutetium texaphyrin RNA conjugate for light induced cleavage of DNA.
XX KW Photosensitive; texaphyrin; DNA cleavage; light induced; photocleavage;
XX KW lutetium; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT misc_binding 1..15 /tag= b
FT /note= "this region binds to AAT89134"
FT misc_feature 1 /tag= a
FT /mod_base
FT /note= "cytosine is modified by lutetium(III)texaphyrin
FT compound"
FT misc_feature 15 /tag= c
FT /note= "Guanine is modified by a methoxy group"
```

[illegible]

PI Stuyver L, Louwagie J, Rossau R;  
 XX WPI; 1997-393716/36.  
 XX  
 XX Determining susceptibility to antiviral drugs of reverse transcriptase  
 PT containing viruses - useful for genotyping HIV RT and detecting antiviral  
 PT resistant HIV.  
 XX  
 XX Claim 13; Page 36; 59pp; English.  
 XX  
 XX This sequence represents a probe for a wild type HIV reverse  
 CC transcriptase (RT) gene fragment. This sequence can be used in the method  
 CC of the invention for determining the susceptibility to antiviral drugs of  
 CC viruses which contain RT genes and are present in a biological sample. It  
 CC comprises: (1) releasing, isolating or concentrating the polynucleic  
 CC acids present in a sample; (2) amplifying the relevant part of the RT  
 CC genes present with at least one suitable primer pair; (3) hybridising the  
 CC polynucleic acids of step (1) or (2) with at least two RT gene probes.  
 CC The probes being applied to known locations on a solid support, and are  
 CC capable of simultaneously hybridising to their respective target regions  
 CC under appropriate hybridisation and wash condition allowing the detection  
 CC of homologous targets, or with the probes hybridising specifically with a  
 CC sequence complementary to any of the target sequences; (4) detecting the  
 CC hybrids formed in step (3); and (4) inferring the nucleotide sequence at  
 CC the codons of interest (codons 38-44, 47-53, 65-72, 73-77, 148-154, 180-  
 CC 187, 212-216, and 217-220), and/or the amino acids of the codons of  
 CC interest and/or antiviral drug resistance spectrum, and possible the type  
 CC of viral isolates involved from the differential hybridisation signals  
 CC obtained in step (4). The method is specifically used to detect antiviral  
 CC drug resistant strains of viruses containing RT genes, especially HIV  
 CC retroviruses and Hepadnaviridae. The method can also be used for  
 CC genotyping HIV RT  
 XX  
 XX Sequence 15 BP; 7 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.5%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 3.3e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1717 GTACGGAGATGGAGA 1731  
 DB 1 GTACAGAGATGGAAA 15  
 RESULT 326  
 AAV07304/C  
 ID AAV07304 standard; DNA; 15 BP.  
 XX  
 XX AAV07304;  
 AC  
 DT 14-AUG-1998 (first entry)  
 XX  
 XX Metallotexaphyrin-oligonucleotide conjugate #18.  
 DE  
 XX Metallotexaphyrin; dysprosium; europium; conjugate; RNase H;  
 KW antisense therapy; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /mod\_base  
 FT /note= "DyTxNH-(CH2)6-PSO3-cytosine, where DyTx is  
 FT dysprosium (III) texaphyrin"  
 XX  
 XX US5763172-A.  
 PN  
 XX  
 PD 09-JUN-1998.  
 XX  
 PF 07-JUN-1995; 95US-00486962.  
 XX  
 XX 21-JAN-1992; 92US-00822964.  
 PR

PR 09-JUN-1993; 93US-00075123.  
 PR 14-APR-1994; 94US-00227370.  
 PR 09-JUN-1994; 94WO-US006284.  
 PR 26-MAY-1995; 95US-00452261.  
 PR 07-JUN-1995; 95US-00485581.  
 XX (PHAR-) PHARMACYCLICS INC.  
 FA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 XX Sessler JL, Wright M, Miller RA, Dow WC, Magda D;  
 PI  
 XX WPI; 1998-347306/30.  
 DR  
 XX Enhancing therapeutic activity of oligo-nucleotides in cells - using  
 PT conjugate comprising metallotexaphyrin, which hydrolyses phosphate ester  
 PT bonds of RNA, and oligo-nucleotide, which binds to targetted RNA.  
 XX  
 XX Example 8; Col 29-30; 34pp; English.  
 PS  
 XX The invention relates to a method of enhancing the therapeutic activity  
 CC of oligonucleotides in cells. It comprises contacting a targeted  
 CC intracellular RNA in a cell with a metallotexaphyrin-oligonucleotide  
 CC conjugate. The contact is carried out under physiological conditions for  
 CC a time sufficient to hydrolyse the phosphate ester bond of the targeted  
 CC RNA. The metallotexaphyrin of the conjugate has catalytic activity for  
 CC phosphate ester bond hydrolysis. The oligonucleotide of the conjugate has  
 CC complementary binding affinity to the targeted RNA. The conjugate may be  
 CC used in antisense therapies for treating, e.g. cancer, viral infections,  
 CC autoimmune diseases and restenosis. The conjugate may also be used as  
 CC hydrolysis reagents for the detoxification of di- and trialkyl phosphate  
 CC esters, which are used in solvents, insecticides and chemical nerve  
 CC gases. The metallotexaphyrin complex enhances the therapeutic activity of  
 CC the oligonucleotide, not only by facilitating cellular uptake of the  
 CC oligonucleotide but also by hydrolysing target RNA within the cell.  
 CC independent of RNase H. Attachment to the complex may also cause the  
 CC oligonucleotide to take on some of the pharmacodynamic an biodistribution  
 CC properties of the texaphyrin, such as selective localisation in tumours.  
 CC The present sequence represents a metallo- texaphyrin-oligonucleotide  
 CC conjugate  
 XX  
 SQ Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 3.3e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1659 CCAGGCTCACAGCTG 1673  
 DB 15 CCCGGCTCACAGATG 1  
 RESULT 327  
 AAV54266/C  
 ID AAV54266 standard; cDNA; 15 BP.  
 XX  
 XX AAV54266;  
 AC  
 XX 29-DEC-1998 (first entry)  
 DT  
 XX Primer KCL55 used in the method of the invention.  
 DE  
 XX PCR; primer; amplification; single chain T-cell receptor; scTCR; Vbc;  
 KW bacteriophage coat protein; BCP; V-alpha chain; Vac; V-beta chain;  
 KW immune response; T-cell receptor; TCR; cancer; allergy; T lymphocyte; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9839482-A1.  
 PN  
 XX 11-SEP-1998.  
 PD  
 XX 05-MAR-1998; 98WO-US004274.  
 PF  
 XX

```
PR 07-MAR-1997; 97US-00813781.
XX (SUNO-) SUNOL MOLECULAR CORP.
PA Weidanz JA, Card KF, Wong HC;
XX WPI; 1998-506374/43.
XX WPI; 1999-264000/22.
XX Soluble single-chain T cell receptor proteins.
XX Example; Fig 6D; 145pp; English.
XX The invention relates to a soluble fusion protein that comprises an
CC immunoglobulin (Ig) light chain constant region or fragment, covalently
CC linked to a single-chain T-cell receptor (sc-TCR) comprising a V-alpha
CC chain covalently linked to a V-beta chain by a peptide linker sequence.
CC The soluble fusion protein can induce an immune response in a mammal, so
CC that the mammal is immunized against pathogenic T cell receptor epitopes.
CC It can also be used to inhibit T-cell activation in a mammal. The sc-TCR
CC can be used to kill a cell containing a TCR specific ligand. The sc-TCR
CC proteins can be used in vitro to detect and analyse ligands such as
CC peptides and MHC/HLA molecular components of TCR ligands. They can also
CC be used to detect T-cells with pathogenic properties. Other uses include
CC functional, cellular and molecular assays and structural analysis. In
CC vivo the sc-TCRs can compete with pathogenic T cells or to raise
CC antibodies for use in therapy. Fusion of an Ig light chain constant
CC region to a sc-TCR facilitates soluble expression. The sc-TCR can be
CC isolated in significant quantities without performing difficult
CC solubilisation, cleaving or re-folding steps. The fusion also confers a
CC means of detecting and purifying the fusion proteins by conventional
CC immunological methods. Sequences AAX5301 to AAX55445 represent PCR
CC primers used for constructing the fusion proteins of the invention
XX
XX Sequence 15 BP; 1 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
SQ
Query Match 8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1656 GCACCAGGCTCACAG 1670
DB 15 GAACCACTCTCACAG 1
RESULT 328
AAX5348/c
ID AAX5348 standard; DNA; 15 BP.
XX
XX AAX5348;
XX
XX 08-JUL-1999 (first entry)
XX Soluble sc-TCR fusion protein constructing primer KC155.
XX Fusion protein; soluble; immunoglobulin; Ig; sc-TCR; immune response;
XX single-chain T-cell receptor; T cell activation; therapy; PCR primer; ss.
XX Synthetic.
XX WO9918129-A1.
XX
XX 15-APR-1999.
XX
XX 28-SEP-1998; 98WO-US020263.
XX
XX 02-OCT-1997; 97US-00943086.
XX (SUNO-) SUNOL MOLECULAR CORP.
XX Weidanz JA, Card KF, Wong HC;
XX
```

---

```
DR WPI; 1999-264000/22.
XX Soluble single-chain T cell receptor proteins.
XX Example; Fig 6D; 145pp; English.
XX The invention relates to a soluble fusion protein that comprises an
CC immunoglobulin (Ig) light chain constant region or fragment, covalently
CC linked to a single-chain T-cell receptor (sc-TCR) comprising a V-alpha
CC chain covalently linked to a V-beta chain by a peptide linker sequence.
CC The soluble fusion protein can induce an immune response in a mammal, so
CC that the mammal is immunized against pathogenic T cell receptor epitopes.
CC It can also be used to inhibit T-cell activation in a mammal. The sc-TCR
CC can be used to kill a cell containing a TCR specific ligand. The sc-TCR
CC proteins can be used in vitro to detect and analyse ligands such as
CC peptides and MHC/HLA molecular components of TCR ligands. They can also
CC be used to detect T-cells with pathogenic properties. Other uses include
CC functional, cellular and molecular assays and structural analysis. In
CC vivo the sc-TCRs can compete with pathogenic T cells or to raise
CC antibodies for use in therapy. Fusion of an Ig light chain constant
CC region to a sc-TCR facilitates soluble expression. The sc-TCR can be
CC isolated in significant quantities without performing difficult
CC solubilisation, cleaving or re-folding steps. The fusion also confers a
CC means of detecting and purifying the fusion proteins by conventional
CC immunological methods. Sequences AAX5301 to AAX55445 represent PCR
CC primers used for constructing the fusion proteins of the invention
XX
XX Sequence 15 BP; 1 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
SQ
Query Match 8.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1656 GCACCAGGCTCACAG 1670
DB 15 GAACCACTCTCACAG 1
RESULT 329
AAX66971/c
ID AAX66971 standard; DNA; 15 BP.
XX
XX AAX66971;
XX
XX 19-OCT-2000 (first entry)
XX Human leukocyte antigen A allele DNA probe A539T SEQ ID NO:29.
XX Human leukocyte antigen; HLA; class I allele type; probe; PCR primer;
XX amplification; hybridisation; organ transplant; gene typing; diagnosis;
XX ss.
XX Homo sapiens.
XX WO200031295-A1.
XX
XX 02-JUN-2000.
XX
XX 07-OCT-1999; 99WO-JPC05527.
XX
XX 26-NOV-1998; 98JP-00335151.
XX (SHIO ) SHIONOGI & CO LTD.
XX Moribe T, Kaneshige T;
XX WPI; 2000-400097/34.
XX Simple, rapid and accurate method for distinguishing HLA class I allele
XX type with possibility of mechanization and automation, applicable in
XX judging donor-recipient compatibility during organ transplant and disease
XX diagnosis.
XX
```



PS Claim 8; Page 56; 83pp; Japanese.

XX The present invention describes a method for distinguishing a human

CC leukocyte antigen (HLA) class I antigen or allele by a combination of

CC polymerase chain reaction (PCR) using a primer pair whereby all HLA-A, -B

CC or -C alleles can be amplified or using reverse hybridisation analysis

CC comprising a DNA probe covalently bonded to microtitre plate wells which

CC are hybridisable specifically with the base sequence of at least one

CC specific HLA-A, -B or -C allele. The method is applicable in gene typing,

CC judging donor-recipient compatibility during organ transplant and

CC correlation analysis for diagnosis of various diseases. The method is

CC simple, rapid and accurate, with possibility of mechanisation and

CC automation, without the problems encountered by using the prior-art

CC techniques. AAA66943 to AAA67072 represent oligonucleotide probes and PCR

CC primers for use in the method of the present invention

XX

SQ Sequence 15 BP; 4 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 3.3e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 GGCTCCCAACTCTC 1748

DB 15 GGCTCTCAACTGCTC 1

RESULT 330

AAF47176/c

ID AAF47176 standard; DNA; 15 BP.

XX

AC AAF47176;

XX

DT 30-MAR-2001 (first entry)

DE IGFBP3 oligonucleotide #596.

XX

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

KW neovascular condition of the retina; ss.

XX

OS Homo sapiens.

XX

PN W0200078341-A1.

XX

PD 28-DEC-2000.

XX

XX 21-JUN-2000; 2000WO-AU000693.

PF

XX 21-JUN-1999; 99US-0140345P.

PR

XX (MURD-) MURDOCH CHILDRENS RES INST.

PA

XX Wright CJ, Werther GA, Edmondson SR;

PI

XX WPI; 2001-041421/05.

DR

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX

XX Example 7; Page 48; 201pp; English.

PS

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-

CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia

XX

SQ Sequence 15 BP; 3 A; 9 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 3.3e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1696 GTGFTGGAGTTGGG 1710

DB 15 GGGGTGGAACCTGGG 1

RESULT 331

AAF52890

ID AAF52890 standard; DNA; 15 BP.

XX

AC AAF52890;

XX

DT 30-MAR-2001 (first entry)

DE IGF-I oligonucleotide #3850.

XX

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

KW neovascular condition of the retina; ss.

XX

OS Homo sapiens.

XX

PN W0200078341-A1.

XX

PD 28-DEC-2000.

XX

XX 21-JUN-2000; 2000WO-AU000693.

PF

XX 21-JUN-1999; 99US-0140345P.

PR

XX (MURD-) MURDOCH CHILDRENS RES INST.

PA

XX Wright CJ, Werther GA, Edmondson SR;

PI

XX WPI; 2001-041421/05.

DR

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX

XX Example 8; Page 86; 201pp; English.

PS

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-

CC F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

XX Sequence 15 BP; 3 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

SQ Query Match 8.5%; Score 11.8; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1722 GAGATGGAGATTGGC 1736  
DB 1 GAGATGGAGCTGGC 15

RESULT 332  
AAF47174/c  
ID AAF47174 standard; DNA; 15 BP.  
XX AC AAF47174;  
XX DT 30-MAR-2001 (first entry)  
DE IGFBP3 oligonucleotide #594.  
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.  
XX Homo sapiens.  
OS WO200078341-A1.  
XX PN 28-DEC-2000.  
XX PD 21-JUN-2000; 2000WO-AU000693.  
XX PF 21-JUN-1999; 99US-0140345P.  
XX PR (MURD-) MURDOCH CHILDRENS RES INST.  
XX PA Wright CJ, Werther GA, Edmondson SR;  
PI WPI; 2001-041421/05.  
XX DR Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
XX PT inhibits or reduces growth factor mediated cell proliferation and/or  
XX PT inflammation.  
XX Example 7; Page 48; 201pp; English.

CC The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

CC brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

XX Sequence 15 BP; 4 A; 7 C; 1 G; 3 T; 0 U; 0 Other;

SQ Query Match 8.5%; Score 11.8; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1698 GGTGGAAGTTGGGT 1712  
DB 15 GGTGGAAGTTGGAT 1

RESULT 333  
AAF52891  
ID AAF52891 standard; DNA; 15 BP.  
XX AC AAF52891;  
XX DT 30-MAR-2001 (first entry)  
DE IGF-I oligonucleotide #3851.  
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.  
XX Homo sapiens.  
OS WO200078341-A1.  
XX PN 28-DEC-2000.  
XX PD 21-JUN-2000; 2000WO-AU000693.  
XX PF 21-JUN-1999; 99US-0140345P.  
XX PR (MURD-) MURDOCH CHILDRENS RES INST.  
XX PA Wright CJ, Werther GA, Edmondson SR;  
PI WPI; 2001-041421/05.  
XX DR Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
XX PT inhibits or reduces growth factor mediated cell proliferation and/or  
XX PT inflammation.  
XX Example 8; Page 86; 201pp; English.

CC The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

SQ Sequence 15 BP; 3 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 3.3e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1723 AGATGGAGCTGGCT 1737  
 |||||  
 Db 1 AGATGGAGCTGGCT 15

RESULT 334  
 AAF52889  
 ID AAF52889 standard; DNA; 15 BP.  
 XX  
 AC AAF52889;  
 XX  
 DT 30-MAR-2001 (first entry)  
 XX  
 DE IGF-I oligonucleotide #3849.  
 XX  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytosolic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2000078341-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 PR 21-JUN-1999; 99US-0140345P.  
 XX  
 PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PI Wraight CJ, Werther GA, Edmondson SR;  
 XX  
 DR WPI; 2001-041421/05.  
 XX  
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 PS Example 8; Page 86; 201pp; English.  
 XX  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 3 A; 2 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 3.3e+02;

SQ Sequence 15 BP; 0 A; 6 C; 3 G; 5 T; 0 U; 1 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 3.3e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1677 CCTGTGTCTCTC 1691  
 |||||  
 Db 1 CCTGTGTCTCTC 15

RESULT 336  
 AAS99376/C  
 ID AAS99376 standard; DNA; 15 BP.  
 XX  
 AC AAS99376;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1721 GGAGATGGAGATTGG 1735  
 |||||  
 Db 1 GGAGATGGAGCTGG 15

RESULT 335  
 ABV99795  
 ID ABV99795 standard; DNA; 15 BP.  
 XX  
 AC ABV99795;  
 XX  
 DT 24-FEB-2003 (first entry)  
 XX  
 DE Human PFKFB2 allele specific oligonucleotide primer #21.  
 XX  
 KW Human; 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2; PFKFB2;  
 KW cytosolic; antidiabetic; gene therapy; cancer; diabetes; ss; ASO;  
 KW allele specific oligonucleotide; primer; polymorphism.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200194363-A2.  
 XX  
 PD 13-DEC-2001.  
 XX  
 PF 07-JUN-2001; 2001WO-US018458.  
 XX  
 PR 07-JUN-2000; 2000US-0209935P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Duda A, Kazemi A, Koshy B;  
 XX  
 DR WPI; 2002-566434/60.  
 XX  
 PT New 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 (PFKFB2) gene  
 PT variants, for improving efficiency and reliability in the development of  
 PT drugs for treating diseases associated with PFKFB2 activity e.g. cancer.  
 XX  
 PS Claim 16; Page 13; 95pp; English.  
 XX  
 CC The invention relates to a novel human 6-phosphofructo-2-kinase/ fructose  
 CC -2,6-bisphosphatase 2 (PFKFB2) isogene. The PFKFB2 of the invention has  
 CC cytosolic and antidiabetic activity. The polynucleotides may have a use  
 CC in gene therapy. The identified candidate agents targeting PFKFB2, are  
 CC useful for treating cancer and diabetes. The methods of the invention are  
 CC useful for improving the efficiency and reliability of several steps in  
 CC the discovery and development of drugs for treating diseases associated  
 CC with PFKFB2 activity. The present sequence represents a allele specific  
 CC oligonucleotide (ASO) primer used in the invention to detect PFKFB2 gene  
 CC polymorphisms  
 XX  
 SQ Sequence 15 BP; 0 A; 6 C; 3 G; 5 T; 0 U; 1 Other;



RESULT 338  
ACD56644  
ID ACD56644 standard; RNA; 15 BP.  
XX  
AC ACD56644;  
DT 24-SEP-2003 (first entry)  
XX  
DE HBV enzymatic nucleic acid substrate sequence #241.  
XX  
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;  
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX  
OS Hepatitis B virus.  
XX  
PN WO200281494-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 26-MAR-2002; 2002WO-US009187.  
XX  
PR 26-MAR-2001; 2001US-00817879.  
PR 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX  
DR WPI; 2003-229207/22.  
XX  
PT Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
PS Example 1; Page 224; 387pp; English.  
XX  
CC The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HBV  
XX enzymatic nucleic acid sequences disclosed in the present invention  
SQ Sequence 15 BP; 0 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 15;  
Best Local Similarity 53.3%; Pred. No. 3.3e+02;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 1677 CCTGGTGTCTCTC 1691  
DB 1 CCUUGUGUCUCCUC 15  
RESULT 339  
AAQ91451/c  
ID AAQ91451 standard; DNA; 16 BP.  
XX  
AC AAQ91451;  
DT 25-MAR-2003 (revised)  
DT 30-AUG-1995 (first entry)  
XX  
DE Dysprosium (III) texaphyrin (DyTx) DNA conjugate.  
XX  
KW Dysprosium (III) texaphyrin (DyTx) DNA conjugate; liver disease;  
KW targeted intracellular mRNA hydrolysis; gene expression inhibition;  
KW hormone regulation; hydrolysis reagents; alkyl phosphate esters;  
KW detoxification; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "DyTx-NH(CH2)6-PO4-thymine"  
XX  
PN WO9429316-A2.  
XX  
PD 22-DEC-1994.  
XX  
PF 09-JUN-1994; 94WO-US006284.  
PR 09-JUN-1993; 93US-00075123.  
PR 14-APR-1994; 94US-00227370.  
XX  
XX (TEXA) UNIV TEXAS SYSTEM.  
PA (PHAR-) PHARMACYCLICS INC.  
XX  
PI Sessler JU, Ross KL, Wright M, Hemmi GW, Dow WC, Smith DA;  
PI Kral VA, Iverson B, Mody T, Miller RA, Magda D;  
XX  
DR WPI; 1995-036382/05.  
XX  
PT Texaphyrin metal complex mediated ester hydrolysis - esp. useful for  
PT targeted intracellular hydrolysis of mRNA and for inhibiting gene  
PT expression.  
XX  
PS Disclosure; Fig 21; 125pp; English.  
XX  
CC AAQ91451-Q91457 are texaphyrin lanthanide metal DNA conjugates, which are  
CC esp. useful for the targeted intracellular hydrolysis of mRNA; inhibiting  
CC gene expression. They may also be used for the treatment of liver disease,  
CC as hormone regulation agents and as hydrolysis reagents for the  
CC detoxification of alkyl phosphate esters. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX  
SQ Sequence 16 BP; 1 A; 2 C; 8 G; 5 T; 0 U; 0 Other;  
Query Match 8.5%; Score 11.8; DB 1; Length 16;  
Best Local Similarity 86.7%; Pred. No. 3.6e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1655 AGCACCAGGCTCACA 1669  
DB 15 AACACCCGGCTCACA 1

RESULT 340  
 AAV07300/c  
 ID AAV07300 standard; DNA; 16 BP.  
 XX  
 AC AAV07300;  
 XX  
 DT 14-AUG-1998 (first entry)  
 XX  
 DE Metallotexaphyrin-oligonucleotide conjugate #14.  
 XX  
 KW Metallotexapyrin; dysprosium; europium; conjugate; RNase H;  
 KW antisense therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1 /\*tag= a  
 FT /mod\_base  
 FT /note= "DyTXNH-(CH2)6-PO4-thymine, where DyTx is  
 FT dysprosium (III) texaphyrin"  
 XX  
 PN US5763172-A.  
 XX  
 PD 09-JUN-1998.  
 XX  
 PF 07-JUN-1995; 95US-00486962.  
 XX  
 PR 21-JAN-1992; 92US-00822964.  
 PR 09-JUN-1993; 93US-00075123.  
 PR 14-APR-1994; 94US-00227370.  
 PR 09-JUN-1994; 94WO-US006284.  
 PR 26-MAY-1995; 95US-00452261.  
 PR 07-JUN-1995; 95US-00485581.  
 XX  
 PA (PHAR-) PHARMACYCLICS INC.  
 PA (TEXA) UNIV TEXAS SYSTEM.  
 XX  
 PI Sessler JL, Wright M, Miller RA, Dow WC, Magda D;  
 XX WPI; 1998-347306/30.  
 DR  
 XX  
 PT Enhancing therapeutic activity of oligo-nucleotides in cells - using  
 PT conjugate comprising metallotexaphyrin, which hydrolyses phosphate ester  
 PT bonds of RNA, and oligo-nucleotide, which binds to targetted RNA.  
 XX  
 PS Example 6; Fig 5; 34pp; English.  
 XX  
 CC The invention relates to a method of enhancing the therapeutic activity  
 CC of oligonucleotides in cells. It comprises contacting a targeted  
 CC intracellular RNA in a cell with a metallotexaphyrin-oligonucleotide  
 CC conjugate. The contact is carried out under physiological conditions for  
 CC a time sufficient to hydrolyse the phosphate ester bond of the targeted  
 CC RNA. The metallotexaphyrin of the conjugate has catalytic activity for  
 CC phosphate ester bond hydrolysis. The oligonucleotide of the conjugate has  
 CC complementary binding affinity to the targeted RNA. The conjugate may be  
 CC used in antisense therapies for treating, e.g. cancer, viral infections,  
 CC autoimmune diseases and restenosis. The conjugate may also be used as  
 CC hydrolysis reagents for the detoxification of di- and trialkyl phosphate  
 CC esters, which are used in solvents, insecticides and chemical nerve  
 CC gases. The metallotexaphyrin complex enhances the therapeutic activity of  
 CC the oligonucleotide, not only by facilitating cellular uptake of the  
 CC oligonucleotide but also by hydrolysing target RNA within the cell,  
 CC independent of RNase H. Attachment to the complex may also cause the  
 CC oligonucleotide to take on some of the pharmacodynamic and biodistribution  
 CC properties of the texaphyrin, such as selective localisation in tumours.  
 CC The present sequence represents a metallo- texaphyrin-oligonucleotide  
 CC conjugate  
 XX  
 SQ Sequence 16 BP; 1 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 16;  
 Best Local Similarity 86.7%; Pred. No. 3.6e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1655 AGCACCAGGCTCACA 1669  
 Db 15 AACACCCGGCTCACA 1  
 |||||  
 RESULT 341  
 AAV07038/c  
 ID AAV07038 standard; DNA; 16 BP.  
 XX  
 AC AAV07038;  
 XX  
 DT 08-JUL-1998 (first entry)  
 XX  
 DE Texaphyrin oligonucleotide conjugate.  
 XX  
 KW Texaphyrin oligonucleotide conjugate; dysprosium; metal complex;  
 KW hydrolytic cleavage activity; ribonucleic acid cleavage; RNA; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1 /\*tag= a  
 FT /note= "A texaphyrin dysprosium metal complex, bound to  
 FT thymine via a linking phosphate group"  
 XX  
 PN WO9807733-A1.  
 XX  
 PD 26-FEB-1998.  
 XX  
 PF 20-AUG-1997; 97WO-US014682.  
 XX  
 PR 20-AUG-1996; 96US-00700277.  
 XX  
 PA (PHAR-) PHARMACYCLICS INC.  
 XX  
 PI Magda D, Crofts SP, Wright M;  
 XX WPI; 1998-179049/16.  
 DR  
 XX  
 PT New conjugates which have hydrolytic cleavage activity for RNA - comprise  
 PT a texaphyrin metal complex bound to an internal linkage of an  
 PT oligonucleotide.  
 XX  
 PS Example 4; Page 53; 77fp; English.  
 XX  
 CC This sequence is shown in the specification. The invention relates to a  
 CC texaphyrin oligonucleotide conjugate, which has hydrolytic cleavage  
 CC activity for ribonucleic acid (RNA). It comprises a texaphyrin metal  
 CC complex bound to an internal linkage of an oligonucleotide or  
 CC oligonucleotide analogue. The conjugates may be used for the destruction  
 CC of retroviral RNA, messenger RNA, ribosomal RNA, RNA cofactors, transfer  
 CC RNA, small nuclear RNA and small cytoplasmic RNA. They may be used for  
 CC eliminating diseased or cancerous cells or tissues, in blood purification  
 CC protocols (in vivo or in vitro), in antiviral treatments, or as  
 CC diagnostic probes (e.g. in determination of the nucleotide sequence of  
 CC RNA or to detect polymorphisms in RNA). Administration of the conjugates  
 CC is, e.g., oral, topical or parenteral, especially topical or intravenous.  
 CC The conjugates are especially effective under conditions where the  
 CC concentration of RNA target exceeds that of available conjugate  
 CC  
 SQ Sequence 16 BP; 1 A; 2 C; 8 G; 5 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 16;  
 Best Local Similarity 86.7%; Pred. No. 3.6e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1655 AGCACCAGGCTCACA 1669  
 |||||

```
Db      15 AACACCCGGCTCAC 1
RESULT 342
AAZ97664
ID AAZ97664 standard; DNA; 16 BP.
XX AC AAZ97664;
XX DT 15-SEP-2003 (revised)
XX DT 26-APR-2000 (first entry)
XX DE HIV-1 protease gene probe SEQ ID NO:154.
XX KW Human immunodeficiency virus; HIV; protease; probe; detection;
XX KW drug selected mutation; hybridisation; genotyping; infection;
XX KW drug resistance; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9967428-A2.
XX PD 29-DEC-1999.
XX PF 22-JUN-1999; 99WO-EP004317.
XX PR 24-JUN-1998; 98EP-00870143.
XX PA (INNO-) INNOGENETICS NV.
XX FI Stuyver L;
XX DR WPI; 2000-147219/13.
XX PT Detection of drug-selected mutations in the HIV protease gene used to
XX PT treat HIV infections.
XX PS Claim 3; Page 35; 76pp; English.
XX CC The present invention describes the detection of drug-selected mutations
XX CC in the HIV protease gene. The method of detection allows the simultaneous
XX CC characterisation of a range of codons involved in drug resistance using
XX CC sets of probes optimised to function together in a reverse-hybridisation
XX CC assay. AAZ97517 to AAZ97997 represent specifically claimed probes for use
XX CC in the assay, and AAZ97479 to AAZ97501 represent specifically claimed HIV
XX CC protease gene polymorphic nucleotide sequences. AAZ97502 to AAZ97515, and
XX CC AAZ98004 to AAZ98007, represent PCR primers for the HIV protease gene,
XX CC and AAZ97516 represents an HIV protease probe used in an example from the
XX CC present invention. The method, probes and primers can be used for the
XX CC detection of drug-selected mutations in the HIV protease gene. The method
XX CC allows the simultaneous characterisation of a range of codons involved in
XX CC drug resistance. The method may also be used for HIV protease genotyping
XX CC assays. The probes are able to discriminate between wild type and mutated
XX CC protease sequences. The method allows rapid and reliable detection of
XX CC drug-selected mutation in HIV. (Updated on 15-SEP-2003 to standardise OS
XX CC field)
XX SQ Sequence 16 BP; 2 A; 0 C; 10 G; 4 T; 0 U; 0 Other;

Query Match      8.5%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1721 GGAGTTGGAGATTGG 1735
      ||||| ||||| |||||
Db      2 GGAGTTGGAGATTGG 16

RESULT 343
AAZ88440/c
ID AAZ88440 standard; DNA; 16 BP.
XX AC AAZ88440;
```

```
XX DT 08-MAY-2000 (first entry)
XX DE Exemplary texaphyrin oligonucleotide conjugate SEQ ID NO:6.
XX KW Texaphyrin; metal complex; catalytic; RNA hydrolysis; virucide;
XX KW antibacterial; cytostatic; antiinflammatory; antitumour; antiviral; ss.
XX OS Synthetic.
XX PN US6022959-A.
XX PD 08-FEB-2000.
XX PF 20-NOV-1997; 97US-00975522.
XX PR 20-AUG-1996; 96US-0077185P.
XX PR 20-AUG-1997; 97WO-US014682.
XX PA (PHAR-) PHARMACYCLICS INC.
XX PI Wright M, Crofts SP, Magda D;
XX DR WPI; 2000-160391/14.
XX PT Texaphyrin metal complex derivatized ribonucleic acids possessing
XX PT hydrolytic cleavage activity against RNA are useful as e.g. antiviral,
XX PT antibacterial, antitumor and antiinflammatory agents.
XX PS Example 4; Col 33; 30pp; English.
XX CC The present invention describes a conjugate with hydrolytic cleavage
XX CC activity for ribonucleic acid (RNA), which comprises a texaphyrin metal
XX CC complex bound to an internal linkage of an oligonucleotide or
XX CC oligonucleotide analogue. AAZ88435 to AAZ88440 represent exemplary
XX CC texaphyrin oligonucleotide conjugates used in the exemplification of the
XX CC present invention. The novel conjugates have virucide, antibacterial,
XX CC cytostatic and antiinflammatory properties, and are involved in RNA
XX CC hydrolysis. The conjugates are useful for inhibiting the expression of a
XX CC gene by targeted intracellular mRNA (messenger ribonucleic acid)
XX CC hydrolysis. The conjugates have applications for anti-viral and anti-
XX CC bacterial therapy as well as cancers and inflammatory responses caused by
XX CC overexpression of certain proteins
XX SQ Sequence 16 BP; 1 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

Query Match      8.5%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1655 AGCACCAGGCTCAC 1669
      ||||| ||||| |||||
Db      15 AACACCCGGCTCAC 1

RESULT 344
ABX14989
ID ABX14989 standard; DNA; 16 BP.
XX AC ABX14989;
XX DT 14-MAR-2003 (first entry)
XX DE Human delta opioid receptor OPRD1-1 SNP genotyping PCR primer #1.
XX KW Human; delta opioid receptor; OPRD1-1; ss; PCR; primer; SNP;
XX KW single nucleotide polymorphism; eating disorder; anorexia nervosa;
XX KW energy homeostasis disorder; chromosome 1.
XX OS Homo sapiens.
XX PN WO200292838-A2.
```

PD		21-NOV-2002.
XX		
PF		13-MAY-2002; 2002WO-US014940.
XX		
PPR		11-MAY-2001; 2001US-0290016P.
XX		(BIOI-) BIOINVEST LTD.
PA		Bergen AW;
PI		
XX		
PS		WPI; 2003-129306/12.
DR		
XX		
PT		New isolated nucleic acid molecule encoding a delta opioid receptor variant associated with an eating or energy homeostasis disorder, useful for diagnosing a genetic predisposition to such disorder, e.g. anorexia nervosa.
PT		
PT		
XX		
XX		Example; Page 19; 39pp; English.
XX		
CC		The invention relates to an isolated nucleic acid molecule encoding a delta opioid receptor variant associated with an eating or energy homeostasis disorder. Also included are a delta opioid receptor variant encoded by the nucleic acid, an isolated antibody that specifically recognises the delta opioid receptor variant, a vector comprising the nucleic acid, a host cell transformed to contain the vector, producing the polypeptide by culturing the host cell, identifying an agent which modulates the expression of the nucleic acid, diagnosing a genetic predisposition to an eating or energy homeostasis disorder by detecting the presence or absence of the variant nucleic acid in a patient sample, an allele specific primer that detects a polymorphism in the gene encoding a delta opioid receptor associated with an eating or energy homeostasis disorder and a non-human transgenic animal modified to contain the variant nucleic acids. The variants are named OPRD1-1 to OPRD1-8. The human opioid receptor gene is located on chromosome 1. The nucleic acid molecules and delta opioid receptor variant are useful for diagnosing a genetic predisposition to an eating or energy homeostasis disorder, such as anorexia nervosa. The allele specific primer is useful for detecting polymorphism in the gene encoding a delta opioid receptor associated with the disorder cited. The present sequence is a genotyping PCR primer for detecting the presence of a particular SNP (single nucleotide polymorphism) in a sample
XX		
XX		Sequence 16 BP; 4 A; 5 C; 3 G; 4 T; 0 U; 0 Other;
SQ		
	Query Match	8.5%; Score 11.8; DB 1; Length 16;
	Best Local Similarity	86.7%; Pred. No. 3.6e+02;
	Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1662 GGCTCAGCTGGAA 1676             2 GGCTCACACCTGTAA 16	
DB		
	RESULT 345	
	ABT34281	
ID	ABT34281 standard; DNA; 16 BP.	
XX		
XX	ABT34281;	
AC		
XX		
DT	12-JUN-2003 (first entry)	
XX		
DE	Opioid receptor D1 PCR primer SEQ ID NO 67.	
XX		
KW	Eating disorder; polymorphism; dataset; allele; HGBASE identification;	
KW	serotonin receptor 1b; delta-opioid receptor; dopamine receptor D2;	
KW	anorexia nervosa; bulimia nervosa; PCR; primer; ss.	
XX		
OS	Unidentified.	
XX		
FN	WO2003012143-A1.	
XX		
PD	13-FEB-2003.	
XX		



XX WPI; 1997-259017/23.  
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 59; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 5 A; 7 C; 1 G; 0 T; 4 U; 0 Other;  
 CC  
 CC Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 CC Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
 CC Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 1745 CCTCCTATCCTATAA 1759  
 Db ||:||:|:||||  
 2 CCUCUUAUCCGAAA 16  
 XX  
 RESULT 347  
 AAX69126  
 ID AAX69126 standard; RNA; 17 BP.  
 XX  
 AC AAX69126;  
 XX  
 XX 28-JUL-1999 (first entry)  
 DT Human flt1 VEGF receptor hammerhead ribozyme substrate #421.  
 XX  
 DE Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 PN WO9715662-A2.  
 XX  
 XX 01-MAY-1997.  
 PD  
 XX 25-OCT-1996; 96WO-US017480.  
 PF  
 XX 26-OCT-1995; 95US-0005974P.  
 PR  
 XX 11-JAN-1996; 96US-00584040.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR ) CHIRON CORP.  
 XX  
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 PI WPI; 1997-259017/23.  
 XX  
 DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 XX Claim 4; Page 59; 218pp; English.  
 PS  
 XX The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more

CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 5 A; 7 C; 1 G; 0 T; 4 U; 0 Other;  
 CC  
 CC Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 CC Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
 CC Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 1745 CCTCCTATCCTATAA 1759  
 Db ||:||:|:||||  
 3 CCUCUUAUCCGAAA 17  
 XX  
 RESULT 348  
 AAV97558  
 ID AAV97558 standard; RNA; 17 BP.  
 XX  
 AC AAV97558;  
 XX  
 XX 17-MAR-1999 (first entry)  
 DT Human EGF-R target sequence nucleotide position 2960.  
 XX  
 DE Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;  
 KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;  
 KW cancer; genetic drift; detection; mutation; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 PN WO9833893-A2.  
 XX  
 XX 06-AUG-1998.  
 PD  
 XX 14-JAN-1998; 96WO-US000730.  
 PF  
 XX 31-JAN-1997; 97US-0036476P.  
 PR  
 XX 04-DEC-1997; 97US-00985162.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (UVAS-) UNIV ASTON.  
 XX  
 XX Akhtar S, Fell P, Mcswiggen JA;  
 PI WPI; 1998-437449/37.  
 DR  
 XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal  
 PT growth factor receptor, useful for inhibiting cell proliferation and for  
 PT treating cancers.  
 XX  
 XX Claim 5; Page 75; 109pp; English.  
 PS  
 XX The present invention describes enzymatic nucleic acid molecules (NAMS)  
 CC which specifically cleave RNA derived from an epidermal growth factor  
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090  
 CC represent specifically claimed target sequence from human EGF-R. AAV98044  
 CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and  
 CC hairpin ribozymes respectively for human EGF-R. The NAMS are useful for  
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR  
 CC expression levels e.g. to inhibit cell proliferation in the prevention or  
 CC treatment of cancers. The NAMS can also be used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of EGF-R RNA in a cell  
 XX  
 SQ Sequence 17 BP; 2 A; 7 C; 3 G; 0 T; 5 U; 0 Other;  
 CC  
 CC Query Match 8.5%; Score 11.8; DB 1; Length 17;

DT 19-JUN-2000 (first entry)

18520/c

RESULT 351  
AAA18520/C

ID AA18520 standard; RNA; 17 BP.  
 XX AA18520;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Human TIE-2 substrate sequence SEQ ID NO:1746.  
 XX  
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;  
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;  
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
 KW age related macular degeneration; inflammation; neovascular glaucoma;  
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;  
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9950403-A2.  
 XX  
 XX 07-OCT-1999.  
 PD  
 XX 24-MAR-1999; 99WO-US006507.  
 PF  
 XX 27-MAR-1998; 98US-0079678P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA  
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;  
 PI WPI; 1999-591315/50.  
 XX  
 DR Novel ribozymes for modulating the synthesis, expression and/or stability  
 PT of an mRNA encoding an angiogenic factors.  
 XX  
 PS Claim 56; Page 100; 305pp; English.  
 CC  
 CC The present invention describes enzymatic nucleic acid molecules with RNA  
 CC cleaving activity, which specifically cleave RNA encoded by an aryl  
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their  
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to  
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
 CC sequences for integrin alpha 6 subunit, and AAA20361 to AAA21500 and  
 CC AAA21596 to AAA21688 represent their corresponding target sequences;  
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme  
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
 CC AAA21596 to AAA21688 represent their corresponding target sequences;  
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme  
 CC sequences for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to  
 CC AAA23422 represent their corresponding target sequences. The ribozymes of  
 CC the invention are used for modulating the synthesis, expression and/or  
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
 CC especially used to treat cancer, diabetic retinopathy, age related  
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber  
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,  
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
 CC integrin subunit alpha-6, or integrin subunit beta-3  
 XX  
 SQ Sequence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 17 GCAGTACGAGATGG 3  
 RESULT 352  
 AAA22628  
 ID AAA22628 standard; RNA; 17 BP.  
 XX  
 AC AAA22628;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5854.  
 XX  
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;  
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;  
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
 KW age related macular degeneration; inflammation; neovascular glaucoma;  
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;  
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9950403-A2.  
 XX  
 XX 07-OCT-1999.  
 PD  
 XX 24-MAR-1999; 99WO-US006507.  
 PF  
 XX 27-MAR-1998; 98US-0079678P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA  
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;  
 PI WPI; 1999-591315/50.  
 XX  
 DR Novel ribozymes for modulating the synthesis, expression and/or stability  
 PT of an mRNA encoding an angiogenic factors.  
 XX  
 PS Claim 54; Page 232; 305pp; English.  
 CC  
 CC The present invention describes enzymatic nucleic acid molecules with RNA  
 CC cleaving activity, which specifically cleave RNA encoded by an aryl  
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their  
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to  
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
 CC sequences for integrin alpha 6 subunit, and AAA20361 to AAA21595 represent ribozyme  
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
 CC AAA21596 to AAA21688 represent their corresponding target sequences;  
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme  
 CC sequences for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to  
 CC AAA23422 represent their corresponding target sequences. The ribozymes of  
 CC the invention are used for modulating the synthesis, expression and/or  
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
 CC especially used to treat cancer, diabetic retinopathy, age related  
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber  
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,  
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
 CC integrin subunit alpha-6, or integrin subunit beta-3  
 XX  
 SQ Sequence 17 BP; 1 A; 8 C; 3 G; 0 T; 5 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;

CC activity. AAV90922 to AAV93877 represent NACs that can be used in the					
CC	method, specifically for: modulating the expression of a Raf gene				
XX	Sequence 17 BP; 5 A; 7 C; 0 G; 0 T; 5 U; 0 Other;				
Query Match		8.5%;	Score 11.8;	DB 1;	length 17;
Best Local Similarity		86.7%;	Pred. NO. 3.9e+02;		
XX	Matches 13; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1718 TACGGAGATGGAGAT 1732				
Db	15 TATGGAGATGGTGTAT 1				
RESULT 354					
AAV91355/c					
ID	AAV91355 standard; RNA; 17 BP.				
XX					
AC	AAV91355;				
XX					
DT	18-FEB-1999 (first entry)				
XX					
DE	Human C-raf target site nucleotide position 2701.				
XX					
KW	Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;				
KW	target; substrate; catalyst; modulation; expression; Raf gene; delivery;				
KW	screening; identification; synthesis; deprotection; purification; cancer;				
KW	inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;				
KW	restenosis; rheumatoid arthritis; ss.				
OS	Homo sapiens.				
XX					
PN	WO9850530-A2.				
XX					
PD	12-NOV-1998.				
XX					
PF	05-MAY-1998; 98WO-US009249.				
XX					
PR	09-MAY-1997; 97US-0046059P.				
PR	09-JUN-1997; 97US-0049002P.				
PR	03-JUL-1997; 97US-0051718P.				
PR	22-AUG-1997; 97US-0056808P.				
PR	02-OCT-1997; 97US-0061321P.				
PR	02-OCT-1997; 97US-0061324P.				
PR	05-NOV-1997; 97US-0064866P.				
PR	19-DEC-1997; 97US-0068212P.				
XX					
PA	(RIBO-) RIBOZYME PHARM INC.				
XX					
PI	Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;				
PI	Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;				
PI	Thompson J, Workman CT, Beaudry A, Sweedler D;				
XX					
DR	WPI; 1999-009494/01.				
XX					
PT	Identifying new catalytic nucleic acid that modulates selected processes				
PT	- especially ribozymes that cleave Raf RNA for treating cancer,				
PT	restenosis, and also new ribozymes and modified nucleoside triphosphates				
PT	used as antiviral agents and synthons.				
XX					
PS	Claim 177; Page 153; 259pp; English.				
XX					
CC	A method has been developed for the identification of a nucleic acid				
CC	capable of modulating a process in a biological system. The method				
CC	comprises: (a) introducing into the system a random library of nucleic				
CC	acid catalysts (NAC) having a substrate binding domain (SBD), comprising				
CC	a random sequence, and a catalytic domain (CD); and (b) identifying NAC				
CC	in systems where modulation has occurred and/or determining the sequence				
CC	of at least part of the SBDs in such systems. Nucleic acid molecules with				
CC	endonuclease activity and catalytic activity, from the present invention,				
CC	are used to modulate gene expression in plant and mammalian cells and to				
CC	cleave target nucleic acid, particularly for treating systemic diseases				
CC	caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic				
CC	ascites and infection. They may also be used to detect genetic drift and				
CC	mutations in diseased cells and to determine c-raf RNA. Specifically NACs				
CC	with RNA-cleaving activity that modulate expression of the Raf gene, are				
CC	used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or				
CC	generally any condition associated with the level of c-raf. Introduction				
CC	of sugar/phosphate modifications increases stability against nuclease and				

ascites and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-raf. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. AAV90922 to AAV93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene

Sequence 17 BP; 3 A; 8 C; 3 G; 0 T; 3 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1722 GAGATGGGATTGGC 1736

DB 17 GAGATGGGATTGGC 3

RESULT 355

AAV92633  
 ID AAV92633 standard; RNA; 17 BP.

XX AC AAV92633;

DT 18-FEB-1999 (first entry)

DE Human A-Raf substrate position 2219.

XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
 KW screening; identification; synthesis; deprotection; purification; cancer;  
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
 KW restenosis; rheumatoid arthritis; ss.

OS Homo sapiens.

XX WO9850530-A2.

PN 12-NOV-1998.

XX 05-MAY-1998; 98WO-US009249.

XX 09-MAY-1997; 97US-0046059P.

PR 09-JUN-1997; 97US-0049002P.

PR 03-JUL-1997; 97US-0051718P.

PR 22-AUG-1997; 97US-0056808P.

PR 02-OCT-1997; 97US-0061321P.

PR 02-OCT-1997; 97US-0061324P.

PR 05-NOV-1997; 97US-0064866P.

PR 19-DEC-1997; 97US-0068212P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;  
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;

XX WPI; 1998-009494/01.

XX Identifying new catalytic nucleic acid that modulates selected processes  
 PT - especially ribozymes that cleave Raf RNA for treating cancer,  
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
 PT used as antiviral agents and synthons.

XX Claim 177; Page 161; 259pp; English.

XX A method has been developed for the identification of a nucleic acid  
 CC capable of modulating a process in a biological system. The method  
 CC comprises: (a) introducing into the system a random library of nucleic  
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC

CC in systems where modulation has occurred and/or determining the sequence  
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
 CC endonuclease activity and catalytic activity, from the present invention,  
 CC are used to modulate gene expression in plant and mammalian cells and to  
 CC cleave target nucleic acid, particularly for treating systemic diseases  
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
 CC ascites and infection. They may also be used to detect genetic drift and  
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs  
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
 CC generally any condition associated with the level of c-raf. Introduction  
 CC of sugar/phosphate modifications increases stability against nuclease and  
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the  
 CC method, specifically for modulating the expression of a Raf gene

XX Sequence 17 BP; 2 A; 6 C; 1 G; 0 T; 8 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 53.3%; Pred. No. 3.9e+02;

Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1683 TGTCTCTCCAGCGT 1697

DB 1 UGUUCCUCCAUCAU 15

RESULT 356

AAAX15355  
 ID AAAX15355 standard; DNA; 17 BP.

XX AC AAAX15355;

XX 22-JUN-1999 (first entry)

DE HSV-1 thymidine kinase gene mutagenic primer #3.

XX HSV-1; thymidine kinase; mutation; DRH nucleoside binding site; enzyme;  
 KW pathogen; tumour; hyperkeratosis; psoriasis; prostate hypertrophy;  
 KW hyperthyroidism; endocrinopathy; autoimmune disease; allergy; restenosis;  
 KW viral disease; AIDS; hepatitis; parasite; bacterial infection; ss.

OS Synthetic.

OS Herpes simplex virus unknown type.

XX US5877010-A.

XX 02-MAR-1999.

XX 02-MAY-1995; 95US-00432871.

XX 02-MAY-1994; 94US-00237592.

XX (UNIW ) UNIV WASHINGTON.

XX Black ME, Loeb LA;  
 XX WPI; 1999-189650/16.

XX New Herpesviridae thymidine kinase mutant nucleic acids - used to  
 PT develop products for treating e.g. tumours, autoimmune diseases,  
 PT allergies, restenosis or viral, bacterial or parasitic diseases.  
 XX Example 1; Col 20; 72pp; English.

XX This sequence represents a primer used to construct a mutation in the  
 CC herpes simplex virus type 1 (HSV-1) thymidine kinase (TK) gene  
 CC (AAAX15352). The invention relates to the generation of novel HSV-1 TK  
 CC gene with a mutation upstream, within or downstream from a DRH nucleoside  
 CC binding site. The TK enzymes can be used for inhibiting pathogenic  
 CC agents, e.g. tumours, hyperkeratosis, psoriasis, prostate hypertrophy,  
 CC hyperthyroidism, endocrinopathies, autoimmune diseases, allergies,  
 CC restenosis, viral diseases such as AIDS, hepatitis, intracellular  
 CC parasitic diseases or bacterial infection

[illegible]

PR 22-OCT-1999; 99US-0160901P.

PA (MITO-) MITOKOR.

PI Herrnstadt C, Davis RE;

PR WPI; 2000-672748/65.

PT Diagnosing a subject at the risk for or having Alzheimer's disease  
PT comprises determining at least one single nucleotide polymorphism in  
PT mitochondrial DNA associated with the disease in the sample from the  
PT subject.

PS Example 4; Page 38; 89pp; English.

CC The present invention describes a novel method for determining the risk  
CC of or diagnosing Alzheimer's disease using single nucleotide  
CC polymorphisms (SNPs) present in an individual's mitochondrial DNA  
CC (mtDNA). In addition, the SNPs identified can be used to identify agents  
CC suitable for use in treating Alzheimer's disease. Sequences AAC67301-  
CC C67610 are PCR primers used to demonstrate the method of the invention

XX Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1652 GCAAGCACACAGGCTC 1666

Db 1 GCTATCACACAGGCTC 15

RESULT 360

AAC67310  
ID AAC67310 standard; DNA; 17 BP.

AC AAC67310;

DT 14-FEB-2001 (first entry)

XX Alzheimer's disease-linked mitochondrial SNP PCR primer #10.

XX Human; mitochondrial genome; single nucleotide polymorphism; SNP;  
XX Alzheimer's disease; mtDNA; PCR primer; ss.

OS Homo sapiens.

XX WO200063441-A2.

PN 26-OCT-2000.

XX 19-APR-2000; 2000WO-US010906.

XX 20-APR-1999; 99US-0130447P.

PR 22-OCT-1999; 99US-0160901P.

PA (MITO-) MITOKOR.

PI Herrnstadt C, Davis RE;

PR WPI; 2000-672748/65.

PT Diagnosing a subject at the risk for or having Alzheimer's disease  
PT comprises determining at least one single nucleotide polymorphism in  
PT mitochondrial DNA associated with the disease in the sample from the  
PT subject.

PS Example 2; Page 33; 89pp; English.

CC The present invention describes a novel method for determining the risk  
CC of or diagnosing Alzheimer's disease using single nucleotide  
CC polymorphisms (SNPs) present in an individual's mitochondrial DNA

CC (mtDNA). In addition, the SNPs identified can be used to identify agents  
CC suitable for use in treating Alzheimer's disease. Sequences AAC67301-  
CC C67610 are PCR primers used to demonstrate the method of the invention

XX Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1652 GCAAGCACACAGGCTC 1666

Db 1 GCTATCACACAGGCTC 15

RESULT 361

ABA81112

ID ABA81112 standard; DNA; 17 BP.

XX ABA81112;

DT 24-JAN-2002 (first entry)

XX LDLR mutation correcting oligonucleotide SEQ ID NO: 3958.

XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;  
XX retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;  
XX cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;  
XX adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;  
XX haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;  
XX mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;  
XX familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;  
XX UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;  
XX Alzheimer's disease; cytostatic; antitickling; antianaemic; haemostatic;  
XX antileptic; ss.

XX Homo sapiens.

XX WO200173002-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US009761.

XX 27-MAR-2000; 2000US-0192176P.

PR 07-JUN-2000; 2000US-0192179P.

PR 01-JUN-2000; 2000US-0208538P.

PR 30-OCT-2000; 2000US-0244989P.

XX (UYDE ) UNIV DELAWARE.

XX Kmiec EB, Gamper HB, Rice MC;

XX WPI; 2001-639230/73.

XX Oligonucleotide for targeted alterations of genetic sequences and for  
XX treating cystic fibrosis, comprises at least one mismatch and chemical  
XX modification.

XX Claim 7; Page 257; 294pp; English.

XX The present invention provides single-stranded oligonucleotides which can  
XX be used for the targeted alteration of genomic sequences, where the  
XX oligonucleotide has at least one mismatch compared with the genomic  
XX sequence to be altered. In particular, these sequences are directed at  
XX the following genes: adenosine deaminase, p53, beta-globin,  
XX retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A  
XX (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus  
XX 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,  
XX apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase  
XX (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and  
XX presenilin-2 (PSEN2). These can be used in the gene therapy of diseases  
XX such as cancer, adenosine deaminase deficiency, cystic fibrosis,

CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,  
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and  
CC various syndromes. The present sequence is one of the gene correcting  
CC oligonucleotides of the invention

XX  
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1661 AGGCTCAGCTGGA 1675  
||||| |||||||  
DB 2 AGGCTTCCAGCTGGA 16

RESULT 362  
ABA77557  
ID ABA77557 standard; DNA; 17 BP.  
XX  
AC ABA77557;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Beta globin mutation correcting oligonucleotide SEQ ID NO: 403.  
XX  
KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;  
KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;  
KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;  
KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;  
KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;  
KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;  
KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;  
KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;  
KW Alzheimer's disease; cytostatic; antiskilling; antianaemic; haemostatic;  
KW antilipemic; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200173002-A2.  
XX  
PD 04-OCT-2001.  
XX  
PF 27-MAR-2001; 2001WO-US009761.  
XX  
PR 27-MAR-2000; 2000US-0192176P.  
PR 27-MAR-2000; 2000US-0192179P.  
PR 01-JUN-2000; 2000US-0208538P.  
PR 30-OCT-2000; 2000US-0244989P.  
XX  
PA (UYDE ) UNIV DELAWARE.  
XX  
PI Kmiec EB, Gamper HB, Rice MC;  
XX  
DR WPI; 2001-639230/73.  
XX  
PT Oligonucleotide for targeted alterations of genetic sequences and for  
PT treating cystic fibrosis, comprises at least one mismatch and chemical  
PT modification.  
XX  
PS Claim 7; Page 67; 294pp; English.  
XX  
CC The present invention provides single-stranded oligonucleotides which can  
CC be used for the targeted alteration of genomic sequences, where the  
CC oligonucleotide has at least one mismatch compared with the genomic  
CC sequence to be altered. In particular, these sequences are directed at  
CC the following genes: adenosine deaminase, p53, beta-globin,  
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A  
CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus  
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,  
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase  
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and  
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases

CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,  
CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,  
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and  
CC various syndromes. The present sequence is one of the gene correcting  
CC oligonucleotides of the invention

XX  
SQ Sequence 17 BP; 3 A; 1 C; 8 G; 5 T; 0 U; 0 Other;  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1695 CGTGTGGAAGTTG3 1709  
||||| |||||||  
DB 1 CGTGGATGAAGTTG3 15

RESULT 363  
ABA77558/c  
ID ABA77558 standard; DNA; 17 BP.  
XX  
AC ABA77558;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Beta globin mutation correcting oligonucleotide SEQ ID NO: 404.  
XX  
KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;  
KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;  
KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;  
KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;  
KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;  
KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;  
KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;  
KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;  
KW Alzheimer's disease; cytostatic; antiskilling; antianaemic; haemostatic;  
KW antilipemic; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200173002-A2.  
XX  
PD 04-OCT-2001.  
XX  
PF 27-MAR-2001; 2001WO-US009761.  
XX  
PR 27-MAR-2000; 2000US-0192176P.  
PR 27-MAR-2000; 2000US-0192179P.  
PR 01-JUN-2000; 2000US-0208538P.  
PR 30-OCT-2000; 2000US-0244989P.  
XX  
PA (UYDE ) UNIV DELAWARE.  
XX  
PI Kmiec EB, Gamper HB, Rice MC;  
XX  
DR WPI; 2001-639230/73.  
XX  
PT Oligonucleotide for targeted alterations of genetic sequences and for  
PT treating cystic fibrosis, comprises at least one mismatch and chemical  
PT modification.  
XX  
PS Claim 7; Page 67; 294pp; English.  
XX  
CC The present invention provides single-stranded oligonucleotides which can  
CC be used for the targeted alteration of genomic sequences, where the  
CC oligonucleotide has at least one mismatch compared with the genomic  
CC sequence to be altered. In particular, these sequences are directed at  
CC the following genes: adenosine deaminase, p53, beta-globin,  
CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A  
CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus  
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,  
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase  
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and



CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases  
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,  
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,  
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and  
 CC various syndromes. The present sequence is one of the gene correcting  
 CC oligonucleotides of the invention  
 XX  
 SQ Sequence 17 BP; 5 A; 8 C; 1 G; 3 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1695 CGTGGTGAAGTTGG 1709  
 ||||| |||||  
 Db 17 CGTGGATGAGTTGG 3  
 RESULT 364  
 ABA77561  
 ID ABA77561 standard; DNA; 17 BP.  
 XX  
 AC ABA77561;  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE Beta globin mutation correcting oligonucleotide SEQ ID NO: 407.  
 XX  
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;  
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;  
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;  
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;  
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;  
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;  
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;  
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;  
 KW Alzheimer's disease; cytostatic; antiskickling; antianaemic; haemostatic;  
 KW antilipemic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 EN WO200173002-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 27-MAR-2001; 2001WO-US009761.  
 XX  
 PR 27-MAR-2000; 2000US-0192176P.  
 PR 27-MAR-2000; 2000US-0192179P.  
 PR 01-JUN-2000; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 XX  
 PA (UYDE ) UNIV DELAWARE.  
 XX  
 XX Kmiec EB, Gamper HB, Rice MC;  
 PI WPI; 2001-639230/73.  
 XX  
 DR Oligonucleotide for targeted alterations of genetic sequences and for  
 PT treating cystic fibrosis, comprises at least one mismatch and chemical  
 PT modification.  
 XX  
 PS Claim 7; Page 68; 294pp; English.  
 XX  
 CC The present invention provides single-stranded oligonucleotides which can  
 CC be used for the targeted alteration of genomic sequences, where the  
 CC oligonucleotide has at least one mismatch compared with the genomic  
 CC sequence to be altered. In particular, these sequences are directed at  
 CC the following genes: adenosine deaminase, p53, beta-globin,  
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A  
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus  
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,  
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase

CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and  
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases  
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,  
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,  
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and  
 CC various syndromes. The present sequence is one of the gene correcting  
 CC oligonucleotides of the invention  
 XX  
 SQ Sequence 17 BP; 4 A; 1 C; 7 G; 5 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1695 CGTGGTGAAGTTGG 1709  
 ||||| |||||  
 Db 2 CGTGGATGAGTTGG 16  
 RESULT 365  
 ABA81113/c  
 ID ABA81113 standard; DNA; 17 BP.  
 XX  
 AC ABA81113;  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE LDLR mutation correcting oligonucleotide SEQ ID NO: 3959.  
 XX  
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;  
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;  
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;  
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;  
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;  
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;  
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;  
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;  
 KW Alzheimer's disease; cytostatic; antiskickling; antianaemic; haemostatic;  
 KW antilipemic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 EN WO200173002-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 27-MAR-2001; 2001WO-US009761.  
 XX  
 PR 27-MAR-2000; 2000US-0192176P.  
 PR 27-MAR-2000; 2000US-0192179P.  
 PR 01-JUN-2000; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 XX  
 PA (UYDE ) UNIV DELAWARE.  
 XX  
 XX Kmiec EB, Gamper HB, Rice MC;  
 PI WPI; 2001-639230/73.  
 XX  
 DR Oligonucleotide for targeted alterations of genetic sequences and for  
 PT treating cystic fibrosis, comprises at least one mismatch and chemical  
 PT modification.  
 XX  
 PS Claim 7; Page 257; 294pp; English.  
 XX  
 CC The present invention provides single-stranded oligonucleotides which can  
 CC be used for the targeted alteration of genomic sequences, where the  
 CC oligonucleotide has at least one mismatch compared with the genomic  
 CC sequence to be altered. In particular, these sequences are directed at  
 CC the following genes: adenosine deaminase, p53, beta-globin,  
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A  
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus  
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,

CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase  
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and  
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases  
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,  
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,  
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and  
 CC various syndromes. The present sequence is one of the gene correcting  
 CC oligonucleotides of the invention  
 XX  
 SQ Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e-02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1661 AGGCTCAGCTGGGA 1675  
 ||||| |||||  
 Db 16 AGGCTCAGCTGGGA 2

RESULT 366  
 ABA77562/c  
 ID ABA77562 standard; DNA; 17 BP.

XX ABA77562;

XX 24-JAN-2002 (first entry)

DE Beta globin mutation correcting oligonucleotide SEQ ID NO: 408.

XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;  
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;  
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;  
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;  
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;  
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;  
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;  
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;  
 KW Alzheimer's disease; cytosolic; antislacking; antianaemic; haemostatic;  
 KW antileptic; ss.

XX Homo sapiens.

XX WO200173002-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US009761.

XX 27-MAR-2000; 2000US-0192176P.

XX 27-MAR-2000; 2000US-0192179P.

XX 01-JUN-2000; 2000US-0208538P.

XX 30-OCT-2000; 2000US-0244989P.

XX (UYDE ) UNIV DELAWARE.

XX Kmlec EB, Gamper HB, Rice MC;

XX WPI; 2001-639230/73.

XX Oligonucleotide for targeted alterations of genetic sequences and for  
 PT treating cystic fibrosis, comprises at least one mismatch and chemical  
 PT modification.

XX Claim 7; Page 68; 294pp; English.

XX The present invention provides single-stranded oligonucleotides which can  
 CC be used for the targeted alteration of genomic sequences, where the  
 CC oligonucleotide has at least one mismatch compared with the genomic  
 CC sequence to be altered. In particular, these sequences are directed at  
 CC the following genes: adenosine deaminase, p53, beta-globin,  
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A  
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus

CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,  
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase  
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and  
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases  
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,  
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,  
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and  
 CC various syndromes. The present sequence is one of the gene correcting  
 CC oligonucleotides of the invention  
 XX  
 SQ Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e-02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1695 CGTGGTGAAGTTGG 1709  
 ||||| |||||  
 Db 16 CGTGGTGAAGTTGG 2

RESULT 367

AAH24589

ID AAH24589 standard; DNA; 17 BP.

XX AAH24589;

XX 07-AUG-2001 (first entry)

DE Human endometrium cDNA clone 3-7-SP6 PCR primer #1.

XX Human; endometrium; gynaecological; cytostatic; gene therapy;  
 KW peptide therapy; endometriosis; gene expression; drug screening;  
 KW PCR primer; ss.

XX Homo sapiens.

XX WO200132920-A2.

XX 10-MAY-2001.

XX 03-NOV-2000; 2000WO-GB04228.

XX 03-NOV-1999; 99GB-00026074.

XX 03-NOV-1999; 99GB-00026076.

XX 03-NOV-1999; 99GB-00026079.

XX 03-NOV-1999; 99GB-00026081.

XX (METR-) METRIS THERAPEUTICS LTD.

XX Pappa H, Lnenicek M;

XX WPI; 2001-328804/34.

XX Screening for a gene or gene product associated with endometriosis, for  
 PT diagnosing or treating endometriosis, comprises selecting a gene whose  
 PT level of expression differs between healthy and diseased endometrium  
 PT tissues.

XX Example; Fig 3; 106pp; English.

XX The invention relates to a method for screening for a gene or gene  
 CC product associated with endometriosis. The method comprises comparing the  
 CC pattern of gene expression in a diseased endometrium tissue from a  
 CC patient suffering from endometriosis to the pattern of gene expression in  
 CC healthy endometrium tissue from the same patient, and selecting a gene  
 CC whose level of expression differs between healthy and diseased tissues.  
 CC The gene, gene product and their antagonists and agonists are useful in  
 CC the manufacture of a medicament for diagnosing or treating endometriosis.  
 CC The method is useful for screening genes or gene products that are  
 CC implicated in endometriosis. It is particularly useful in diagnosing  
 CC endometriosis, as well as for screening for agents for treating  
 CC endometriosis. Prior methods of diagnosing endometriosis are more

CC difficult to perform and are more expensive, normally involving surgery.  
 CC The present method allows the disease to be diagnosed and treated at  
 CC earlier stage. The present sequence is a primer used in a reverse  
 CC transcription polymerase chain reaction (RT-PCR) procedure to validate  
 CC the results of differential gene expression studies. It was used to  
 CC amplify human endometrium cDNA encoding ferritin L chain  
 XX Sequence 17 BP; 5 A; 4 C; 7 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1648 GAAGGCAAGCACCAG 1662  
 Db 3 GAAGGCTGACACCAG 17  
 RESULT 368  
 ABNO2361/c  
 ID ABNO2361 standard; DNA; 17 BP.  
 AC ABNO2361;  
 XX  
 XX  
 DT 29-MAY-2002 (first entry)  
 XX  
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2353.  
 DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200192524-A2.  
 PN  
 XX  
 XX 06-DEC-2001.  
 PD  
 XX  
 XX 25-MAY-2001; 2001WO-US016981.  
 XX  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 05-FEB-2001; 2001WO-US000670.  
 XX (AEOM-) AEOMICA INC.  
 PA  
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 PI WPI; 2002-179446/23.  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 FT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
 PT  
 XX Disclosure; SEQ ID NO 2353; 214pp; English.  
 PS  
 XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to

CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1632 GATGGGGCTTGTAGC 1646  
 Db 15 GATGGGGCTTGTAGC 1  
 RESULT 369  
 ABNO2360/c  
 ID ABNO2360 standard; DNA; 17 BP.  
 AC ABNO2360;  
 XX  
 XX 29-MAY-2002 (first entry)  
 DT  
 XX  
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2352.  
 DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200192524-A2.  
 PN  
 XX  
 XX 06-DEC-2001.  
 PD  
 XX  
 XX 25-MAY-2001; 2001WO-US016981.  
 XX  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 05-FEB-2001; 2001WO-US000670.  
 XX (AEOM-) AEOMICA INC.  
 PA  
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 PI WPI; 2002-179446/23.  
 XX

PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

XX Disclosure; SEQ ID NO 2352; 214pp; English.

XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens in assays used to determine the concentration  
CC of -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence

XX Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. No. 3.9e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1632 GATGGCGCTGTAGC 1646

Db ||||| ||||| ||||| |||||  
16 GATGGCGCGCTGTAGC 2

RESULT 370

ABN00533  
ID ABN00533 standard; DNA, 17 BP.

XX AC ABN00533;

XX 29-MAY-2002 (first entry)

XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:525.

XX Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;  
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
XX skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

XX WO200192524-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016981.

XX 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 30-JAN-2001; 2001WO-US000461.

XX 30-JAN-2001; 2001WO-US000862.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

30-JAN-2001; 2001WO-US000668.  
30-JAN-2001; 2001WO-US000669.  
30-JAN-2001; 2001WO-US000670.  
05-FEB-2001; 2001US-0266860P.

XX (ABCM-) ABOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX WPI; 2002-179446/23.

XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

XX Disclosure; SEQ ID NO 525; 214pp; English.

XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens in assays used to determine the concentration  
CC of -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence

XX Sequence 17 BP; 7 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. No. 3.9e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AGCAGAGGCACGCA 1658

Db ||||| ||||| ||||| |||||  
3 AGCAGATGACAGCA 17

RESULT 371

ABN00534  
ID ABN00534 standard; DNA, 17 BP.

XX AC ABN00534;

XX 29-MAY-2002 (first entry)

XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:526.

XX Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;  
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
XX skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

XX WO200192524-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016981.

PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 05-FEB-2001; 2001US-0266860P.  
 XX (AEOM-) AEOMICA INC.  
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX WPI; 2002-179446/23.  
 DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX Disclosure; SEQ ID NO 526; 214pp; English.  
 XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 SQ Sequence 17 BP; 7 A; 3 C; 5 G; 2 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1644 AGCAGAGGCAAGCA 1658  
 DB 2 AGCAGATGACAAGCA 16  
 RESULT 372  
 ABNO7838  
 ID ABNO7838 standard; DNA; 17 BP.  
 XX  
 AC ABNO7838;  
 XX  
 XX 29-MAY-2002 (first entry)  
 DT Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7830.  
 DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 XX  
 KW

KW muscle, myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX Homo sapiens.  
 XX WO200192524-A2.  
 XX 06-DEC-2001.  
 XX 25-MAY-2001; 2001WO-US016981.  
 XX 26-MAY-2000; 2000US-0207456P.  
 XX 21-SEP-2000; 2000US-0234687P.  
 XX 27-SEP-2000; 2000US-0236359P.  
 XX 04-OCT-2000; 2000GB-00024263.  
 XX 30-JAN-2001; 2001WO-US000661.  
 XX 30-JAN-2001; 2001WO-US000662.  
 XX 30-JAN-2001; 2001WO-US000663.  
 XX 30-JAN-2001; 2001WO-US000664.  
 XX 30-JAN-2001; 2001WO-US000665.  
 XX 30-JAN-2001; 2001WO-US000666.  
 XX 30-JAN-2001; 2001WO-US000667.  
 XX 30-JAN-2001; 2001WO-US000668.  
 XX 30-JAN-2001; 2001WO-US000669.  
 XX 05-FEB-2001; 2001US-0266860P.  
 XX (AEOM-) AEOMICA INC.  
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX WPI; 2002-179446/23.  
 DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX Disclosure; SEQ ID NO 7830; 214pp; English.  
 XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 SQ Sequence 17 BP; 6 A; 5 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1661 AGGCTCACAGCTGGA 1675  
 DB 2 AGCTCACAGCTGAA 16  
 RESULT 372  
 ABNO7838  
 ID ABNO7838 standard; DNA; 17 BP.  
 XX  
 AC ABNO7838;  
 XX  
 XX 29-MAY-2002 (first entry)  
 DT Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7830.  
 DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 XX  
 KW

RESULT 373  
ABN02359/C  
ID ABN02359 standard; DNA; 17 BP.  
XX  
XX  
AC ABN02359;  
XX  
XX 29-MAY-2002 (first entry)  
DT Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2351.  
DE  
XX  
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX WO200192524-A2.  
PN  
XX  
XX 06-DEC-2001.  
PD  
XX  
XX 25-MAY-2001; 2001WO-US016981.  
PF  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
XX (AEOM-) AEOMICA INC.  
PA  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX  
XX WPI; 2002-179446/23.  
DR  
XX  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
PT  
XX  
XX Disclosure; SEQ ID NO 2351; 214pp; English.  
PS  
XX  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX

SQ Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1632 GATGGGCTGTAGC 1646  
DB 17 GATGGGCTGTAGC 3  
RESULT 374  
ABN07837  
ID ABN07837 standard; DNA; 17 BP.  
XX  
XX AC ABN07837;  
XX  
XX 29-MAY-2002 (first entry)  
DT Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7829.  
DE  
XX  
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX WO200192524-A2.  
PN  
XX  
XX 06-DEC-2001.  
PD  
XX  
XX 25-MAY-2001; 2001WO-US016981.  
PF  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
XX (AEOM-) AEOMICA INC.  
PA  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX  
XX WPI; 2002-179446/23.  
DR  
XX  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
PT  
XX  
XX Disclosure; SEQ ID NO 7829; 214pp; English.  
PS  
XX  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX

therapeutic supplement in patients having specific deficiency in hGDMPLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a disorder associated with the expression of hGDMPLP-1, in particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMPLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequence

Sequence 17 BP; 6 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. No. 3.9e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1661 AGGCTCAGCTGGA 1675

Db 3 AGCCTCAGCTGAA 17

RESULT 375

ABV79508

ID ABV79508 standard; DNA; 17 BP.

AC ABV79508;

XX 03-JAN-2003 (first entry)

XX Human HTPL scanning oligonucleotide SEQ ID 754.

DE Human; Gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;

KW human testis expressed Patched like protein; testis; adrenal; liver;

KW male germ cell development; bone marrow; brain; kidney; lung; placenta;

KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX Homo sapiens.

OS EPI229046-A2.

PN 07-AUG-2002.

XX 28-JAN-2002; 2002EP-00001167.

XX 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 23-MAY-2001; 2001US-00864761.

PR 09-OCT-2001; 2001US-0327898P.

XX (AEOM-) AEOMICA INC.

PA Zhan J;

XX WPI; 2002-676582/73.

XX Novel isolated human testis expressed Patched like protein (HTPL), useful

PT for identifying agonist and antagonist and specific binding partners, and

PT for treating subjects having defects in HTPL.

XX Example 2; Page 162; 718pp; English.

XX The present invention relates to human testis expressed Patched like

CC protein (HTPL, see ABV79508 to ABV79508 and ABV79508 to ABV79508).

CC has two isoforms, with a few single base pair differences between the

CC two. One of the single base pair changes introduces a premature stop

CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL

CC shares an overall structure organisation with the Patched protein. The

CC shared structural features strongly imply that HTPL plays a role similar

to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10p12.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potential therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention

Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. No. 3.9e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1664 CTCACGCTGGAACC 1678

Db 1 CTCACGCTGGAACC 15

RESULT 376

ABV79507

ID ABV79507 standard; DNA; 17 BP.

AC ABV79507;

XX 03-JAN-2003 (first entry)

XX Human HTPL scanning oligonucleotide SEQ ID 753.

DE Human; Gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;

KW human testis expressed Patched like protein; testis; adrenal; liver;

KW male germ cell development; bone marrow; brain; kidney; lung; placenta;

KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX Homo sapiens.

OS EPI229046-A2.

PN 07-AUG-2002.

XX 28-JAN-2002; 2002EP-00001167.

XX 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 23-MAY-2001; 2001US-00864761.

PR 09-OCT-2001; 2001US-0327898P.

XX (AEOM-) AEOMICA INC.

PA Zhan J;

XX WPI; 2002-676582/73.

XX Novel isolated human testis expressed Patched like protein (HTPL), useful

PT for identifying agonist and antagonist and specific binding partners, and

PT for treating subjects having defects in HTPL.

XX Example 2; Page 162; 718pp; English.

XX The present invention relates to human testis expressed Patched like

CC protein (HTPL, see ABV79508 to ABV79508 and ABV79508 to ABV79508).

CC has two isoforms, with a few single base pair differences between the

CC two. One of the single base pair changes introduces a premature stop

CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL

CC shares an overall structure organisation with the Patched protein. The

CC shared structural features strongly imply that HTPL plays a role similar

CC shares an overall structure organisation with the Patched protein. The

CC shared structural features strongly imply that HTPL plays a role similar

CC to that of Patched, and is a potential tumour suppressor. HTPL is

CC important in regulating male germ cell development, and the HTPL gene was

CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are

CC useful for diagnosing a disorder caused by mutation in HTPL, and in

CC therapy and manufacture of a medicament for treatment or prevention of

CC such disorder associated with decreased expression or activity of human

CC HTPL. Such disorders include disorders of testis, or adrenal, adult and

CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,

CC skeletal muscle or colon function. HTPL proteins and nucleic acids are

CC clinically useful diagnostic markers and potential therapeutic agents for

CC male infertility and cancer. The present oligonucleotide was used in an

CC example from the invention

XX

XX Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Seq Query Match 8.5%; Score 11.8; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. No. 3.9e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1664 CTCACGCTGGGAACC 1678

Db 2 CTCACGCTGGGAACC 16

RESULT 377

ABV78965

ID ABV78965 standard; DNA; 17 BP.

XX AC ABV78965;

XX DT 03-JAN-2003 (first entry)

XX DE Human HTPL scanning oligonucleotide SEQ ID 211.

XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;

XX KW human testis expressed Patched like protein; testis; adrenal; liver;

XX KW male germ cell development; bone marrow; brain; kidney; lung; placenta;

XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX XX EF1229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX WI; 2002-676582/73.

XX Novel isolated human testis expressed Patched like protein (HTPL), useful

XX PT for identifying agonist and antagonist and specific binding partners, and

XX PT for treating subjects having defects in HTPL.

XX Example 2; Page 91; 718pp; English.

XX The present invention relates to human testis expressed Patched like

XX protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL

XX has two isoforms, with a few single base pair differences between the

CC

CC two. One of the single base pair changes introduces a premature stop

CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL

CC shares an overall structure organisation with the Patched protein. The

CC shared structural features strongly imply that HTPL plays a role similar

CC to that of Patched, and is a potential tumour suppressor. HTPL is

CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are

CC important in regulating male germ cell development, and the HTPL gene was

CC useful for diagnosing a disorder caused by mutation in HTPL, and in

CC therapy and manufacture of a medicament for treatment or prevention of

CC such disorder associated with decreased expression or activity of human

CC HTPL. Such disorders include disorders of testis, or adrenal, adult and

CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,

CC skeletal muscle or colon function. HTPL proteins and nucleic acids are

CC clinically useful diagnostic markers and potential therapeutic agents for

CC male infertility and cancer. The present oligonucleotide was used in an

CC example from the invention

XX

XX Sequence 17 BP; 5 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Seq Query Match 8.5%; Score 11.8; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. No. 3.9e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1646 CAGAAGCGCAAGCACC 1660

Db 3 CGGAAGCGCAAGCAGC 17

RESULT 378

ABV78967

ID ABV78967 standard; DNA; 17 BP.

XX AC ABV78967;

XX DT 03-JAN-2003 (first entry)

XX DE Human HTPL scanning oligonucleotide SEQ ID 213.

XX KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;

XX KW human testis expressed Patched like protein; testis; adrenal; liver;

XX KW male germ cell development; bone marrow; brain; kidney; lung; placenta;

XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX XX EF1229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX WI; 2002-676582/73.

XX Novel isolated human testis expressed Patched like protein (HTPL), useful

XX PT for identifying agonist and antagonist and specific binding partners, and

XX PT for treating subjects having defects in HTPL.

XX Example 2; Page 91; 713pp; English.

XX The present invention relates to human testis expressed Patched like

XX protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL

XX has two isoforms, with a few single base pair differences between the

CC



CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was  
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention  
 XX  
 SQ Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1646 CAGAAGCGCAGCACC 1660  
 Db 1 CGGAAGCGCAGCAGC 15  
 RESULT 379  
 ABV78966  
 ID ABV78966 standard; DNA; 17 BP.  
 AC ABV78966;  
 XX  
 DT 03-JAN-2003 (first entry)  
 XX  
 DE Human HTPL scanning oligonucleotide SEQ ID 212.  
 XX  
 KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
 KW human testis expressed patched like protein; testis; adrenal; liver;  
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1229046-A2.  
 XX  
 PD 07-AUG-2002.  
 XX  
 PF 28-JAN-2002; 2002EP-00001167.  
 XX  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 09-OCT-2001; 2001US-0327898P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Zhan J;  
 XX  
 DR WPI; 2002-676582/73.  
 XX  
 XX Novel isolated human testis expressed Patched like protein (HTPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPL.  
 XX  
 PS Example 2; Page 91; 718pp; English.

XX The present invention relates to human testis expressed Patched like  
 CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was  
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention  
 XX  
 SQ Sequence 17 BP; 5 A; 5 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1646 CAGAAGCGCAGCACC 1660  
 Db 2 CGGAAGCGCAGCAGC 16  
 RESULT 380  
 ABK18405/C  
 ID ABK18405 standard; RNA; 17 BP.  
 AC ABK18405;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Human ERG hammerhead ribozyme target sequence, Seq ID No 1052.  
 XX  
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;  
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;  
 KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;  
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;  
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;  
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;  
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;  
 KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNazyme; inozyme;  
 KW amberzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200188124-A2.  
 XX  
 PD 22-NOV-2001.  
 XX  
 PF 16-MAY-2001; 2001WO-US015866.  
 XX  
 PR 16-MAY-2000; 2000US-00572021.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (GLAX ) GLAXO GROUP LTD.  
 XX  
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;  
 XX WPI; 2002-082995/11.  
 DR  
 XX Novel polynucleotide which down regulates expression of Ets-related gene,  
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,  
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.  
 XX

PS Claim 4; Page 78; 149pp; English.

xx The invention relates to a nucleic acid molecule (I) which down regulates

CC expression of an Ets-related gene (ERG). (I) is useful for treating

CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,

CC tumour angiogenesis, diabetic retinopathy, macular degeneration,

CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca

CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge

CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu

CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for

CC treating a patient having a condition associated with the level of ERG,

CC by contacting cells of the patient with (I) under conditions suitable for

CC the treatment. The method comprises the use of one or more therapies

CC under conditions suitable for the treatment. Leukaemia or tumour

CC angiogenesis is treated by administering (I) to the patient in

CC conjunction with one or more of other therapies such as radiation or

CC chemotherapy treatment. (I) is useful for reducing ERG activity in a

CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of

CC ERG gene, by contacting (I) with RNA, in the presence of a divalent

CC cation such as Mg2+. (I) is useful for diagnosis of conditions and

CC diseases related to the expression of ERG, and as diagnostic tool to

CC examine genetic drift and mutations within diseased cells or to detect

CC the presence of ERG RNA in a cell. (I) is useful for specifically

CC targeting genes that share homology with ERG gene or ERG fusion genes.

CC ABK7354-ABK2719 represent nucleic acids, including antisense and

CC enzymatic nucleic acid molecules which regulate expression of ERG, and

CC related PCR primers of the invention

xx Sequence 17 BP; 4 A; 2 C; 7 G; 0 T; 4 U; 0 Other;

SQ Query Match 8.5%; Score 11.8; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. No. 3.9e+02; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 2;

QY 1675 AACCTCGGTCTCC 1689

Db 17 AACCTCGGTCTCC 3

RESULT 381

ABV90894

ID ABV90894 standard; DNA; 17 BP.

XX AC ABV90894;

XX 23-DEC-2002 (first entry)

DT Human POSHL1 scanning oligonucleotide SEQ ID NO 1607.

DE Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;

XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;

KW gene therapy; transgenic; ss.

XX Homo sapiens.

XX EF1239051-A2.

PN 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

XX 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.

PR 23-MAY-2001; 2001US-00864761.

PR 10-OCT-2001; 2001US-0328205P.

XX (ABOM-) AEOMICA INC.

PA

xx Shannon M;

PI WPI; 2002-684061/74.

DR Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide. POSHL

XX -1, useful for treating disorders associated with decreased expression or

PT activity of human POSHL1.

XX Example 2; SEQ ID NO 1607; 60pp + Sequence Listing; English.

PS The invention relates to an isolated SH3 domain (POSH)-like signalling

CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino

CC acids (S1, AB83999), a sequence having 65% sequence identity to (S1),

CC (S1) having 95% deviations, especially conservative substitutions or a

CC fragment of the sequences comprising at least 8 contiguous amino acids.

CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an

CC adaptor protein that interacts with Rho family small GTPases as well as

CC downstream components of the signal transduction pathway. (I) is useful

CC for identifying a specific binding partner. (I) and nucleic acids (II)

CC encoding (I) are useful for diagnosing, monitoring disease and treating

CC caused by altered expression of human POSHL1 including diagnosing and

CC treating cancer, they are useful in the development of vaccines and (II) is

CC useful in gene therapy. (II) is useful for constructing microarrays which

CC are useful for measuring and for surveying gene expression and creating

CC transgenic non-human animals capable of producing the proteins. The

CC present sequence is that of a scanning oligonucleotide useful in examples

CC of the invention. Note: The present sequence did not form part of the

CC printed specification, but is based on sequence information supplied to

CC Derwent by the European Patent Office

xx Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

SQ Query Match 8.5%; Score 11.8; DB 1; Length 17;

Best Local Similarity 86.7%; Pred. No. 3.9e+02; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 2;

QY 1673 GGAAACCCCTGGTCTCT 1687

Db 2 GGAGCCCTGGTCTCT 16

RESULT 382

ABV91048/c

ID ABV91048 standard; DNA; 17 BP.

XX AC ABV91048;

XX 23-DEC-2002 (first entry)

DT Human POSHL1 scanning oligonucleotide SEQ ID NO 1761.

DE Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;

XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;

KW gene therapy; transgenic; ss.

XX Homo sapiens.

XX EF1239051-A2.

PN 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

XX 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.

PR 23-MAY-2001; 2001US-00864761.

PR 23-MAY-2001; 2001US-00864761.

PR

```

PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
PA Shannon M;
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 1761; 60pp + Sequence Listing; English.
PS
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
XX Sequence 17 BP; 5 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1751 TATCCTAAAGGCCCA 1765
Db | ||||| |||||
16 TGTCTAAAGTCCCA 2

RESULT 383
ABV91047/c
XX ID ABV91047 standard; DNA; 17 BP.
XX AC ABV91047;
XX
XX 23-DEC-2002 (first entry)
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1760.
XX
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
XX Homo sapiens.
XX OS
XX EPI239051-A2.
XX PN
XX 11-SEP-2002.
XX PD
XX
XX 28-JAN-2002; 2002EP-00001165.
XX PF
XX
XX 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR

```

```

PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 1760; 60pp + Sequence Listing; English.
PS
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
XX Sequence 17 BP; 4 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1751 TATCCTAAAGGCCCA 1765
Db | ||||| |||||
17 TGTCTAAAGTCCCA 3

RESULT 384
ACCS2599
XX ID ACCS2599 standard; DNA; 17 BP.
XX AC ACCS2599;
XX
XX 27-JUN-2003 (first entry)
XX DT
XX DE Human tumour suppressor sequence #1366.
XX
XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX
XX Homo sapiens.
XX OS
XX FR2826373-A1.
XX PN
XX 27-DEC-2002.
XX PD
XX
XX 20-JUN-2001; 2001FR-00008139.
XX PF
XX
XX 20-JUN-2001; 2001FR-00008139.
XX PR
XX (MOLE-) MOLECULAR ENGINES LAB SA.
XX PA

```

XX Tuijnder M, Telerman A, Amson R;  
PI WPI; 2003-250498/25.  
XX New nucleic acid sequences associated with tumor suppression, regression,  
PT apoptosis or virus resistance are useful to diagnose and treat viral  
PT disease, development of tumor cells and cell degeneration.  
XX Claim 1; Page 356; 798pp; French.  
XX This sequence represents an isolated nucleic acid sequence associated  
CC with tumor suppression or regression, apoptosis or virus resistance. The  
CC invention relates to these sequences or sequences having at least 80%  
CC identity to them, and polypeptides encoded by the sequences or  
CC polypeptides having 80% identity to the polypeptide sequences. The  
CC invention is used to diagnose or treat viral disease or disease  
CC characterized by development of tumor cells or cellular degeneration  
XX  
XX Sequence 17 BP; 3 A; 8 C; 2 G; 4 T; 0 U; 0 Other;  
SQ Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1735 GCTCCCAACTCTCTCC 1749  
DB 1 GATCCCAACTGCTCC 15  
RESULT 385  
ABT40179  
ID ABT40179 standard; DNA; 17 BP.  
XX AC ABT40179;  
XX 13-JUN-2003 (first entry)  
XX Tumour suppression related human fukutin oligo SEQ ID No 5816.  
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; protein chip; gene therapy; tumour suppression;  
KW human fukutin; ds.  
XX Homo sapiens.  
XX WO2003025175-A2.  
XX 27-MAR-2003.  
XX 17-SEP-2002; 2002WO-IB004208.  
XX 17-SEP-2001; 2001FR-00011978.  
XX (MOLE-) MOLECULAR ENGINES LAB.  
XX Telerman A, Amson R, Tuijnder M;  
XX WPI; 2003-313353/30.  
XX New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX Disclosure; Page 713; 720pp; French.  
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,  
CC given in the specification, a sequence containing at least 15 consecutive  
CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
CC hybridizes to them under highly stringent conditions, or the complement  
CC of any of them, or the corresponding RNA. The novel isolated nucleic  
CC acid, of any of them, or the corresponding RNA. The novel isolated nucleic  
XX acids of the invention are useful as probes and primers for detecting,  
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
XX component of a gene chip, in vitro as (anti)sense reagents, and for  
XX production of recombinant polypeptides. Any of the nucleic acids,  
XX polypeptides, vectors containing the nucleic acids, cells containing the  
XX vector or antibodies directed against the polypeptides are useful for  
XX preparation of pharmaceuticals for prevention and/or treatment of viral  
XX diseases that are characterised by development of tumours or cell  
XX degeneration, specifically cancer but also Alzheimer's disease and  
XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
XX patient samples is useful for diagnosis and/or prognosis of these  
XX diseases. The polypeptides can also be used to generate antibodies, and  
XX both the polypeptide and antibodies are useful as components of protein  
XX chips. The nucleic acid sequences of the invention can be used in gene  
XX therapy. This polynucleotide sequence represents a tumour suppression  
XX related human fukutin oligonucleotide of the invention  
SQ Sequence 17 BP; 3 A; 8 C; 2 G; 4 T; 0 U; 0 Other;  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1735 GCTCCCAACTCTCTCC 1749  
DB 1 GATCCCAACTGCTCC 15  
RESULT 386  
ABT40171  
ID ABT40171 standard; DNA; 17 BP.  
XX AC ABT40171;  
XX 13-JUN-2003 (first entry)  
XX Tumour suppression related human fukutin oligo SEQ ID No 5808.  
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; protein chip; gene therapy; tumour suppression;  
KW human fukutin; ds.  
XX Homo sapiens.  
XX WO2003025175-A2.  
XX 27-MAR-2003.  
XX 17-SEP-2002; 2002WO-IB004208.  
XX 17-SEP-2001; 2001FR-00011978.  
XX (MOLE-) MOLECULAR ENGINES LAB.  
XX Telerman A, Amson R, Tuijnder M;  
XX WPI; 2003-313353/30.  
XX New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX Disclosure; Page 713; 720pp; French.  
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,  
CC given in the specification, a sequence containing at least 15 consecutive  
CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
CC hybridizes to them under highly stringent conditions, or the complement  
CC of any of them, or the corresponding RNA. The novel isolated nucleic  
CC acid, of any of them, or the corresponding RNA. The novel isolated nucleic

CC component of a gene chip, in vitro as (anti)sense reagents, and for  
 CC production of recombinant polypeptides. Any of the nucleic acids,  
 CC polypeptides, vectors containing the nucleic acids, cells containing the  
 CC vector or antibodies directed against the polypeptides are useful for  
 CC preparation of pharmaceuticals for prevention and/or treatment of viral  
 CC diseases that are characterised by development of tumours or cell  
 CC degeneration, specifically cancer but also Alzheimer's disease and  
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
 CC patient samples is useful for diagnosis and/or prognosis of these  
 CC diseases. The polypeptides can also be used to generate antibodies, and  
 CC both the polypeptide and antibodies are useful as components of protein  
 CC chips. The nucleic acid sequences of the invention can be used in gene  
 CC therapy. This polynucleotide sequence represents a tumour suppression  
 CC related human fukutin oligonucleotide of the invention  
 CC  
 XX Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e-02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1735 GCTCCCACTCTCTCC 1749  
 | | | | | | | | | |  
 Db 1 GATCCCACTCTCTCC 15  
 RESULT 387  
 ID ABT36364/C  
 AC ABT36364 standard; DNA; 17 BP.  
 XX ABT36364;  
 DT 12-JUN-2003 (first entry)  
 DE Tumour suppression related human fukutin oligo SEQ ID No 2001.  
 KW Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; gene chip;  
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrenia; protein chip; gene therapy; tumour suppression;  
 KW human fukutin; ds.  
 XX Homo sapiens.  
 OS  
 PN WO2003025175-A2.  
 XX 27-MAR-2003.  
 PD  
 XX 17-SEP-2002; 2002WO-IB004208.  
 PF  
 XX 17-SEP-2001; 2001FR-00011978.  
 PR  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 PA  
 XX Telerman A, Amson R, Tuijnder M;  
 PI WPI; 2003-313353/30.  
 XX  
 DR New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 PT  
 XX Disclosure; Page 267; 720pp; French.  
 PS  
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,  
 CC given in the specification, a sequence containing at least 15 consecutive  
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
 CC hybridizes to them under highly stringent conditions, or the complement  
 CC of any of them, or the corresponding RNA. The novel isolated nucleic  
 CC acids of the invention are useful as probes and primers for detecting,  
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
 CC component of a gene chip, in vitro as (anti)sense reagents, and for  
 CC production of recombinant polypeptides. Any of the nucleic acids,  
 CC vector or antibodies directed against the polypeptides are useful for

CC polypeptides, vectors containing the nucleic acids, cells containing the  
 CC vector or antibodies directed against the polypeptides are useful for  
 CC preparation of pharmaceuticals for prevention and/or treatment of viral  
 CC diseases that are characterised by development of tumours or cell  
 CC degeneration, specifically cancer but also Alzheimer's disease and  
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
 CC patient samples is useful for diagnosis and/or prognosis of these  
 CC diseases. The polypeptides can also be used to generate antibodies, and  
 CC both the polypeptide and antibodies are useful as components of protein  
 CC chips. The nucleic acid sequences of the invention can be used in gene  
 CC therapy. This polynucleotide sequence represents a tumour suppression  
 CC related human fukutin oligonucleotide of the invention  
 CC  
 XX Sequence 17 BP; 2 A; 7 C; 1 G; 7 T; 0 U; 0 Other;  
 SQ

Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e-02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1712 TAGGAGTAGGAGAT 1726  
 | | | | | | | | | |  
 Db 16 TAGGAGGAGGAGAT 2

RESULT 388  
 ID ABT38111/C  
 AC ABT38111 standard; DNA; 17 BP.  
 XX ABT38111;  
 DT 12-JUN-2003 (first entry)  
 DE Tumour suppression related human fukutin oligo SEQ ID No 3748.

KW Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; gene chip;  
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrenia; protein chip; gene therapy; tumour suppression;  
 KW human fukutin; ds.  
 XX Homo sapiens.  
 OS  
 PN WO2003025175-A2.  
 XX 27-MAR-2003.  
 PD  
 XX 17-SEP-2002; 2002WO-IB004208.  
 PF  
 XX 17-SEP-2001; 2001FR-00011978.  
 PR  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 PA  
 XX Telerman A, Amson R, Tuijnder M;  
 PI WPI; 2003-313353/30.  
 XX

PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.

PS Disclosure; Page 472; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,  
 CC given in the specification, a sequence containing at least 15 consecutive  
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
 CC hybridizes to them under highly stringent conditions, or the complement  
 CC of any of them, or the corresponding RNA. The novel isolated nucleic  
 CC acids of the invention are useful as probes and primers for detecting,  
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
 CC component of a gene chip, in vitro as (anti)sense reagents, and for  
 CC production of recombinant polypeptides. Any of the nucleic acids,  
 CC polypeptides, vectors containing the nucleic acids, cells containing the  
 CC vector or antibodies directed against the polypeptides are useful for

preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention

SQ	Sequence	17 BP; 5 A; 6 C; 1 G; 5 T; 0 U; 0 Other;
Query Match	8.5%;	Score 11.8; DB 1; Length 17;
Best Local Similarity	86.7%;	Pred. No. 3.9e+02;
Matches	13; Conservative	0; Mismatches 2; Indels 0; Gaps 0;

Qy		1702	GAACTTGGGTTAGGA	1716
Dd		17	GAGATGTGTTAGGA	3

RESULT 389	
ACA07737	
ID	ACA07737 standard; RNA; 17 BP.
XX	
XX	
AC	ACA07737;
XX	
XX	
DT	03-JUN-2003 (first entry)
XX	
XX	
DE	NFKB sub-unit modulating zincyme substrate #136.

XX	Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinyzyme;
KW	G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
KW	lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW	oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW	cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW	lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW	chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW	cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW	gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW	rheumatoid arthritis; stenosis; Crohn's disease; obesity; ischaemia;
KW	gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW	transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW	allergic rhinitis; inflammation. inflammatory bowel disease infection; ss.

XX	Homo sapiens.	
OS	US2002177568-A1.	
XX	28-NOV-2002.	
PN	23-MAY-2001; 2001US-00864785.	
XX	07-DEC-1992;	92US-00987132.
PR	18-MAY-1994;	94US-00245466.
PR	15-AUG-1994;	94US-00291932.
PR	23-DEC-1996;	96US-00777916.

PA (STIN/) STINCHOMB D T.  
PA (MCSW/) MCSWIGEN J.  
PA (DRAP/) DRAPER K G.  
XX  
pi Stinchcomb DT, Mcswiggen J, Draper KG;  
XX  
XX  
DR WPI: 2003-340953/32.

Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.

xx  
ps  
Claim 3: Page 39: 72pp: English.

The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFkB), where (I) is an inozyme, zynzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of the REL-A gene, in the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, stenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents the substrate of a novel enzymatic nucleic acid molecule

Sequence 17 BP: 2 A; 6 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 53.3%; Pred. No. 3.9e+02;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0

QY 1676 ACCCTGGTGTCCT 1690  
 ||| : ||| : ||| :  
 Db 3 ACCAUGGUGUUCCU 17

RESULT 390  
ADA99592/C  
ID ADA99592 standard; DNA; 17 Bp.  
XX  
XX  
AC  
ADA99592;  
XX  
XX  
DT  
20-NOV-2003 (first entry)  
XX  
XX  
DE Human MP23 scanning oligonucleotide SEQ ID 581.

XX	Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW	zinc finger protein; MD23; MD24; MD27; MD12; chromosome 7q22.1;
KW	zinc finger protein; MD23; MD24; MD27; MD12; chromosome 7q22.1; cancer;
KW	chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; developmental disorder; ss.

xx Homo sapiens.

PN EP1281758-A2.

PD 05-FEB-2003.

PF 30-JUL-2002; 2002EP-00016874.

PR 02-AUG-2001; 2001US-00922181.

PA (AEOM-) AEOMICA INC.

PI Shannon M, Gu Y, Nguyen C;

DR WPI; 2003-423107/40.

PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of  
MD23, MD24, MD27 or MN212, e.g. cancer.

Example 8: SEO ID NO 581; 103pp; English.

XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder,  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 17 BP; 3 A; 6 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1668 CAGCTGGACCTGG 1682  
 Db ||||||| |||||  
 16 CAGCTGGATGCTCTG 2  
 RESULT 391  
 ADA99303  
 ID ADA99303 standard; DNA; 17 BP.  
 AC ADA99303;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human MD23 scanning oligonucleotide SEQ ID 292.  
 XX  
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1281758-A2.  
 XX  
 PD 05-FEB-2003.  
 XX  
 PF 30-JUL-2002; 2002EP-00016874.  
 XX  
 PR 02-AUG-2001; 2001US-00922181.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Shannon M, Gu Y, Nguyen C;  
 XX  
 DR WPI; 2003-423107/40.  
 XX  
 PT New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. cancer.  
 XX  
 PS Example 8; SEQ ID NO 292; 103pp; English.  
 XX  
 CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder,  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX

CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 17 BP; 5 A; 6 C; 5 G; 1 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1668 CAGCTGGACCTGG 1682  
 Db ||||||| |||||  
 1 CAGCTGGACCCGAG 15  
 RESULT 392  
 ADA99591/c  
 ID ADA99591 standard; DNA; 17 BP.  
 XX  
 AC ADA99591;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human MD23 scanning oligonucleotide SEQ ID 580.  
 XX  
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1281758-A2.  
 XX  
 PD 05-FEB-2003.  
 XX  
 PF 30-JUL-2002; 2002EP-00016874.  
 XX  
 PR 02-AUG-2001; 2001US-00922181.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Shannon M, Gu Y, Nguyen C;  
 XX  
 DR WPI; 2003-423107/40.  
 XX  
 PT New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. cancer.  
 XX  
 PS Example 8; SEQ ID NO 580; 103pp; English.  
 XX  
 CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder,  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX

Mon Aug 30 09:26:45 2004

schultz139-3.rng

```
XX SQ Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGACCCCTGG 1682
Dbb ||||| ||||| |||||
2 CAGCTGGACCCCTGG 16

RESULT 394
ADA99301
ID ADA99301 standard; DNA; 17 BP.
XX ADA99301;
XX 20-NOV-2003 (first entry)
XX Human MDZ3 scanning oligonucleotide SEQ ID 290.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX Homo sapiens.
XX EP1281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX Example 8; SEQ ID NO 290; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX Sequence 17 BP; 3 A; 6 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 8.5%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGACCCCTGG 1682
Dbb ||||| ||||| |||||
3 CAGCTGGACCCCTGG 17

RESULT 395
ABZ64947/c
ID ABZ64947 standard; RNA; 17 BP.
XX
```



AC ABZ64947;  
 XX  
 DT 21-MAR-2003 (first entry)  
 XX  
 DE Human HER2 DNzyme substrate #404.  
 XX  
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
 KW anti-rheumatic; cancer; AIDS; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200297114-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 29-MAY-2002; 2002WO-US016840.  
 XX  
 PR 29-MAY-2001; 2001US-0294140P.  
 PR 06-JUN-2001; 2001US-0296249P.  
 PR 10-SEP-2001; 2001US-0318471P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Mcswiggen J;  
 XX  
 DR WPI; 2003-140484/13.  
 XX  
 PT Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
 XX  
 PS Claim 4; Page 140; 185pp; English.  
 XX  
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
 CC rheumatic activity. The nucleic acid molecules are useful for reducing  
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
 CC ribozymes of the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 7 C; 6 G; 0 T; 2 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1660 CAGGCTCACAGCTGG 1674  
 DB 15 CCGGCGCACAGCTGG 1  
 RESULT 396  
 ABZ65447  
 ID ABZ65447 standard; RNA; 17 BP.  
 XX  
 AC ABZ65447;  
 XX  
 DT 21-MAR-2003 (first entry)  
 XX  
 DE Human HER2 DNzyme substrate #904.  
 XX  
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
 KW anti-rheumatic; cancer; AIDS; ss.  
 XX  
 OS Homo sapiens.

XX WO200297114-A2.  
 PN  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 29-MAY-2002; 2002WO-US016840.  
 XX  
 PR 29-MAY-2001; 2001US-0294140P.  
 PR 06-JUN-2001; 2001US-0296249P.  
 PR 10-SEP-2001; 2001US-0318471P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Mcswiggen J;  
 XX  
 DR WPI; 2003-140484/13.  
 XX  
 PT Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
 XX  
 PS Claim 4; Page 150; 185pp; English.  
 XX  
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
 CC rheumatic activity. The nucleic acid molecules are useful for reducing  
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
 CC ribozymes of the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 6 C; 4 G; 0 T; 5 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1;  
 Best Local Similarity 53.3%; Pred. No. 3.9e+02;  
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 QY 1677 CCCTGGTGTCTCCNC 1691  
 DB 2 CCCTGAUGUGUCCUC 16  
 RESULT 397  
 ABZ64946/c  
 ID ABZ64946 standard; RNA; 17 BP.  
 XX  
 AC ABZ64946;  
 XX  
 DT 21-MAR-2003 (first entry)  
 XX  
 DE Human HER2 DNzyme substrate #403.  
 XX  
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
 KW anti-rheumatic; cancer; AIDS; ss.  
 OS Homo sapiens.  
 XX  
 FN WO200297114-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 29-MAY-2002; 2002WO-US016840.  
 XX  
 PR 29-MAY-2001; 2001US-0294140P.  
 PR 06-JUN-2001; 2001US-0296249P.  
 PR 10-SEP-2001; 2001US-0318471P.  
 XX

PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J;  
XX  
XX WPI; 2003-140484/13.  
DR  
XX Novel short interfering RNA and enzymatic nucleic acid useful for  
XX treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
PT  
XX  
XX Claim 4; Page 140; 185pp; English.  
PS  
XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
XX acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
CC rheumatic activity. The nucleic acid molecules are useful for reducing  
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
CC ribozymes of the invention  
XX  
XX Sequence 17 BP; 2 A; 8 C; 5 G; 0 T; 2 U; 0 Other;  
SQ  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1660 CAGGCTCACAGCTGG 1674  
DB 17 CGGGCGCACAGCTGG 3  
RESULT 398  
ABZ64792/c  
ID ABZ64792 standard; RNA; 17 BP.  
XX  
XX ABZ64792;  
AC  
XX 21-MAR-2003 (first entry)  
DT  
DE Human HER2 DNzyme substrate #249.  
XX  
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
KW anti-rheumatic; cancer; AIDS; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200297114-A2.  
PN  
XX 05-DEC-2002.  
PD  
XX 29-MAY-2002; 2002WO-US016840.  
PF  
XX 29-MAY-2001; 2001US-0294140P.  
PR  
XX 06-JUN-2001; 2001US-0296249P.  
PR  
XX 10-SEP-2001; 2001US-0318471P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
XX Mcswiggen J;  
PI  
XX WPI; 2003-140484/13.  
DR  
XX Novel short interfering RNA and enzymatic nucleic acid useful for  
XX treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
PT  
XX  
XX Claim 4; Page 137; 185pp; English.  
PS  
XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
XX acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
CC rheumatic activity. The nucleic acid molecules are useful for reducing  
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
CC ribozymes of the invention  
XX  
XX Sequence 17 BP; 2 A; 6 C; 5 G; 0 T; 4 U; 0 Other;  
SQ  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1660 CAGGCTCACAGCTGG 1674  
DB 15 CAGTCACACAGCTGG 1  
RESULT 399  
ABZ64791/c  
ID ABZ64791 standard; RNA; 17 BP.  
XX  
XX ABZ64791;  
AC  
XX 21-MAR-2003 (first entry)  
DT  
DE Human HER2 DNzyme substrate #248.  
XX  
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
KW anti-rheumatic; cancer; AIDS; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200297114-A2.  
PN  
XX 05-DEC-2002.  
PD  
XX 29-MAY-2002; 2002WO-US016840.  
PF  
XX 29-MAY-2001; 2001US-0294140P.  
PR  
XX 06-JUN-2001; 2001US-0296249P.  
PR  
XX 10-SEP-2001; 2001US-0318471P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
XX Mcswiggen J;  
PI  
XX WPI; 2003-140484/13.  
DR  
XX Novel short interfering RNA and enzymatic nucleic acid useful for  
XX treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
PT  
XX  
XX Claim 4; Page 137; 185pp; English.  
PS  
XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
XX acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
CC rheumatic activity. The nucleic acid molecules are useful for reducing  
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
CC ribozymes of the invention

CC AB266530 - AB266585 represent substrate/target sequences for the human  
 CC ribozymes of the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 6 G; 0 T; 4 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1660 CAGGCTCACAGCTGG 1674  
 |||||  
 Db 17 CAGTCACACAGCTGG 3  
 RESULT 400  
 ACD62967/c  
 ID ACD62967 standard; RNA; 17 BP.  
 XX  
 AC ACD62967;  
 XX  
 DT 24-SEP-2003 (first entry)  
 XX  
 DE HCV minus strand DNazyme substrate sequence #830.  
 XX  
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX  
 DR WPI; 2003-229207/22.  
 XX  
 PT Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 PS Claim 1; Page 289; 387pp; English.  
 XX  
 CC The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed

CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNazyme or minus strand DNazyme sequences disclosed in the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 5 A; 8 C; 1 G; 0 T; 3 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1631 GCATGGGGCTTTGTAG 1645  
 |||||  
 Db 15 GGAAGGTGCTTTGTAG 1  
 RESULT 401  
 ACD52213  
 ID ACD52213 standard; RNA; 17 BP.  
 XX  
 AC ACD52213;  
 XX  
 DT 24-SEP-2003 (first entry)  
 XX  
 DE HBV inozyme substrate sequence #292.  
 XX  
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis B virus.  
 XX  
 PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX  
 DR WPI; 2003-229207/22.

PT Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX Example 1; Page 155; 387pp; English.  
XX The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HBV  
CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberyzyme sequences  
CC disclosed in the present invention  
XX Sequence 17 BP; 2 A; 4 C; 5 G; 0 T; 6 U; 0 Other;  
XX  
XX Query Match 8.5%; Score 11.8; DB 1; Length 17;  
XX Best Local Similarity 60.0%; Pred. No. 3.9e+02;  
XX Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 1672 TGGAACTCCCTGGTGC 1696  
DB 3 UGACACCUUGUGUC 17  
XX  
XX RESULT 402  
XX ACDS9647  
XX ID ACDS9647 standard; RNA; 17 BP.  
XX AC ACDS9647;  
XX DT 24-SEP-2003 (first entry)  
XX DE HCV DNazyme substrate sequence #1449.  
XX  
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
XX RNA stability; RNA expression; RNA synthesis; antisense;  
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
XX amberyzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
XX HBV reverse transcriptase; Enhancer I region; viral replication;  
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
XX virucide; antiinflammatory; substrate; ss.  
XX  
XX Hepatitis C virus.  
XX  
XX WO200281494-A1.  
XX PD 17-OCT-2002.  
XX  
XX 26-MAR-2002; 2002WO-US009187.  
XX  
XX 26-MAR-2001; 2001US-00817879.  
XX 08-JUN-2001; 2001US-00877478.  
XX 08-JUN-2001; 2001US-0296876P.  
XX 24-OCT-2001; 2001US-0335059P.  
XX 05-DEC-2001; 2001US-0337055P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
XX (MACE/) MACEJAK D.  
XX (MCSW/) MCSWIGGEN J.

PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
XX Draper K, Roberts E;  
XX WPI; 2003-229207/22.  
XX  
XX Novel compound useful for treating cirrhosis, liver failure,  
XX hepatocellular carcinoma, or condition associated with hepatitis C virus  
XX infection.  
XX Claim 1; Page 259; 387pp; English.  
XX  
XX The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HCV  
CC DNazyme or minus strand DNazyme sequences disclosed in the present  
XX invention  
XX Sequence 17 BP; 4 A; 1 C; 8 G; 0 T; 4 U; 0 Other;  
XX  
XX Query Match 8.5%; Score 11.8; DB 1; Length 17;  
XX Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
XX Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 1631 GGATGGGCTTGTAG 1645  
DB 2 GGNAGGUGUUGUAG 16  
XX  
XX RESULT 403  
XX ACDS9666/c  
XX ID ACDS9666 standard; RNA; 17 BP.  
XX AC ACDS9666;  
XX DT 24-SEP-2003 (first entry)  
XX DE HCV minus strand DNazyme substrate sequence #829.  
XX  
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
XX RNA stability; RNA expression; RNA synthesis; antisense;  
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
XX amberyzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
XX HBV reverse transcriptase; Enhancer I region; viral replication;  
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
XX virucide; antiinflammatory; substrate; ss.  
XX  
XX Hepatitis C virus.  
XX  
XX WO200281494-A1.  
XX PD 17-OCT-2002.  
XX  
XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEPP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX WPI; 2003-229207/22.  
 XX Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 PS Claim 1; Page 289; 387pp; English.  
 XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNazyme or minus strand DNazyme sequences disclosed in the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 4 A; 7 C; 2 G; 0 T; 4 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1631 GGATGGGCTGTAG 1645  
 Db 17 GGAAGTGCTGTAG 3  
 RESULT 404  
 ACC65896/C  
 ID ACC65896 standard; DNA; 17 BP.  
 AC ACC65896;  
 XX  
 DT 01-JUL-2003 (first entry)  
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 3143.  
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrania; ss.  
 XX

OS Mus musculus.  
 XX WO2003025176-A2.  
 XX 27-MAR-2003.  
 XX 17-SEP-2002; 2002WO-IB004210.  
 XX 17-SEP-2001; 2001FR-00011979.  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 XX Telerman A, Amson R, Tuijnder M;  
 XX WPI; 2003-333167/31.  
 XX New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 PS Disclosure; Page 398; 738pp; French.  
 XX The present invention relates to murine oligonucleotides (ACC62754-  
 CC ACC68806), which are associated with tumour suppression, tumour  
 CC reversion, apoptosis and virus resistance. The oligonucleotides are  
 CC useful as (1) as probes and primers for detecting, identifying,  
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a  
 CC recombinant polypeptides. The oligonucleotides are useful for preparation  
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrania  
 XX  
 SQ Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1663 GCTCACAGCTGGAAC 1677  
 Db 15 GCTCACAGTTGGATC 1  
 RESULT 405  
 ACC67445  
 ID ACC67445 standard; DNA; 17 BP.  
 AC ACC67445;  
 XX  
 DT 01-JUL-2003 (first entry)  
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 4692.  
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrania; ss.  
 XX Mus musculus.  
 XX WO2003025176-A2.  
 XX 27-MAR-2003.  
 XX 17-SEP-2002; 2002WO-IB004210.  
 XX 17-SEP-2001; 2001FR-00011979.  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 XX Telerman A, Amson R, Tuijnder M;  
 XX

CC recombinant polypeptides. The oligonucleotides are useful for preparation  
CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
CC are characterised by development of tumours or cell degeneration,  
CC specifically cancer but also Alzheimer's disease and schizophrenia  
XX  
SQ Sequence 17 BP; 6 A; 5 C; 2 G; 4 T; 0 U; 0 Other;  
  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1724 GATGAGATTGGCTC 1738  
Db 15 GATGAGATTGGATC 1  
|||||  
  
RESULT 407  
ACC63888/c  
ID ACC63888 standard; DNA; 17 BP.  
XX  
AC ACC63888;  
XX  
DT 01-JUL-2003 (first entry)  
XX  
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 1135.  
XX  
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; ss.  
XX  
OS Mus musculus.  
XX  
PN WO2003025176-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 17-SEP-2002; 2002WO-IB004210.  
XX  
PR 17-SEP-2001; 2001FR-00011979.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
PI Telerman A, Amson R, Tuijnder M;  
XX  
XX WPI; 2003-333167/31.  
XX  
PT New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
PS Disclosure; Page 163; 738pp; French.  
XX  
CC The present invention relates to murine oligonucleotides (ACC62754-  
CC ACC68806), which are associated with tumour suppression, tumour  
CC reversion, apoptosis and virus resistance. The oligonucleotides are  
CC useful as (1) as probes and primers for detecting, identifying,  
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a  
CC recombinant polypeptides. The oligonucleotides are useful for preparation  
CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
CC are characterised by development of tumours or cell degeneration,  
CC specifically cancer but also Alzheimer's disease and schizophrenia  
XX  
SQ Sequence 17 BP; 6 A; 5 C; 2 G; 4 T; 0 U; 0 Other;  
  
Query Match 9.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1635 GGGGCTTGTCAGCA 1649  
Db 17 GGGGTTTGTATCAGA 3  
|||||

DR WPI; 2003-333167/31.  
XX  
PT New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
PS Disclosure; Page 579; 738pp; French.  
XX  
CC The present invention relates to murine oligonucleotides (ACC62754-  
CC ACC68806), which are associated with tumour suppression, tumour  
CC reversion, apoptosis and virus resistance. The oligonucleotides are  
CC useful as (1) as probes and primers for detecting, identifying,  
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a  
CC recombinant polypeptides. The oligonucleotides are useful for preparation  
CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
CC are characterised by development of tumours or cell degeneration,  
CC specifically cancer but also Alzheimer's disease and schizophrenia  
XX  
SQ Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;  
  
Query Match 8.5%; Score 11.8; DB 1; Length 17;  
Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1687 TCCTCCAGCGTGTG 1701  
Db 3 TCCTCTCGGTGTG 17  
|||||  
  
RESULT 406  
ACC63689/c  
ID ACC63689 standard; DNA; 17 BP.  
XX  
AC ACC63689;  
XX  
DT 01-JUL-2003 (first entry)  
XX  
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 936.  
XX  
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; ss.  
XX  
OS Mus musculus.  
XX  
PN WO2003025176-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 17-SEP-2002; 2002WO-IB004210.  
XX  
PR 17-SEP-2001; 2001FR-00011979.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
PI Telerman A, Amson R, Tuijnder M;  
XX  
XX WPI; 2003-333167/31.  
XX  
PT New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
PS Disclosure; Page 140; 738pp; French.  
XX  
CC The present invention relates to murine oligonucleotides (ACC62754-  
CC ACC68806), which are associated with tumour suppression, tumour  
CC reversion, apoptosis and virus resistance. The oligonucleotides are  
CC useful as (1) as probes and primers for detecting, identifying,  
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a

RESULT 408  
ABX04768  
ID ABX04768 standard; DNA; 17 BP.  
XX  
XX AC ABX04768;  
XX  
XX DT 15-JAN-2003 (first entry)  
XX  
XX Thymidine kinase (TK) mutant associated oligonucleotide #4.  
XX  
XX Herpesviridae; thymidine kinase; TK; DRH nucleoside binding region;  
KW viral inhibitor; bacterial inhibitor; parvovirus inhibitor; tumour;  
KW autoreactive immune cell; cancer; hyperkeratosis; psoriasis;  
KW prostate hypertrophy; hyperthyroidism; endocrinopathy; allergy;  
KW autoimmune disease; restenosis; viral disease; AIDS; hepatitis; HCV; HBV;  
KW acquired immunodeficiency syndrome; intracellular parasitic disease;  
KW gene therapy; adenosine deaminase deficiency; Alzheimer's disease; ss.  
XX  
XX OS Synthetic.  
XX  
XX US6451571-B1.  
XX  
XX PN 17-SEP-2002.  
XX  
XX PD 17-SEP-2002.  
XX  
XX PF 17-MAR-1999; 99US-00270956.  
XX  
XX PR 02-MAY-1994; 94US-00237592.  
XX  
XX PR 02-MAY-1995; 95US-00432871.  
XX  
XX PR 02-NOV-1995; 95US-00522304.  
XX  
XX PA (UNIW ) UNIV WASHINGTON.  
XX  
XX PI Loeb LA, Black ME;  
XX  
XX WPI; 2003-045581/04.  
XX  
XX Novel Herpesviridae thymidine kinase mutant useful for inhibiting  
PT pathogens e.g. viruses, bacteria, tumor in animals, has one or more  
PT mutations encoding amino acid substitutions upstream from the DRH  
PT nucleoside binding site.  
XX  
XX Example 1; Col 21; 78pp; English.  
XX  
XX The invention describes an isolated Herpesviridae thymidine kinase (TK)  
CC comprising a 12 amino acid (aa) nucleoside binding region having a site 3  
CC made up of a DRH nucleoside binding site and a site 4 and mutation(s), at  
CC least one of the mutations being an aa substitution 2 or 3 aa upstream or  
CC 5 or more aa downstream from the DRH motif that increases a biological  
CC activity, preferably ability of TK to phosphorylate a nucleoside  
CC analogue, as compared to unmutated TK. TK mutants are useful for  
CC inhibiting a pathogenic agent such as viruses, bacteria, parasites,  
CC tumour cells or autoreactive immune cells in a warm-blooded animal. TK  
CC mutant is useful for inhibiting a tumour or cancer in a warm-blooded  
CC animal, for treating a variety of disease e.g., hyperkeratosis  
CC (psoriasis), prostate hypertrophy, hyperthyroidism, endocrinopathies,  
CC autoimmune diseases, allergies, restenosis, viral diseases such as  
CC acquired immunodeficiency syndrome (AIDS) hepatitis (HCV or HBV),  
CC intracellular parasitic diseases, and to correct aberrant expression of a  
CC gene within a cell, or to replace a specific gene which is defective in  
CC proper expression using gene therapy, e.g. including adenosine deaminase  
CC deficiency, and Alzheimer's diseases. The mutants are utilised as a  
CC conditionally lethal marker for homologous recombination. This sequence  
CC represents an oligonucleotide used in the creation of thymidine kinase  
XX mutants  
XX  
XX Sequence 17 BP; 2 A; 9 C; 4 G; 2 T; 0 U; 0 Other;  
XX  
XX Query Match 8.5%; Score 11.8; DB 1; Length 17;  
XX Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1686 CTCTCCAGCGTGGT 1700  
Db | | | | | | | | | |  
1 CCCCTCCAGCGGT 15  
RESULT 409  
ADC37712  
ID ADC37712 standard; DNA; 17 BP.  
XX  
XX AC ADC37712;  
XX  
XX DT 18-DEC-2003 (first entry)  
XX  
XX Human AMLP1a scanning 17-mer oligonucleotide SEQ ID NO:61.  
DE human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;  
KW AMLP1a; ss.  
XX  
XX OS Synthetic.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO2003037931-A2.  
XX  
XX PD 08-MAY-2003.  
XX  
XX PF 01-NOV-2002; 2002WO-US035129.  
XX  
XX PR 01-NOV-2001; 2001US-0334773P.  
XX  
XX PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.  
XX  
XX PI Shannon M, Phan T;  
XX  
XX WPI; 2003-430501/40.  
XX  
XX New isolated nucleic acid molecule encoding a human angiominotin-like  
PT protein, useful for treating or preventing a disorder associated with  
PT decreased or increased expression or activity of AMLP1.  
XX  
XX Example 2; SEQ ID NO 61; 172pp; English.  
XX  
XX The present invention describes the human angiominotin-like protein 1  
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene  
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and  
CC compositions of the present invention can be used for treating or  
CC preventing a disorder associated with decreased or increased expression  
CC or activity of AMLP1. The present sequence represents a scanning  
CC oligonucleotide for human AMLP1a, which is used in an example from the  
XX present invention.  
XX  
XX Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 8.5%; Score 11.8; DB 1; Length 17;  
XX Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1716 AGTACGAGATGGAG 1730  
Db | | | | | | | | | |  
3 AATACGATGGAG 17  
RESULT 410  
AAQ20431  
ID AAQ20431 standard; DNA; 18 BP.  
XX  
XX AC AAQ20431;  
XX  
XX DT 07-APR-1992 (first entry)  
XX  
XX DE Debrisoquine polymorphism PCR primer.  
XX  
XX KW Polymerase chain reaction; ss.  
XX

PS Disclosure; Fig 7C-2; 1C4pp; English.

XX The method aims to provide a collection of highly reproducible

CC microsatellite marker sequences (MMS) at approx. 10-50 cm intervals

CC throughout the human genome which can be detectably labelled. The MSS are

CC polymorphic, simple sequence repeats and can be used in automated

CC genotyping, esp. fluorescence-based. The primers correspond to the unique

CC DNA sequence surrounding each marker, and PCR is used to detect each

CC polymorphism. When the MSS show considerable polymorphism (ie. a

CC difference in the number of repeats) between individuals, the markers can

CC be particularly informative. The MSS can be ideal for linkage studies.

CC Kits comprise at least 4 groups, of at least 3 sets, each comprising

CC labelled primers for PCR amplification of the DNA. Group 3 primer pairs

CC are shown in AA095417-454. The published size range of the DIS243 allele

CC is 142-170 bp, and the degree of heterozygosity in the population is

CC about 87%

XX Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

SQ

Query Match 8.5%; Score 11.8; DB 1; Length 18;

Best Local Similarity 86.7%; Pred. NO. 4.2e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1689 CTCACGCTGGTGGG 1703

Db 2 CTCACGCTGGTGGG 16

RESULT 412

AAV49520/c

ID AAV49520 standard; DNA; 18 BP.

XX

AC AAV49520;

XX

DT 20-OCT-1998 (first entry)

XX

DE Mycobacterium sp. AlAdE oligonucleotide AlAdH-R2.

XX

KW Alanine dehydrogenase; AlAdH; ADH; diagnosis; tuberculosis; pathogen;

KW swimmers disease; vaccine; epidemic; infection; identification; ss.

XX

OS Synthetic.

OS Mycobacterium sp.

PN WO9832862-A2.

XX

PD 30-JUL-1998.

XX

PF 29-JAN-1998; 98WO-EP000484.

XX

PR 29-JAN-1997; 97EP-00101339.

XX

PA (FLOH/) FLOHE L.

XX

PI Flohe L, Singh M, Hunter B, Kolk A;

XX

XX WPI; 1998-427958/36.

XX

PT Nucleic acid encoding alanine dehydrogenase of Mycobacterium marinum -

PT used for diagnosis of tuberculosis and other mycobacterial diseases, also

PT for treatment and prevention, for drug screening and for bio-

PT transformation.

XX

PS Disclosure; Page 10; 57pp; German.

XX

CC AAV49512-V49526 are oligonucleotides used in a method to isolate an

CC alanine dehydrogenase (ADH) protein from a Mycobacterium sp. This protein

CC is used to diagnose tuberculosis and other mycobacterial infections

CC (including 'swimmers' disease', caused by M. marinum, a fish pathogen) in

CC humans or animals. The protein can also be used for control of epidemics

CC and for vaccination, to screen for agents with anti-mycobacterial

CC activity, and in bio-transformations that are specific for L-alanine.

CC Also mycobacteria can be identified by analysis of genomic ADH sequences.

OS Synthetic.

XX

PN EP463395-A.

XX

PD 02-JAN-1992.

XX

PF 29-MAY-1991; 91EP-00108867.

XX

PR 22-JUN-1990; 90EP-00810467.

XX

PA (HOFF ) HOFFMANN-LA ROCHE AG.

XX

XX WPI; 1992-009068/02.

XX

PT New PCR primers for detecting poor metaboliser of drugs - useful to

PT highlight cases of debrisoquine, mephenytoin and acetylation-

PT polymorphism.

XX

PS Claim 11; Page 18; 31pp; English.

XX

CC The sequence is that of an oligonucleotide primer which is used in a

CC polymerase chain reaction (PCR) for the detection of normal and genes

CC coding for drug metabolising enzymes which allow the phenotyping of poor

CC metabolisers. Detection of debrisoquine polymorphism (CY2D6 gene -

CC encodes the P450IID6 enzyme) is possible using this primer. See also

CC AAQ20421-Q20436

XX

SQ Sequence 18 BP; 4 A; 6 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;

Best Local Similarity 86.7%; Pred. NO. 4.2e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1665 TCACAGCTGGAACCC 1679

Db 4 TCACAGCTGGAATCC 18

RESULT 411

AAQ95428

ID AAQ95428 standard; DNA; 18 BP.

XX

AC AAQ95428;

XX

DT 08-FEB-1996 (first entry)

XX

DE Primer B (Group 3, Set A) for marker DIS243, chromosome 1.

XX

KW primer; polymerase chain reaction; PCR; linkage study; locus;

KW microsatellite marker sequence; automated genotyping; allele;

KW polymorphism; detection; Homo sapiens; ss.

XX

OS Synthetic.

XX

PN WO9515400-A1.

XX

PD 08-JUN-1995.

XX

PF 05-DEC-1994; 94WO-US013945.

XX

PR 03-DEC-1993; 93US-00160837.

XX

PA (UVJO ) UNIV JOHNS HOPKINS.

XX

PI Levitt RC;

XX

XX WPI; 1995-215278/28.

XX

PT Kit for automated genotyping contg. pairs of PCR primers - designed to

PT amplify polymorphic nucleotide repeat sequences, arranged in sets each

PT with a characteristic fluorescence label, useful e.g. in detection of

PT disease related genetic rearrangement.

XX



therapy; diagnosis; ss.

XX Synthetic.  
 XX Key Location/Qualifiers  
 XX modified\_base 1..18  
 XX /\*tag= a  
 XX /note= "phosphorothioate linkages"  
 XX  
 XX WO9842722-A1.  
 XX 01-OCT-1998.  
 XX 20-MAR-1998; 98WO-US005651.  
 XX 21-MAR-1997; 97US-0041182P.  
 XX (HARD ) HARVARD COLLEGE.  
 XX Fett JW, Olson KA;  
 XX WPI; 1998-531944/45.  
 XX New oligo:nucleotide(s) that inhibit expression of angiogenin - for  
 XX treatment of tumours and metastases, or other conditions involving  
 XX abnormal angiogenesis.  
 XX Claim 10; Page 38; 71pp; English.  
 XX Antisense phosphorothioate oligonucleotide JF2S encompasses the AUG  
 XX initiation codon of the human angiogenin gene (see AAV60918). JF2S, and  
 XX other claimed antisense oligonucleotides (see AAV60912-17) with base  
 XX sequences complementary to a target region of the angiogenin gene, are  
 XX able to inhibit expression of angiogenin. They are used in claimed  
 XX methods to decrease production of angiogenin, particularly to reduce the  
 XX size of tumours associated with angiogenesis, to inhibit metastases,  
 XX establishment of tumour cells or growth of tumours and, when labelled, to  
 XX detect angiogenin for diagnosis of conditions associated with abnormal  
 XX angiogenesis. They can also be used to treat a wide range of non-cancer  
 XX conditions that involve angiogenesis, e.g. age-related macular  
 XX degeneration, diabetic retinopathy, bacterial or fungal ulcers,  
 XX rheumatoid arthritis, Paget's disease, Crohn's disease, haemangioma and  
 XX many others listed  
 XX Sequence 18 BP; 3 A; 9 C; 1 G; 5 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 18;  
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1722 GAGATGGAGATTGGC 1736  
 DB 15 GAGATGGTGTGGGC 1  
 |||||  
 RESULT 416  
 AAV60919  
 ID AAV60919 standard; DNA; 18 BP.  
 XX  
 XX AC AAV60919;  
 XX 11-JAN-1999 (first entry)  
 XX Angiogenin sense oligonucleotide JF1S.  
 XX Angiogenin; antisense; inhibitor; cancer; metastasis; angiogenesis;  
 XX therapy; diagnosis; ss.  
 XX Synthetic.  
 XX WO9842722-A1.  
 XX 01-OCT-1998.  
 XX

PF 20-MAR-1998; 98WO-US005651.  
 XX  
 XX 21-MAR-1997; 97US-0041182P.  
 XX (HARD ) HARVARD COLLEGE.  
 XX Fett JW, Olson KA;  
 XX WPI; 1998-531944/45.  
 XX New oligo:nucleotide(s) that inhibit expression of angiogenin - for  
 XX treatment of tumours and metastases, or other conditions involving  
 XX abnormal angiogenesis.  
 XX Example 4; Page 26; 71pp; English.  
 XX Sense oligonucleotide JF1S encompasses the AUG initiation codon of the  
 XX human angiogenin gene (see AAV60918). Its sequence is complementary to  
 XX claimed antisense phosphorothioate oligonucleotide JF2S. JF2S, and other  
 XX claimed antisense oligonucleotides (see AAV60912-17) with base sequences  
 XX complementary to target regions of the angiogenin gene, are able to  
 XX inhibit expression of angiogenin. JF1S is used as a control  
 XX oligonucleotide in experiments with these antisense sequences. The  
 XX antisense oligonucleotides are used in claimed methods to decrease  
 XX production of angiogenin, particularly to reduce the size of tumours  
 XX associated with angiogenesis, to inhibit metastases, establishment of  
 XX tumour cells or growth of tumours and, when labelled, to detect  
 XX angiogenin for diagnosis of conditions associated with abnormal  
 XX angiogenesis  
 XX Sequence 18 BP; 5 A; 1 C; 9 G; 3 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 18;  
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1722 GAGATGGAGATTGGC 1736  
 DB 4 GAGATGGTGTGGGC 18  
 |||||  
 RESULT 417  
 AAX86530  
 ID AAX86530 standard; DNA; 18 BP.  
 XX  
 XX AC AAX86530;  
 XX 04-OCT-1999 (first entry)  
 XX Primer rb21 used for amplification and sequencing of Rhd gene exons.  
 XX Allele; Rhesus D antigen; Rhd; weak D phenotype; blood transfusion;  
 XX PCR primer; ss.  
 XX Synthetic.  
 XX Homo sapiens.  
 XX WO9937763-A2.  
 XX 29-JUL-1999.  
 XX 18-DEC-1998; 98WO-EP008319.  
 XX 23-JAN-1998; 98EP-00101203.  
 XX (DRKB-) DRK BLUTSPENDEDIENST BADEN WUERTTEMBERG.  
 XX Flegel WA, Wagner FF;  
 XX WPI; 1999-469127/39.  
 XX Nucleic acid sequences correlated with Rhesus weak D phenotype, useful  
 XX for screening blood from donors and recipients for transfusion methods.  
 XX

XX  
XX  
XX Example; Page 33; 64pp; English.

CC PCR primers AAX86523-62 were used for amplification and sequencing of  
CC exons of the Rhesus D (RhD) antigen gene. The specification describes a  
CC RhD contributing to or indicative of the weak D phenotype, where the RhD  
CC polynucleotide carries at least one missense mutation as compared to the  
CC wild-type RhD, in its transmembrane and/or intracellular regions,  
CC especially in amino acid positions 2-16, 114-149, 179-225 or/and 267-397,  
CC with the proviso that the D antigen does not carry a single missense  
CC mutation leading to a F223V or T283I substitution. The probes and  
CC antibodies are useful in the methods for detection of weak D phenotypes.  
CC Red blood cells, from probands, are useful for the assessment of the  
CC affinity, avidity and/or reactivity of monoclonal anti-D antibodies.  
CC Polyclonal anti-D antisera or of anti-globulin or anti-human-globulin  
CC antisera. Detecting the presence of the RhD associated with weak D  
CC phenotype is useful for determining that a patient in need of a blood  
CC transfusion is to be transfused with RhD negative blood from a donor.  
CC Alternatively, testing for weak D phenotype RhD in the blood of a donor  
CC is useful for determining whether the donor blood should be excluded for  
CC transfusion to patients having wild type RhD or weak D types, other than  
CC that of the donor weak D type

XX  
XX  
XX SQ Sequence 18 BP; 3 A; 9 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;  
Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1681 GGTGTCCTCTCCAGC 1695  
||| |||||  
Db 2 GGTCCCTCTCCAGC 16

RESULT 418  
AAA74957/c  
ID AAA74957 standard; DNA; 18 BP.  
XX  
XX AC AAA74957;  
XX  
XX DT 02-JAN-2001 (first entry)  
XX  
XX DE PCR primer used to amplify a 316 bp fragment of murine VEGF-B gene.  
XX  
XX KW VEGF-B; vascular endothelial growth factor-B; heart abnormality;  
XX KW ischemia; atrioventricular conduction defect; myocardium; heart disease;  
XX KW PCR primer; ss.  
XX  
XX OS Mus sp.  
XX  
XX PN W0200052462-A1.  
XX  
XX PD 08-SEP-2000.  
XX  
XX PF 03-MAR-2000; 2000WO-US005465.  
XX  
XX PR 03-MAR-1999; 99US-0160083P.  
XX  
XX PA (LUDW-) LUDWIG INST CANCER RES.  
XX  
XX PI Aase K, Thoren P, Eriksson U;  
XX  
XX DR WPI; 2000-638114/61.  
XX  
XX PT Use of vascular endothelial growth factor B deficient animals for  
XX screening atrioventricular conduction or ischemia modulating compounds,  
XX and characterization of the biological roles of the growth factor.  
XX  
XX PS Example 4; Page 31; 58pp; English.  
XX  
XX CC PCR primers AAA74956-57 were used to amplify a 316 bp fragment from exons  
XX 3 and 4 of the VEGF (vascular endothelial growth factor)-B. The primers  
XX were used to analyse VEGF-B deficient transgenic mice. VEGF-B deficient

CC animals show heart abnormalities that appear to be caused by  
CC atrioventricular conduction defects and ischemia of the myocardium. The  
CC specification describes methods for screening a compound for  
CC atrioventricular conduction or ischemia modulating activity. The method  
CC comprises introducing the compound into a VEGF-B deficient non-human  
CC animal, and assaying the effect on atrioventricular conduction or  
CC ischemia. The methods are used for screening atrioventricular conduction  
CC or ischemia modulating compounds, treatment or alleviation of these  
CC conditions, diagnosis of heart disease characterized by loss of VEGF-B  
CC expression, and detecting or diagnosing VEGF-B deficiency in heart of a  
CC test subject

XX  
XX SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;  
Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1660 CAGGCTCACAGCTGG 1674  
||| |||||  
Db 17 CAGTCACACAGCTGG 3

RESULT 419  
AAZ65415  
ID AAZ65415 standard; DNA; 18 BP.  
XX  
XX AC AAZ65415;  
XX  
XX DT 10-APR-2000 (first entry)  
XX  
XX DE Human CD71 phosphorothioate antisense oligonucleotide SEQ ID NO:66.  
XX  
XX KW Human; CD71; transferrin receptor; antisense; phosphorothioate;  
XX KW antiproliferative; anticancer; anti-inflammatory; gene therapy; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX PN US6004814-A.  
XX  
XX PD 21-DEC-1999.  
XX  
XX PF 25-SEP-1998; 98US-00161244.  
XX  
XX PR 25-SEP-1998; 98US-00161244.  
XX  
XX PA (ISIS-) ISIS PHARM INC.  
XX  
XX PI Bennett CF, Cowser LM;  
XX  
XX DR WPI; 2000-105082/09.  
XX  
XX PT Antisense oligonucleotides targeted to genes encoding CD71, useful for  
XX preventing, diagnosing and treating inflammatory disorders and tumors.  
XX  
XX PS Claim 1; Col 27; 34pp; English.  
XX  
XX CC Sequences AAZ65357-Z65440 represent novel phosphorothioate antisense  
XX oligonucleotides targeted against the human CD71 gene, which encodes the  
XX CD71 transferrin receptor. Upon uptake in the small intestine, iron  
XX immediately combines with the ubiquitous serum protein transferrin, the  
XX primary vehicle by which iron is transported around the body. The uptake  
XX of circulating iron-transferrin complexes is mediated by the transferrin  
XX receptor, CD71. The requirement of both iron-transferrin complexes and  
XX CD71 for cell proliferation suggests that inhibition of iron utilisation  
XX could represent a strategy for the treatment of cancer. The  
XX oligonucleotides may be used in the treatment of an animal suspected of  
XX having a disease or disorder which can be treated by inhibition of CD71  
XX expression. Use of the antisense compounds and methods of the invention  
XX may also be useful prophylactically to prevent or delay infection,  
XX inflammation or tumour formation. The antisense compounds may  
XX additionally be useful for research and as diagnostic tools. The  
XX antisense oligonucleotides provide a tool for effectively downregulating

CD71 expression. Prior art methods utilised antibodies specific for CD71 proteins; however, this resulted in the development of resistant tumour cells, due to the development of mutations in CD71 which altered the epitope recognised by the antibodies

Sequence 18 BP; 4 A; 6 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;  
Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1676 ACCCTGGTGTCTCT 1690  
| | | | | | | | | |  
Db 3 AACCTGGTATCTCT 17

RESULT 420  
AAZ71696/C  
ID AAZ71696 standard; DNA; 18 BP.  
XX AAZ71696;  
AC AAZ71696;  
XX  
DT 10-SEP-2001 (first entry)  
DE Human biallelic marker upstream amplification primer SEQ ID NO:6052.  
XX Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
KW diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO954500-A2.  
XX  
PD 28-OCT-1999.  
XX  
PF 21-APR-1999; 99WO-IB000822.  
XX  
PR 21-APR-1998; 98US-0082614P.  
XX  
PR 23-NOV-1998; 98US-0109732P.  
XX  
PA (GEST ) GENSET.  
XX  
PI Cohen D, Blumenfeld M, Chumakov I;  
XX  
DR WPI; 2000-013267/01.  
XX  
PT Novel biallelic markers used to construct a high density disequilibrium map of the human genome.  
XX  
XX Claim 8; Page 1521; 2745pp; English.  
XX  
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment. N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the present invention

Sequence 18 BP; 4 A; 9 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;

Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1721 GGAGATCGAGATTGG 1735  
| | | | | | | | | |  
Db 18 GAAGTTGGAGATTGG 4

RESULT 421  
AAA63106  
ID AAA63106 standard; DNA; 18 BP.  
XX AAA63106;  
AC AAA63106;  
XX  
DT 07-DEC-2000 (first entry)  
DE Antisense oligonucleotide for use in RNase H mapping assay SEQ ID NO: 10.  
XX Antisense oligonucleotide; antisense oligonucleotide; cancer; tumour cell vaccine;  
KW rheumatoid arthritis; autoimmune disease; diabetes mellitus; thyroiditis;  
KW ss.  
XX  
OS Mus sp.  
XX  
PN WO200034467-A1.  
XX  
PD 15-JUN-2000.  
XX  
PF 24-NOV-1999; 99WO-US028096.  
XX  
PR 04-DEC-1998; 98US-00205995.  
XX  
PA (ANTI-) ANTIGEN EXPRESS INC.  
XX  
PI Xu M, Qiu G, Humphreys R;  
XX  
DR WPI; 2000-423417/36.  
XX  
PT Cancer cell vaccine for treating malignancies, autoimmune disorders and isolating autoteterminant peptides comprises a regulator of invariant chain protein expression or immunoregulatory function.  
XX  
XX Example 1; Page 46; 94pp; English.  
XX  
XX The present sequence is an antisense oligonucleotide which was used in an Rhase mapping experiment. This enables the identification of sites within the 11 RNA strand which hybridise to antisense DNA. These sites can then be used as targets for antisense strands which may, using gene therapy, be used as targets for tumour cell vaccines (for example to treat carcinomas, melanoma, leukaemia, lymphomas, stomach, breast, colon or rectum, lung, prostate, bladder, pancreas, brain and ovarian cancers), or they can be used to treat autoimmune diseases including rheumatoid arthritis, diabetes mellitus and thyroiditis

Sequence 18 BP; 3 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;  
Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1656 GCACGAGCTCACAG 1670  
| | | | | | | | | |  
Db 3 GCATCTGGCTCACAG 17

RESULT 422  
AAF84596  
ID AAF84596 standard; DNA; 18 BP.  
XX  
AC AAF84596;  
XX  
DT 29-JUN-2001 (first entry)  
XX

DE Probe and primer for plant pathogen resistance proteins.

KW DNA-binding domain; pathogen resistance protein; RRS1-S; RRS1-R;  
KW Ralstonia solanacearum; probe; primer; ss.

OS Arabidopsis thaliana.

PN FR279204-A1.

XX 06-APR-2001.

XX 01-OCT-1999; 99FR-00012315.

XX 01-OCT-1999; 99FR-00012315.

XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.

XX Olivier J, Deslandes L, Marco Y;

XX WPI; 2001-275284/29.

XX New nucleic acid encoding pathogen-resistance protein from plants, useful  
PT for producing transgenic plants resistant particularly to Ralstonia  
PT solanacearum.

PS Claim 13; Page 67; 142pp; French.

XX AAF84555-AAF84605 represent probes and primers for DNA encoding plant  
CC pathogen resistance proteins, designated RRS1-S and RRS1-R. The pathogen  
CC resistance proteins contain a N-terminal region containing at least one  
CC Leu-rich sequence and at least one nucleotide-binding site, and a C-  
CC terminal region with a DNA-binding domain containing the present  
CC sequence. RRS1 polynucleotides are used for in vivo or in vitro  
CC expression of the RRS1-S or RRS1-R proteins (or their fragments),  
CC especially in transgenic plants, or as antisense sequences, for blocking  
CC or inhibiting expression of these genes. Fragments of these  
CC polynucleotides are useful as probes and primers for detection/  
CC amplification of these genes. The RRS1-R protein confers resistance to  
CC pathogens, specifically the bacterium Ralstonia solanacearum. The 3'- and  
CC 5'-regulatory regions from these genes may be used to control expression  
CC of other genes, e.g. those encoding toxic peptides that induce death of  
CC plant cells, thus blocking spread of pathogens. RRS1 proteins are used to  
CC raise antibodies, and to screen for agents that bind to RRS1-R or RRS1-S  
CC proteins

XX SQ Sequence 18 BP; 3 A; 8 C; 2 G; 5 T; 0 U; 0 Other;  
Query Match 8.5%; Score 11.8; DB 1; Length 18;  
Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1741 AACTCTCTCCCTATCC 1755

Db 1 AACTCTCTCCATGCC 15

XX RESULT 423

XX AAS03672

XX ID AAS03672 standard; DNA; 18 BP.

XX AC AAS03672;

XX 29-AUG-2001 (first entry)

XX PCR primer rb21, used to detect RHD positive haplotypes.

XX Rhesus box; RHD positive; sequence length polymorphism; SSP; RHD; SMP1;  
KW RHCE; RHD negative; blood group typing; blood transfusion; antigen C;  
KW haemolytic disease of the newborn; chromosome 1 p34.1-p36; primer; ss.

OS Homo sapiens.

XX WO200132702-A2.

PN

XX 10-MAY-2001.

XX 31-OCT-2000; 2000WO-EP010745.

XX 02-NOV-1999; 99EP-00121686.

XX 31-MAY-2000; 2000EP-00111696.

XX (DRKB-) DRK BLUTSPENDEDIENST BADEN WUERTTEMBERG.

XX Flegel WA, Wagner FF;

XX WPI; 2001-291052/30.

XX New nucleic acid molecular structure, useful for detection of common RHD  
PT positive haplotypes in D-negative individuals, comprises RHD, SMP1 and  
PT RHCE genes.

XX Example 12; Page 66; 135pp; English.

XX The sequence represents PCR primer rb21, used to detect RHD positive  
CC haplotypes in RHD negative individuals. The primer was used in DNA typing  
CC using PCR-sequence length polymorphism (SSP) of the Rhesus genes locus  
CC comprising the RHD, SMP1 and RHCE (all undefined) genes and/or the Rhesus  
CC box(es), preferably the hybrid Rhesus box, the upstream Rhesus box and/or  
CC the downstream Rhesus box. The RHD and RHCE genes are located at  
CC chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the  
CC RHD deletion in the common RHD negative haplotypes. The primers of the  
CC invention are useful for: (1) the specific detection of the common RHD  
CC positive haplotypes in D-negative individuals; (2) blood group typing;  
CC (3) determining whether a patient can be transfused with RHD negative  
CC blood and whether blood is suitable for transfusion to patients who  
CC should not be exposed to antigen C; (4) assessing the risk of a RHD  
CC negative mother of conceiving or carrying an RHD positive foetus. Anti-D  
CC antibodies are useful for treating pregnant women who are Rhesus D  
CC negative, where the foetus is not homozygous for the RHD gene to treat or  
CC prevent haemolytic disease of the newborn

XX SQ Sequence 18 BP; 3 A; 9 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;  
Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1681 GGTGTCTCTCTCCAGC 1695

Db 2 GGTCTCTCTCTCCAGC 16

XX RESULT 424

XX ABZ72191/c

XX ID ABZ72191 standard; DNA; 18 BP.

XX AC ABZ72191;

XX 03-APR-2003 (first entry)

XX Gene 216 SSCP sequencing primer SEQ ID NO 163.

XX Human; Gene 216; chromosome 20p13-p12; antiasthmatic; anorectic;  
KW antiinflammatory; gastrointestinal; gene therapy; vaccine; asthma;  
KW obesity; inflammatory bowel disease; primer; ss.

XX Synthetic.

XX WO200178894-A2.

XX 25-OCT-2001.

XX 13-APR-2001; 2001WO-US012245.

XX 13-APR-2000; 2000US-00548797.

XX



PT Collection of binding groups for determining or typing samples,  
 PT especially clinical samples, has groups capable to identify essentially  
 PT all members of the family of nucleic acids of relatively high  
 XX significance.  
 XX  
 PS Disclosure; Page 9; 166pp; English.  
 XX  
 CC The present invention describes a collection of binding groups for a  
 CC family of nucleic acids comprising members of relative high and relative  
 CC low significance, where the binding groups are selected to be capable to  
 CC identify, alone or in combination, essentially all members of the family  
 CC of nucleic acids of relatively high significance. The collection of  
 CC binding groups is useful for typing of nucleic acid in a clinical sample,  
 CC by contacting the nucleic acid with the collection and determining  
 CC whether one or more binding groups bound to the nucleic acid of the  
 CC sample. This method is useful for determining whether the sample  
 CC comprises at least a part of a member of relatively high significance of  
 CC a family of nucleic acids. The collection of binding groups is useful for  
 CC diagnosing the severity of a disease caused by a pathogen containing a  
 CC member of a family of nucleic acids. ABL88779 to ABL89321 represent  
 CC oligonucleotide sequences used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 18 BP; 8 A; 1 C; 7 G; 2 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 18;  
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1717 GTACGAGATGGAGA 1731  
 ||||| |||||  
 Db 1 GTACAGAGATGGAAA 15  
 RESULT 427  
 ABA97088/C  
 ID ABA97088 standard; DNA; 18 BP.  
 XX AC ABA97088;  
 XX  
 XX ABA97088;  
 XX  
 XX 17-APR-2002 (first entry)  
 XX Human cathepsin B PCR primer #2.  
 XX Human; PCR; primer; detection; cathepsin; leucocystatin; metastasis;  
 KW tumour; asparaginyl endopeptidase; cathepsin B; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200198475-A2.  
 XX  
 XX 27-DEC-2001.  
 XX  
 XX 15-JUN-2001; 2001WO-EP006791.  
 XX  
 XX 23-JUN-2000; 2000DR-01030827.  
 XX (UYTU-) UNIV TUEBINGEN EBERHARD-KARLS.  
 PA  
 PI Melms A, Wienhold W, Tolosa E;  
 XX  
 XX WPI; 2002-122278/16.  
 XX  
 PT Detecting nucleic acid that encodes cathepsins and related proteins, for  
 PT diagnosis of tumors, comprises amplification with specific primers.  
 XX  
 XX Claim 4; Page 35; 39pp; German.  
 XX  
 CC This invention describes a novel method for the selective detection of  
 CC nucleic acids that are specific for cathepsins, asparaginyl endopeptidase  
 CC or leucocystatin. The method is used for diagnosis and/or early detection  
 CC of tumors and/or their metastases, associated with overexpression of  
 CC cathepsins, and also for evaluating treatment. The method is reliable,

CC simple and reproducible, since the PCR primers of the invention have very  
 CC high specificity and sensitivity for their targets, including ability to  
 CC differentiate between closely similar cathepsins. Only a small amount of  
 CC sample, obtained by minimally invasive methods, is required. The PCR  
 CC primers of the invention are designed to generate amplicons of 100-150bp,  
 CC ensuring practically 100 % amplification efficiency, without non-specific  
 CC amplification that could lead to false positives. This sequence  
 CC represents a PCR primer used in the amplification of the human cathepsin  
 CC B and is used to illustrate the method of the invention  
 XX  
 SQ Sequence 18 BP; 5 A; 5 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 18;  
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1733 TGGCTCCCAACTCCT 1747  
 ||||| |||||  
 Db 17 TGGTTGCCCAACTCCT 3  
 RESULT 428  
 ABL44660  
 ID ABL44660 standard; DNA; 18 BP.  
 XX AC ABL44660;  
 XX  
 XX 11-APR-2002 (first entry)  
 XX Human chromosome 1p36-35 PCR primer SEQ ID NO:1704.  
 XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;  
 KW PCR primer; ss.  
 XX Homo sapiens.  
 OS  
 XX JP2001321190-A.  
 XX  
 XX 20-NOV-2001.  
 XX  
 XX 12-MAR-2001; 2001JP-00068285.  
 XX  
 XX 10-MAR-2000; 2000JP-00066716.  
 XX (RIKA) RIKAGAKU KENKYUSHO.  
 PA (GENO-) GENOTEX YG.  
 XX  
 XX WPI; 2002-144136/19.  
 XX  
 XX Arraying genome clones.  
 XX  
 XX Claim 4; Page 38; 528pp; Japanese.  
 XX  
 CC The present invention describes a method of arraying genome clones. The  
 CC method comprises: (a) clones of the genomic libraries contained in  
 CC multiwell plates numbered for discrimination are mixed in each of the  
 CC multiwell plates; (b) a primer designed based on the chromosome marker  
 CC sequence is added to the mixture to carry out an amplification reaction;  
 CC (c) a signal corresponding to the marker is detected from the resultant  
 CC amplified product to specify the discrimination Nos. of the multiwell  
 CC plates containing the clones having said marker sequence; (d) the order  
 CC of the markers is changed so that the same discrimination Nos. succeed to  
 CC the maximum in the specified discrimination Nos. to array the multiwell  
 CC plates; (e) the clones in the multiwell plates of the specified  
 CC discrimination Nos. are mixed respectively in each wells of longitudinal  
 CC and lateral directions; (f) the mixed clones are cultured and the  
 CC resultant cultures are amplified by using the above primer; (g) signals  
 CC are detected from the amplified products; (h) the clones in the multiwell  
 CC plates are specified from the detected result; and (i) the clones are  
 CC reconstructed as the positions on the chromosome and arrayed. The  
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent  
 CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634  
 CC represent PCR primers for human chromosome 21q22.1, which are

CC specifically claimed for use in the present invention

XX Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

SQ Query Match 8.5%; Score 11.8; DB 1; Length 18;  
Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1689 CTCGAGCGTGGTGA 1703  
Db 2 CTCGAGCGTGGTGA 16

RESULT 429

ABK94528

ID ABK94528 standard; DNA; 18 BP.

XX

AC ABK94528;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human BRCA1 gene reverse PCR primer for exon 21.

XX

KW hMLH1; DNA mismatch repair; BRCA1; ss; PCR; primer; BRCA1;

KW breast and ovarian cancer susceptibility gene; TGDS; human;

KW two-dimensional DNA electrophoresis; tumour suppressor gene;

KW breast cancer; ovarian cancer; tumour.

XX

OS Homo sapiens.

XX

PN WO200236819-A1.

XX

PD 10-MAY-2002.

XX

PF 06-NOV-2000; 2000WO-IB001607.

XX

PR 06-NOV-2000; 2000WO-IB001607.

XX

PA (SCSC-) ACAD APPLIED SCI.

XX

PI Vijg J;

XX

DR WPI; 2002-471507/50.

XX

PT Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting

PT amplification products to 2-dimensional gel electrophoresis to produce a

PT characteristic spot pattern for a specific mutation in either the BRCA1

PT or the hMLH1 gene.

XX

PS Claim 1; Page 52; 57pp; English.

XX

CC The invention relates to detecting mutations in the BRCA1 and hMLH1 gene

CC comprising subjecting a set of amplification products to two-dimensional

CC DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a

CC specific mutation in either the BRCA1 or the hMLH1 gene. Also included

CC are test kits for enabling BRCA1 or hMLH1 gene testing comprising short

CC PCR primers given in the specification, mixed in 20 mM of Tris-HCl, 50 mM

CC KCl, 25 mM of dNTP, and 5 % formamide. The method is useful for

CC detecting mutations in the BRCA1 (breast and ovarian cancer

CC susceptibility gene, a tumour suppressor gene) and hMLH1 gene (a DNA

CC mismatch repair gene). The present sequence is a PCR primer specific to

CC BRCA1 used in the method of the invention

XX

SQ Sequence 18 BP; 2 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

XX

Query Match 8.5%; Score 11.8; DB 1; Length 18;

Best Local Similarity 86.7%; Pred. No. 4.2e+02;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1671 CTGGAACCCCTGGT 1685  
Db 1 CTGGAACCTGGGT 15

RESULT 430

ABS97999

ID ABS97999 standard; DNA; 18 BP.

XX

AC ABS97999;

XX

DT 23-DEC-2002 (first entry)

XX

DE Human urokinase gene (uPA) PCR primer #14.

XX

KW Human; ss; primer; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1; PCR;

KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;

KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;

KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathespin S; CTSS;

KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

KW glutathione-S-transferase 2; GSTA2; 5-lipoxygenase activating protein; FLAP;

KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;

KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;

KW NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;

KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;

KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;

KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;

KW multidrug resistance associated protein 3; cancer; prostate;

KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;

KW altered drug metabolism; cardiovascular function; colorectal tumour;

KW central nervous system; pulmonary; immunological.

XX

OS Homo sapiens.

XX

PN WO200257410-A2.

XX

PD 25-JUL-2002.

XX

PF 28-NOV-2001; 2001WO-US044838.

XX

PR 28-NOV-2000; 2000US-00724389.

XX

PA (DNAS-) DNA SCI LAB INC.

XX

PI Guida M, Hall J;

XX

DR WPI; 2002-698522/75.

XX

PT Isolated nucleic acid molecules having polymorphisms in known human genes

PT e.g. cytochrome P450 and cathespin S useful as genetic linkage markers

PT for locating, identifying and characterizing the genes responsible for

PT disorder-related traits.

XX

PS Example 21; Page 139; 714pp; English.

XX

CC This invention relates to the sequence of an isolated nucleic acid

CC molecule comprising at least one base variation from that of a known

CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),

CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),

CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator

CC (ARNT), cathespin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding

CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating

CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl

CC transferase (HNMT), kallikrein 2 (KLK2), nicotinamide -N-methyl

CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),

CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4

CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl

CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1

CC (MRP1), lactotransferrin (LTF), multidrug resistance associated protein 3

CC (MRP3), orphan nuclear receptor (NR112), CHMR2, CHMR3, CHMR4 or CHMR5) sequence.

CC The polymorphisms in the human genes cited in the invention are useful as

CC genetic linkage markers for locating and characterising the genes that

CC are responsible for specific traits within the genome and eventually

CC identifying the genes responsible for a variety of disorder-related

CC traits as a result of their e.g., overexpression, constitutive

CC expression, mutation or underexpression, which may be used in diagnosing



CC and/or treating the disorders. The nucleic acid molecules comprising the  
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,  
 CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,  
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug  
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,  
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for  
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are  
 CC used to screen for altered cardiovascular function, in COX2 for altered  
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central  
 CC nervous system function, in FLAP and NNMT for altered pulmonary,  
 CC immunological or haematological function, in KIK2 for altered serine  
 CC protease activity in the prostate, in LTF for altered immunological or  
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central  
 CC peripheral nervous system function. The present sequence represents a PCR  
 CC primer used to amplify the sequences of the invention  
 XX  
 SQ Sequence 18 BP; 4 A; 9 C; 0 G; 5 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 18;  
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1739 CCAACTCCTCCCTAT 1753  
 Db 4 CCAACTCCTCCCAT 18  
 RESULT 431  
 ABS98011  
 ID ABS98011 standard; DNA; 18 BP.  
 AC ABS98011;  
 XX  
 DT 23-DEC-2002 (first entry)  
 DE Human urokinase gene (uPA) sequencing primer #12.  
 KW Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;  
 KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;  
 KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRE3; NR1I2;  
 KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;  
 KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
 KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;  
 KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;  
 KW NNMT; kallikrein 2; KIK2; nicotinamide-N-methyl transferase; NNMT;  
 KW NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;  
 KW UGT2B7; UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;  
 KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;  
 KW multidrug resistance associated protein 3; cancer; prostate;  
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;  
 KW altered drug metabolism; cardiovascular function; colorectal tumour;  
 KW central nervous system; pulmonary; immunological; sequencing.  
 OS Homo sapiens.  
 XX  
 XX  
 PN WO200257410-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 28-NOV-2001; 2001WO-US044838.  
 XX  
 PR 28-NOV-2000; 2000US-00724389.  
 XX  
 XX (DNAS-) DNA SCI LAB INC.  
 PA  
 XX Guida M, Hall J;  
 PI  
 XX WPI; 2002-698522/75.  
 DR  
 XX Isolated nucleic acid molecules having polymorphisms in known human genes  
 PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers  
 PT for locating, identifying and characterizing the genes responsible for

PT disorder-related traits.  
 XX  
 PS Example 21; Page 139; 714pp; English.  
 XX  
 CC This invention relates to the sequence of an isolated nucleic acid  
 CC molecule comprising at least one base variation from that of a known  
 CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),  
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),  
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
 CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding  
 CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating  
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl  
 CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),  
 CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4  
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl  
 CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1  
 CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3  
 CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic  
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.  
 CC The polymorphisms in the human genes cited in the invention are useful as  
 CC genetic linkage markers for locating and characterising the genes that  
 CC are responsible for specific traits within the genome and eventually  
 CC identifying the genes responsible for a variety of disorder-related  
 CC traits as a result of their e.g., overexpression, constitutive  
 CC expression, mutation or underexpression, which may be used in diagnosing  
 CC and/or treating the disorders. The nucleic acid molecules comprising the  
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,  
 CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,  
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug  
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,  
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for  
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are  
 CC used to screen for altered cardiovascular function, in COX2 for altered  
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central  
 CC nervous system function, in FLAP and NNMT for altered pulmonary,  
 CC immunological or haematological function, in KIK2 for altered serine  
 CC protease activity in the prostate, in LTF for altered immunological or  
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central  
 CC peripheral nervous system function. The present sequence represents a  
 CC sequencing primer used to sequence the polymorphic genes of the invention  
 XX  
 SQ Sequence 18 BP; 4 A; 9 C; 0 G; 5 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 18;  
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1739 CCAACTCCTCCCTAT 1753  
 Db 4 CCAACTCCTCCCAT 18  
 RESULT 432  
 ABL30541/C  
 ID ABL30541 standard; DNA; 18 BP.  
 XX  
 AC ABL30541;  
 XX  
 XX 21-MAR-2002 (first entry)  
 DT  
 XX  
 DE Human HLA genotyping oligonucleotide SEQ ID NO 30.  
 XX  
 XX Human; human leukocyte antigen; HLA; genotype; polymorphism;  
 KW immunogenetic; transplantation; genetic disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200192572-A1.  
 XX  
 PD 06-DEC-2001.  
 XX  
 XX 01-JUN-2001; 2001WO-JF004662.  
 PF

Mon Aug 30 09:26:45 2004

polymorphic bovine acyl CoA-diacylglycerol transferase gene useful for testing a mammal for its predisposition for fat content of milk and for meat marbling.

Example 1; Page 36; 91pp; English.

The present invention describes a nucleic acid molecule (NA) (I) encoding a bovine acyl CoA-diacylglycerol transferase (DGAT) contributing to or indicative for low fat content of milk and to low meat marbling (intramuscular fat content). Human DGAT is located to chromosome 8, and bovine DGAT is located to chromosome 14. (I) is useful for testing a mammal for its predisposition for fat content of milk and/or its predisposition for meat marbling. The method comprises analysing the gene encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide polymorphisms (SNPs)) which are connected with the predisposition. The nucleotide polymorphisms are located in the coding region of the DGAT gene and result in substitution, deletion and/or addition of an amino acid sequence of the polypeptide which is encoded by the gene. The nucleic acid molecule has at the position 10433 and 10434 of the DGAT gene a guanine and a cytosine residue, at position 3343 a cytosine or guanine, 11030 a guanine, 11048 a cytosine or thymine and 11093 a thymine, which correlate with a predisposition for low fat content of milk and low meat marbling. The nucleic acid molecule has at the position corresponding to position 10433 and 10434 of the DGAT gene two adenine residues which correlate with a predisposition for high content of milk and high meat marbling. The nucleotide polymorphisms are located in a region which is responsible for the regulation of the expression of the product of the gene encoding DGAT. ABZ76924 to ABZ77045 and ABP96035 to ABP96046 represent sequences used in the exemplification of the present invention

Sequence 18 BP; 3 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;  
Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1666 CACAGCTGGAAACCT 1680  
DB 1 CACAGCTGGCTCCT 15

RESULT 434  
ABZ75044/c  
ID ABZ75044 standard; DNA: 18 BP.

AC ABZ75044;

XX 25-MAR-2003 (first entry)

XX Human gene 216 polymorphism detection PCR primer #101.

XX Human; mouse; ss; primer; gene 216; antiasthmatic; antiinflammatory;  
XX anorectic; chromosome 20p13-p12; single nucleotide polymorphism; SNP;  
XX gene therapy; respiratory disease; asthma; obesity; PCR;  
XX bronchial hyper-responsiveness; chronic obstructive pulmonary disease;  
XX adult respiratory distress syndrome; inflammatory bowel syndrome.

OS Homo sapiens.

XX WO200283077-A2.

XX 24-OCT-2002.

XX 15-APR-2002; 2002WO-US012063.

XX 13-APR-2001; 2001US-00834597.

XX 13-APR-2001; 2001WO-US012245.

XX (SCHE) SCHERING CORP.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Keith T, Little RD, Van Eerdewegh P, Dupuis J, Del Mastro RG;

PI

XX 01-JUN-2000; 2000JP-00164798.  
XX (NISN) NISSHINEO IND INC.  
XX (SYST-) SYSTEM RES INC.  
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;  
XX WPI; 2002-122074/16.  
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of  
XX individuals e.g. by determining immunogenetic differences when  
XX transplanting between them.  
XX Claim 10; Page 99; 345pp; Japanese.

The invention relates to a typing kit for judging human leukocyte antigen (HLA) genotype of a sample by hybridising a substrate on which 10-24 base oligonucleotides (ABZ30512-ABZ31809) originating in the sequences of genes e.g. belonging to HLA class I antigens on human genome and containing gene polymorphisms as alloantigens have been immobilised as primers for amplification of cleaved nucleic acids relating to gene polymorphisms. The method is useful for judging HLA genotypes of individuals by determining immunogenetic differences before transplanting between them, providing genetic information to decide compatibility of organ and tissue for transplantation e.g. of bone marrow, kidney, liver, pancreas, Langerhans islet in pancreas and cornea, susceptibility diagnosis of genetic diseases and identifying individuals

Sequence 18 BP; 1 A; 4 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 8.5%; Score 11.8; DB 1; Length 18;  
Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1650 AGGCAAGCACCAGGC 1664  
DB 18 AGGCAACACACAGAC 4

RESULT 433  
ABZ76994  
ID ABZ76994 standard; DNA: 18 BP.

AC ABZ76994;

XX 07-MAY-2003 (first entry)

XX Bovine DGAT PCR primer #30.

XX Acyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14; bovine;  
XX milk; meat marbling; low fat; polymorphic; SNP;  
XX single nucleotide polymorphism; PCR primer; ss.

XX Bos taurus.

XX Synthetic.

XX WO2003004630-A2.

XX 16-JAN-2003.

XX 05-JUL-2002; 2002WO-EP007520.

XX 06-JUL-2001; 2001EP-00116412.

XX 13-MAY-2002; 2002US-0379412P.

XX (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.

XX Fries H, Winter A;

XX WPI; 2003-239205/23.

XX New nucleic acid molecule comprising a sequence of an allele of a

PT

PI Simon J, Allen K, Pandit S;  
 DR WPI; 2003-092960/08.  
 XX  
 PT New isolated gene 216 nucleic acids, useful for diagnosing, preventing or  
 PT treating a disorder, such as asthma, bronchial hyper-responsiveness,  
 PT chronic obstructive pulmonary disease, obesity or inflammatory bowel  
 PT syndrome.  
 XX  
 PS Example 10; Page 156; 650pp; English.  
 XX  
 CC This invention relates to a novel isolated nucleic acid, gene 216,  
 CC identified from human chromosome 20p13-p12. The invention also discloses  
 CC regions of the 216 gene that contain single nucleotide polymorphisms  
 CC (SNP's) which may be used as markers for disease susceptibility or  
 CC severity. The nucleotides of the invention may have antiasthmatic,  
 CC antiinflammatory or anorectic activities and may be used in gene therapy.  
 CC The nucleic acids, antibodies or its fragments are useful for diagnosing,  
 CC preventing or treating a disorder, such as respiratory diseases (e.g.  
 CC asthma, bronchial hyper-responsiveness, chronic obstructive pulmonary  
 CC disease or adult respiratory distress syndrome), obesity, or inflammatory  
 CC bowel syndrome. The nucleic acids are also useful for identifying  
 CC increased susceptibility of a subject to the disorders mentioned. The  
 CC nucleic acids can also be used as primers and templates for the  
 CC recombinant production of disorder-associated peptides or polypeptides,  
 CC for chromosome and gene mapping, or for tissue distribution studies. The  
 CC present sequence represents a gene 216 specific PCR primer used in the  
 CC scope of the invention  
 XX  
 SQ Sequence 18 BP; 2 A; 7 C; 3 G; 6 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 18;  
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1649 AAGGCAAGCACCAGG 1663  
 Db 17 ATGGGAAGCACCAGG 3  
 RESULT 435  
 ID ABZ58715 standard; DNA; 18 BP.  
 XX  
 AC ABZ58715;  
 DT 14-APR-2003 (first entry)  
 DE Human HAM cDNA fragment A sequencing sense primer.  
 XX  
 KW HAM; homologue of attractin/mahogany; immunosuppressive; cytostatic;  
 KW antiinflammatory; cardiant; osteopathic; gene therapy; human; PCR;  
 KW primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200297120-Al.  
 XX  
 PD 05-DEC-2002.  
 XX  
 XX 23-MAY-2002; 2002WO-US016391.  
 XX  
 XX 25-MAY-2001; 2001US-0293608P.  
 PR 24-SEP-2001; 2001US-0324626P.  
 XX  
 PA (IMMUNEX CORP.  
 XX  
 PI Anderson DM;  
 XX  
 DR WPI; 2003-140486/13.  
 XX  
 PT New Homologue of Attractin/Mahogany (HAM) polypeptide, useful for  
 PT treating HAM-associated disorder consisting of inflammatory, autoimmune,

PT cell proliferative or cardiovascular disorders.  
 XX  
 PS Example 1; Page 35; 89pp; English.  
 XX  
 CC The invention relates to Homologue of Attractin/Mahogany (HAM)  
 CC polypeptides and encoding polynucleotides. The HAM polypeptides can be  
 CC expressed by standard recombinant methodology. The HAM polypeptides are  
 CC useful for treating HAM-associated disorder consisting of inflammatory,  
 CC autoimmune, graft-versus-host, neurological, myelination, cell  
 CC proliferative, cardiovascular, haematologic, liver, metabolic, weight or  
 CC bone disorder. Sequences ABZ58715-26 represent PCR primers used for  
 CC sequencing the human HAM cDNA  
 XX  
 SQ Sequence 18 BP; 5 A; 1 C; 10 G; 2 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 18;  
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1721 GGAGATGGAGATTGG 1735  
 Db 4 GAAGATGGAGACTGG 18  
 RESULT 436  
 ID ADC59461/c standard; DNA; 18 BP.  
 XX  
 AC ADC59461;  
 DT 18-DEC-2003 (first entry)  
 DE Human precutin PCR primer, SEQ ID NO:14, used in expression analysis.  
 XX  
 KW Human; epiplakin; epidermal autoantigen; autoimmune disease;  
 KW skin disease; transgenic animals; diagnosis; drug screening; pemphigoid;  
 KW pemphigus; dermatological; immunosuppressive; expression analysis;  
 KW precutin; PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP2003047469-A.  
 XX  
 PD 18-FEB-2003.  
 XX  
 PF 16-JUL-2001; 2001JP-00216025.  
 XX  
 PR 16-JUL-2001; 2001JP-00216025.  
 XX  
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 XX  
 DR WPI; 2003-508702/48.  
 XX  
 PT Novel protein having epiplakin activity, useful for screening agents  
 PT which inhibit and activate epiplakin activity, and for treating  
 PT autoimmune skin disease such as pemphigoid or pemphigus.  
 XX  
 PS Example 4; SEQ ID NO 15; 55pp; Japanese.  
 XX  
 CC The invention relates to a 450 kD human epidermal autoantigen, epiplakin  
 CC (ADC59448), and nucleic acids encoding it (ADC59447). The invention also  
 CC encompasses an epiplakin antigenic epitope (ADC59449) which is reactive  
 CC with serum from patients with autoimmune disease, fusion polypeptides  
 CC containing epiplakin or its epitope, an antibody against epiplakin, host  
 CC cells comprising human epiplakin nucleic acids, transgenic animals, which  
 CC under- or over-express epiplakin, epiplakin nucleic acid probes for  
 CC diagnosis of autoimmune disease, and methods of screening for agents  
 CC which modulate epiplakin activity. Epiplakin polypeptides and  
 CC polynucleotides are useful in drug screening for agents which promote or  
 CC inhibit the activity of epiplakin which can be used in the treatment of  
 CC autoimmune disease, particularly those of the skin such as pemphigoid or  
 CC pemphigus. Epiplakin antibodies and nucleic acid probes are useful for  
 CC diagnosis of these diseases. Sequences ADC59461-ADC59462 represent human

Mon Aug 30 09:26:45 2004

CC precutin PCR primers used to generate a probe used in expression analysis  
 CC in an example of the invention.

XX Sequence 18 BP; 5 A; 7 C; 5 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 8.5%; Score 11.8; DB 1; Length 18;  
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1697 TCCTCCAGCGGTG 1701  
 |||||  
 Db 18 TCGTCCACCGTGTG 4

RESULT 437  
 ADE13404  
 ID ADE13404 standard; DNA; 18 BP.

XX AC ADE13404;  
 XX 29-JAN-2004 (first entry)  
 DE HLA class I allele specific primer #20.  
 XX ss; primer; PCR; human; Human Leukocyte Antigen; HLA; genotype.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 PN US2003165884-A1.  
 XX 04-SEP-2003.  
 PD 25-APR-2002; 2002US-00133779.  
 PF 20-DEC-1999; 99US-0172768P.  
 PR 20-DEC-2000; 2000US-00747391.  
 XX (STEM-) STEM-CYTE INC.  
 PA Chow R, Tonai R;  
 PI WPI; 2003-874916/81.  
 DR Identifying class I or II Human Leukocyte Antigen genotypes using  
 PT hybridization and amplification assays.  
 XX Claim 7; SEQ ID NO 20; 66pp; English.

XX The invention relates to a method of identifying a class I or II Human  
 CC Leukocyte Antigen (HLA) genotype of a subject using hybridisation and  
 CC amplification assay. The method is used for determining the HLA genotype  
 CC of a subject. The present sequence represents a HLA class I allele  
 CC specific primer.  
 XX Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;

QY 1653 CAAGCACCAGGTCA 1667  
 |||||  
 Db 2 CAAGCGCCAGGCACA 16

RESULT 438  
 AAH78641/c  
 ID AAH78641 standard; DNA; 20 BP.  
 XX AC AAH78641;  
 XX 10-DEC-2001 (first entry)  
 DT  
 XX

Query Match 8.5%; Score 11.8; DB 1; Length 18;  
 Best Local Similarity 86.7%; Pred. No. 4.2e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1697 TCCTCCAGCGGTG 1701  
 |||||  
 Db 18 TCGTCCACCGTGTG 4

RESULT 437  
 ADE13404  
 ID ADE13404 standard; DNA; 18 BP.

XX AC ADE13404;  
 XX 29-JAN-2004 (first entry)  
 DE HLA class I allele specific primer #20.  
 XX ss; primer; PCR; human; Human Leukocyte Antigen; HLA; genotype.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 PN US2003165884-A1.  
 XX 04-SEP-2003.  
 PD 25-APR-2002; 2002US-00133779.  
 PF 20-DEC-1999; 99US-0172768P.  
 PR 20-DEC-2000; 2000US-00747391.  
 XX (STEM-) STEM-CYTE INC.  
 PA Chow R, Tonai R;  
 PI WPI; 2003-874916/81.  
 DR Identifying class I or II Human Leukocyte Antigen genotypes using  
 PT hybridization and amplification assays.  
 XX Claim 7; SEQ ID NO 20; 66pp; English.

XX The invention relates to a method of identifying a class I or II Human  
 CC Leukocyte Antigen (HLA) genotype of a subject using hybridisation and  
 CC amplification assay. The method is used for determining the HLA genotype  
 CC of a subject. The present sequence represents a HLA class I allele  
 CC specific primer.  
 XX Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;

Probe for mechanically sensitive potassium channel gene fragment.

Human; mechanically sensitive potassium channel; riluzole; TWICK;  
 polyunsaturated fatty acid; arachidonic acid; hTRAAC; chromosome 11q13;  
 neuronal excitation; muscle excitation; cardiac rhythm; anoxia;  
 hormone secretion; cardiac disease; vascular disease; ischemia;  
 nervous system disorder; endocrinal disease; muscle disease;  
 retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration; probe;  
 ss.

Homo sapiens.  
 WO200168670-A2.  
 20-SEP-2001.

14-MAR-2001; 2001WO-FR000758.  
 14-MAR-2000; 2000FR-00003264.

(CNRS ) CNRS CENT NAT RECH SCI.  
 Lazdunski M, Lesage F, Maingret F;  
 WPI; 2001-590037/66.

New mechanically sensitive potassium channel, useful for treating  
 cardiovascular diseases and in drug screening, is activated by  
 polyunsaturated fatty acids.

Disclosure; Page 15; 37pp; French.  
 The present probe was used to detect a gene fragment of the human  
 mechanically sensitive potassium channel gene. The channel is activated  
 by polyunsaturated fatty acids (particularly arachidonic acid (AA)) and  
 by riluzole. The polypeptide is designated human TWICK-related AA-  
 activated potassium channel (hTRAAC). The hTRAAC gene is located on  
 chromosome 11q13. hTRAAC is involved in regulation of neuronal and muscle  
 excitation, cardiac rhythm and secretion of hormones. Cells that express  
 hTRAAC, designated to screen for modulators of hTRAAC activity, in humans  
 modulators are potentially useful for prevention or treatment, in humans  
 and animals, of: cardiac and/or vascular disease; nervous system  
 disorders associated with ischemia and anoxia; endocrinal diseases  
 associated with anomalous hormone secretion or muscle diseases; and  
 retinal diseases. Typical examples are epilepsy, cardiac arrhythmia and  
 neurodegeneration

Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;  
 Query Match 8.5%; Score 11.8; DB 1; Length 20;  
 Best Local Similarity 86.7%; Pred. No. 4.8e+02;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 CAGCTGGACCTCG 1682  
 |||||  
 Db 15 CAGCTGGACCTCG 1

RESULT 439  
 ABH66153/c  
 ID ABH66153 standard; DNA; 13 BP.

XX AC ABH66153;  
 XX 22-FEB-2002 (first entry)  
 DT  
 XX

Oligonucleotide SEQ ID NO 266130 for detecting SNP TSC0064482.  
 SNP; single nucleotide polymorphism; human; diagnosis; PNB; cancer; CNS;  
 peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

XX PN WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 266130; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 1 Other;  
 SQ  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 1 Other;  
 SQ  
 Query Match 8.3%; Score 11.6; DB 1; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 3e+02;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1722 GAGATGGAGATT 1733  
 Db 12 GAGATGGAGATT 1  
 RESULT 440  
 ABH66152  
 ID ABH66152 standard; DNA; 13 BP.  
 XX ABH66152;  
 XX 22-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 266129 for detecting SNP TSC0064482.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX

DR WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 266129; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 1 Other;  
 SQ  
 Query Match 8.3%; Score 11.6; DB 1; Length 13;  
 Best Local Similarity 91.7%; Pred. No. 3e+02;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1722 GAGATGGAGATT 1733  
 Db 2 GAGATGGAGATT 13  
 RESULT 441  
 AAZ44834  
 ID AAZ44834 standard; DNA; 15 BP.  
 XX AAZ44834;  
 XX 27-APR-2000 (first entry)  
 XX H. annuus sld1 homologue primer BN1.  
 XX Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;  
 KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;  
 KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;  
 KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;  
 KW pharmaceutical; food; chemical raw material; primer; ss.  
 XX Helianthus annuus.  
 XX DE19828850-A1.  
 XX 30-DEC-1999.  
 XX 27-JUN-1998; 98DE-01028850.  
 XX 27-JUN-1998; 98DE-01028850.  
 XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.  
 XX Heinz E, Zaehrer U, Schmidt H, Sperling P;  
 XX WPI; 2000-127549/12.  
 XX New sphingolipid desaturase that selectively introduces double bond into  
 PT sphingolipids and capnoids.  
 XX Example 1; Page 24; 62pp; German.  
 XX This invention describes a novel sphingolipid desaturase that selectively  
 CC introduces a double bond into the sphingobase of the ceramide residue of  
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid  
 CC desaturase, or a vector containing the DNA sequence, can be used to

CC produce transgenic plants, especially crop plants, with an increased or  
 CC decreased delta-8-unsaturated long-chain base content or an altered delta  
 CC -8-unsaturated long-chain base cis/trans ratio, especially to compensate  
 CC for a delta-8-unsaturated long-chain base deficiency, to exclude  
 CC production of delta-8-unsaturated bases, to increase tolerance or  
 CC resistance to soil salinity, ion stress or toxicity, drought, wet  
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to  
 CC alter size growth and flowering time. Cells, transgenic organisms or  
 CC plants containing the DNA sequence can be used to produce sphingolipids  
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids  
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw  
 CC materials. This sequence represents a primer used in the isolation of a  
 CC sphingolipid desaturase protein sidi homologue fragment isolated from  
 CC *Halanthus annuus* which is used in the method of the invention  
 XX  
 XX Sequence 15 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 3 Other;

Query Match 8.3%; Score 11.6; DB 1; Length 15;  
 Best Local Similarity 73.3%; Pred. No. 3.7e+02;  
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1694 GCGTGGTGAAGTTG 1708  
 | : ||||| : |  
 DB 1 GSGTGGTGAARTGG 15

RESULT 442  
 ABN81456/c  
 ID ABN81456 standard; DNA; 15 BP.  
 XX  
 AC ABN81456;  
 DT 16-AUG-2002 (first entry)  
 XX  
 DE Human HTATIP allele specific PCR primer SEQ ID NO 57.

XX Human, HIV-1 Tat interactive protein; HTATIP; haplotyping; genotyping;  
 KW transgenic; PCR; primer; ss.  
 XX  
 OS Homo sapiens.

XX WO200229089-A2.  
 XX 11-APR-2002.  
 XX 05-OCT-2001; 2001WO-US031593.  
 XX 06-OCT-2000; 2000US-0238655P.  
 XX (GENA-) GENAISANCE PHARM INC.  
 XX Armstrong B, Bentivegna SC, Choi JY, Gilson CR, Parks KE;  
 PI Sausker EA;  
 XX WPI; 2002-330173/36.

XX New HIV-1 tat interactive protein, 60 kDa (HTATIP) gene polymorphic  
 PT variants, for studying the expression and function of HTATIP and  
 PT screening candidate drugs for treating familial glucocorticoid deficiency  
 PT and cancer.  
 XX  
 PS Claim 14; Page 14; 89pp; English.

XX The invention relates to novel genetic variants of the HIV-1 Tat  
 CC interactive protein, 60 kDa (HTATIP) gene. The polymorphic variants are  
 CC useful in studying the expression and function of HTATIP, in expressing  
 CC HTATIP protein for use in screening for candidate drugs to treat diseases  
 CC related to HTATIP activity, in studying the effect of the variation on  
 CC the biological activity of HTATIP and the binding affinity of candidate  
 CC drugs targeting HTATIP for the treatment of disorders. Haplotyping  
 CC methods are useful in validating HTATIP as a candidate target for  
 CC treating a specific condition or disease predicted to be associated with  
 CC HTATIP activity or in the design of clinical trials of candidate drugs

CC for treating a specific condition or disease associated with HTATIP  
 CC activity. Transgenic animals are useful for studying expression of the  
 CC HTATIP isogenes in vivo, for in vivo screening and testing of drugs  
 CC targeted against HTATIP protein and for testing the efficacy of  
 CC therapeutic agents and compounds for disorders. The present sequence is  
 CC that of a HTATIP allele specific PCR primer of the invention  
 XX  
 XX Sequence 15 BP; 3 A; 3 C; 6 G; 2 T; 0 U; 1 Other;

Query Match 8.3%; Score 11.6; DB 1; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 3.7e+02;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1657 CACCAAGGCTCAC 1668  
 | : ||||| : |  
 DB 15 CRCCAGGCTCAC 4

RESULT 443  
 ABL36320  
 ID ABL36320 standard; DNA; 15 BP.  
 XX  
 AC ABL36320;  
 DT 22-APR-2002 (first entry)  
 XX  
 DE Human lysosomal acid phosphatase 2 (ACP2) allele-specific probe 21.  
 XX  
 KW Human; ss; lysosomal acid phosphatase 2; ACP2; gene; chromosome 11;  
 KW lysosome-specific enzyme; orthophosphoric monoester hydrolysis;  
 KW Hodgkin's disease; HD; acid phosphatase deficiency;  
 KW novel polymorphic site; ACP2 haplotype; ACP2 genotype; polymorphism;  
 KW transgenic animal; primer; probe; primer-extension oligonucleotide; SNP;  
 KW single nucleotide polymorphism.

XX Homo sapiens.  
 OS  
 XX WO200194362-A2.  
 XX 13-DEC-2001.  
 XX 07-JUN-2001; 2001WO-US018457.  
 XX 07-JUN-2000; 2000US-0210047P.  
 XX (GENA-) GENAISANCE PHARM INC.  
 XX Klem SE, Messer C, Tanguay DA;  
 XX WPI; 2002-154563/20.

XX Novel genetic variants of acid phosphatase 2, lysosomal polypeptide gene  
 PT useful in studying expression and function of the protein, and for  
 PT screening drugs to treat diseases e.g. Hodgkin's disease.

XX Claim 17; Page 14; 109pp; English.

XX The invention comprises the human lysosomal acid phosphatase 2 (ACP2)  
 CC nucleic acid and protein sequences. Specifically, the invention relates  
 CC to the discovery of 22 novel polymorphic sites within the ACP2 gene. The  
 CC invention also comprises methods for haplotyping and genotyping the ACP2  
 CC gene in an individual. The ACP2 gene (located on chromosome 11) encodes a  
 CC lysosomal-specific enzyme that catalyses the hydrolysis of  
 CC orthophosphoric monoesters to alcohol and phosphate. The ACP2 gene and  
 CC protein are pharmaceutically important in the treatment of Hodgkin's  
 CC disease (HD) and acid phosphatase deficiency. The novel ACP2 gene  
 CC polymorphisms of the invention are useful in haplotyping the ACP2 gene.  
 CC ACP2 haplotyping is useful in validating ACP2 as a target (and designing  
 CC drugs) for treating an ACP2-related disease or condition (e.g. Hodgkin's  
 CC disease and acid phosphatase deficiency). The ACP2 gene polymorphisms are  
 CC useful for ACP2 genotyping, which can also be used to develop diagnostic  
 CC tests and therapeutic treatments. The ACP2 protein and nucleic acids of  
 CC the invention are useful in the production of a transgenic animal which



```
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1745 CCTCCTATCCTA 1757
    |||||
Db 1 CCTCCTAACCTA 13

RESULT 446
ABC26848/c
ID ABC26848 standard; DNA; 13 BP.
XX
AC ABC26848;
XX
XX
XX 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 26865 for detecting SNP TSC0007227.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 26865; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH99989
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 8 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1739 CCAACTCCTCCCT 1751
    |||||
Db 13 CCACTCCTCCCT 1

RESULT 447
ABF15453
ID ABF15453 standard; DNA; 13 BP.
XX
XX ABF15453;
AC
XX

Matches 12; Conservative 0; Mismatches 0; Gaps 0;

Qy 1739 CCAACTCCTCCCT 1751
    |||||
Db 13 CCACTCCTCCCT 1

RESULT 447
ABF15453
ID ABF15453 standard; DNA; 13 BP.
XX
XX ABF15453;
AC
XX

Matches 12; Conservative 0; Mismatches 0; Gaps 0;

Qy 1739 CCAACTCCTCCCT 1751
    |||||
Db 13 CCACTCCTCCCT 13

RESULT 448
ABC93112/c
ID ABC93112 standard; DNA; 13 BP.
XX
AC ABC93112;
XX
XX 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 93129 for detecting SNP TSC0023277.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PS Claim 1; SEQ ID NO 115450; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH99989
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 9 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```



XX PF 06-APR-2001; 2001WO-IB000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX DR WPI; 2001-657177/75.  
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 93129; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 1 A; 0 C; 10 G; 2 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1738 CCCAACTCCTCC 1750  
 Db 13 CCCAACCCCTCC 1  
 RESULT 449  
 ABC93117  
 ID ABC93117 standard; DNA; 13 BP.  
 AC ABC93117;  
 XX 21-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 93134 for detecting SNP TSC0023277.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.  
 XX Claim 1; SEQ ID NO 93134; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 2 A; 9 C; 1 G; 1 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1738 CCCAACTCCTCC 1750  
 Db 1 CCCAACCCCTCC 13  
 RESULT 450  
 ABC70351  
 ID ABC70351 standard; DNA; 13 BP.  
 AC ABC70351;  
 XX 21-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 70368 for detecting SNP TSC0018290.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 70368; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence

```
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 7 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match      8.2%; Score 11.4; DB 1; Length 13;
  Best Local Similarity 92.3%; Pred. No. 3.3e+02;
  Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1739 CCAACTCCTCCCT 1751
DB 1 CCAACTCTTCCCT 13

RESULT 451
ABC84787
ID ABC84787 standard; DNA; 13 BP.
XX
AC ABC84787;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 84804 for detecting SNP TSC0021342.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
PS Claim 1; SEQ ID NO 84804; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match      8.2%; Score 11.4; DB 1; Length 13;
  Best Local Similarity 92.3%; Pred. No. 3.3e+02;
  Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1746 CTCCTATCCTAA 1758
DB 1 CTCCTACCTAA 13

CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 7 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match      8.2%; Score 11.4; DB 1; Length 13;
  Best Local Similarity 92.3%; Pred. No. 3.3e+02;
  Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1739 CCAACTCCTCCCT 1751
DB 1 CCAACTCTTCCCT 13

RESULT 452
ABF19171
ID ABF19171 standard; DNA; 13 BP.
XX
AC ABF19171;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 119168 for detecting SNP TSC0029760.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
PS Claim 1; SEQ ID NO 119168; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 8 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match      8.2%; Score 11.4; DB 1; Length 13;
  Best Local Similarity 92.3%; Pred. No. 3.3e+02;
  Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1739 CCAACTCCTCCCT 1751
DB 1 CCTACTCTCCCT 13

RESULT 453
ABC47949/C
ID ABC47949 standard; DNA; 13 BP.
XX
AC ABC47949;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 47966 for detecting SNP TSC0013727.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
```

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 47966; 29pp + Sequence Listing; German.  
 PS This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 4 A; 7 C; 0 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1707 TGGCTTAGGAGTA 1719  
 DB 13 TGGCTTAGGAGTA 1  
 RESULT 454  
 ABC49590/c  
 ID ABC49590 standard; DNA; 13 BP.  
 XX ABC49590;  
 AC 21-FEB-2002 (first entry)  
 DT Oligonucleotide SEQ ID NO 49607 for detecting SNP TSC0014014.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 110342; 29pp + Sequence Listing; German.  
 PS This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1745 CTCCTCTATCCTTA 1757  
 DB 13 CTCCTCTATCCTTA 1  
 RESULT 455  
 ABF10345/c  
 ID ABF10345 standard; DNA; 13 BP.  
 XX ABF10345;  
 AC 21-FEB-2002 (first entry)  
 DT Oligonucleotide SEQ ID NO 110342 for detecting SNP TSC0027562.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 110342; 29pp + Sequence Listing; German.  
 PS This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1745 CTCCTCTATCCTTA 1757  
 DB 13 CTCCTCTATCCTTA 1

PA (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 49607; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1745 CTCCTCTATCCTTA 1757  
 DB 13 CTCCTCTATCCTTA 1

RESULT 455  
 ABF10345/c  
 ID ABF10345 standard; DNA; 13 BP.  
 XX ABF10345;  
 AC 21-FEB-2002 (first entry)  
 DT Oligonucleotide SEQ ID NO 110342 for detecting SNP TSC0027562.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 110342; 29pp + Sequence Listing; German.  
 PS This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

RESULT 455  
 ABF10345/c  
 ID ABF10345 standard; DNA; 13 BP.

XX ABF10345;  
 AC 21-FEB-2002 (first entry)

DT Oligonucleotide SEQ ID NO 110342 for detecting SNP TSC0027562.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.

PD 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 110342; 29pp + Sequence Listing; German.  
 PS This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1745 CTCCTCTATCCTTA 1757  
 DB 13 CTCCTCTATCCTTA 1

RESULT 455  
 ABF10345/c  
 ID ABF10345 standard; DNA; 13 BP.

XX ABF10345;  
 AC 21-FEB-2002 (first entry)

DT Oligonucleotide SEQ ID NO 110342 for detecting SNP TSC0027562.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.

PD 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 110342; 29pp + Sequence Listing; German.  
 PS This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1701 GGAAGTGGGTTA 1713  
 DB 13 GGAAGTGGGTTA 1  
 RESULT 456  
 ABC16692  
 ID ABC16692 standard; DNA; 13 BP.  
 XX  
 AC ABC16692;  
 XX  
 XX 20-FEB-2002 (first entry)  
 DT  
 DE Oligonucleotide SEQ ID NO 16699 for detecting SNP TSC0003627.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 PN  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 PR  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PS  
 XX Claim 1; SEQ ID NO 16699; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 13 BP; 2 A; 1 C; 6 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1701 GGAAGTGGGTTA 1713  
 DB 13 GGAAGTGGGTTA 1  
 RESULT 456  
 ABC16692  
 ID ABC16692 standard; DNA; 13 BP.  
 XX  
 AC ABC16692;  
 XX  
 XX 20-FEB-2002 (first entry)  
 DT  
 DE Oligonucleotide SEQ ID NO 16699 for detecting SNP TSC0003627.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 PN  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 PR  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PS  
 XX Claim 1; SEQ ID NO 16699; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 13 BP; 2 A; 1 C; 6 G; 4 T; 0 U; 0 Other;  
 SQ

Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1709 GGTTAGGAGTACG 1721  
 DB 1 GGTTAGGAGTTCG 13  
 RESULT 457  
 ABF16653  
 ID ABF16653 standard; DNA; 13 BP.  
 XX  
 AC ABF16653;  
 XX  
 XX 21-FEB-2002 (first entry)  
 DT  
 DE Oligonucleotide SEQ ID NO 116650 for detecting SNP TSC0029189.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 PN  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 PR  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PS  
 XX Claim 1; SEQ ID NO 116650; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 8.2%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1739 CCAACTCTCCCT 1751  
 DB 1 CCAACTACTCCCT 13  
 RESULT 458  
 ABC47948  
 ID ABC47948 standard; DNA; 13 BP.

```
XX AC ABC47948;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 47965 for detecting SNP TSC0013727.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 47965; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1707 TGGGTTAGGAGTA 1719
XX Db 1 TGGGTTGGGAGTA 13
XX RESULT 459
XX ABC23225/C
XX ID ABC23225 standard; DNA; 13 BP.
XX AC ABC23225;
XX 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 23242 for detecting SNP TSC0004727.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
```

```
PN WO200177384-A2.
XX 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 23242; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 U; 0 Other;
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1701 GGAGTTGGGTTA 1713
XX Db 13 GGAGTTGGGTTA 1
XX RESULT 460
XX ABC62761
XX ID ABC62761 standard; DNA; 13 BP.
XX AC ABC62761;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 62778 for detecting SNP TSC0016623.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
```

CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;  
XX  
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;  
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX QY 1701 GCAAGTTCGGTTA 1713  
XX Db 1 GCGAGTTCGGTTA 13  
XX  
XX RESULT 462  
XX ABF62158  
XX ID ABF62158 standard; DNA; 13 BP.  
XX  
XX AC ABF62158;  
XX  
XX DT 22-FEB-2002 (first entry)  
XX  
XX DE Oligonucleotide SEQ ID NO 162155 for detecting SNP TSC0040797.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200177384-A2.  
XX  
XX PD 18-OCT-2001.  
XX  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX  
XX PR 07-APR-2000; 2000DE-01019173.  
XX  
XX PA (EPIG-) EPIGENOMICS AG.  
XX  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX  
XX PS WPI; 2001-657177/75.  
XX  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX PS Claim 1; SEQ ID NO 162155; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 2 A; 8 C; 0 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 8.2%; Score 11.4; DB 1; Length 13;  
XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX QY 1745 CCTCCCTATCCTA 1757  
XX Db 1 CCCCCCTATCCTA 13  
XX  
XX RESULT 461  
XX ABC65198  
XX ID ABC65198 standard; DNA; 13 BP.  
XX  
XX AC ABC65198;  
XX  
XX DT 21-FEB-2002 (first entry)  
XX  
XX DE Oligonucleotide SEQ ID NO 65215 for detecting SNP TSC0017166.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200177384-A2.  
XX  
XX PD 18-OCT-2001.  
XX  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX  
XX PR 07-APR-2000; 2000DE-01019173.  
XX  
XX PA (EPIG-) EPIGENOMICS AG.  
XX  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX  
XX PS WPI; 2001-657177/75.  
XX  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX PS Claim 1; SEQ ID NO 65215; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The